

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 62.1321 Seconds  
(without alignments)  
821.675 Million cell updates/sec

Title: US-10-006-773A-11

Perfect score: 688

Sequence: 1 MSPAQFLFLVLVLIQETNGD.....VOGTHFPHFGGKLEIKR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	688	100.0	132	6	ABG74244 Mouse ant
2	644	93.6	238	8	ADP45549 Mouse bin
3	638	92.7	238	8	ADM72033 Chimeric
4	636	92.4	132	5	ABG76923 Mouse 3D6
5	636	92.4	132	8	ADR88406 Murine 3D
6	630	91.6	135	5	ABG79729 Anti-Stre
7	626	91.0	133	8	ADO00819 Antibody
8	626	91.0	133	8	ADO43845 Light cha
9	620	90.1	239	6	ABP58274 Humanised
10	617	89.7	132	2	AAR12361 Light (ka
11	616	89.5	239	7	ADD47025 Rat Prote
12	615	89.4	131	2	AAR12239 Mouse MAB
13	608	88.4	132	2	AAR24712 Sequence
14	601	87.4	132	5	ABG76931 Humanised
15	601	87.4	132	8	ADR88415 Humanised
16	599	87.1	238	8	ADM72035 Chimeric
17	596	86.6	142	4	AAE07032 Murine an
18	596	86.6	142	8	ADQ89324 Mouse imm
19	592	86.0	132	5	ABG76925 Humanised
20	592	86.0	132	8	ADR88409 Humanised
21	580	84.3	239	2	AAR24811 Sequence
22	574	83.4	112	6	ABB99636 2A2 monoc
23	565	82.1	113	3	AAU76445 Mouse mon
24	565	82.1	113	3	AAU76445 Mouse HBV
25	560	81.4	112	7	ADE13218 Humanised

26	560	81.4	113	8	ADO76082	Adg76082 Heterorec
27	560	81.4	113	8	ADO76086	Adg76086 Heterorec
28	559	81.2	113	8	ADO76076	Adg76076 Heterorec
29	557	81.0	113	8	ADO76088	Adg76088 Heterorec
30	557	81.0	113	8	ADO76090	Adg76090 Heterorec
31	556	80.8	113	8	ADO76078	Adg76078 Heterorec
32	555	80.7	132	2	AAW79225	AAW79225 Humanised
33	555	80.7	132	2	AAW56349	AAW56349 Humanised
34	555	80.7	132	2	AAW56349	AAW56349 Humanised
35	555	80.7	132	2	AAW56349	AAW56349 Humanised
36	554	80.5	113	8	ADO76092	Adg76092 Heterorec
37	554	80.5	113	8	ADO76080	Adg76080 Heterorec
38	553	80.4	113	3	AB12171	AB12171 Humanised
39	553	80.4	113	4	AAE03751	AAE03751 Murine PS
40	553	80.4	218	4	AAE03756	AAE03756 Chimeric
41	552	80.2	122	8	ADJ95990	Adj95990 Immunoglo
42	552	80.2	130	8	ADJ95992	Adj95992 Immunoglo
43	551	80.1	112	8	ADO76094	Adg76094 Heterorec
44	550	79.9	113	8	ADO76084	Adg76084 Heterorec
45	548	79.7	113	8	ADG25828	ADG25828 Anti-CD30

#### ALIGNMENTS

##### RESULT 1

ABG74244

ID ABG74244 standard; protein; 132 AA.

AC ABG74244;

AC ABG74244;

DT 22-APR-2003 (first entry)

DE Mouse antibody 3D8 light chain variable region.

DE Mouse antibody 3D8 light chain variable region.

DE Mouse antibody 3D8 light chain variable region.

DE Mouse antibody 3D8 light chain variable region.

DE Mouse antibody 3D8 light chain variable region.

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DE Mouse antibody 3D8 light chain variable region.

DE Mouse antibody 3D8 light chain variable region.

DE Mouse antibody 3D8 light chain variable region.

DE Mouse antibody 3D8 light chain variable region.

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),  
CC and/or together with each other or with heterologous constructs to engage  
CC additional stimulatory and functional properties of the effector cells to  
CC enhance the antitumour therapeutic efficacy (claimed). They are  
CC particularly useful in disorders including melanoma, neuroendocrine  
CC tumours and prostate and small cell lung cancer. The present sequence  
CC represents the mouse antibody 3D8 light chain variable region  
XX  
SQ Sequence 132 AA;

Query Match 100.0%; Score 688; DB 6; Length 132;  
Best Local Similarity 100.0%; Pred. No. 3.8e-55;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLIWQETNGDVVMTQPLTLSTVIGQPASISCKSSQSLYSNGKTYLNL 60  
DB 1 MSPAQFLFLVLIWQETNGDVVMTQPLTLSTVIGQPASISCKSSQSLYSNGKTYLNL 60  
QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTFFPH 120  
DB 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTFFPH 120  
QY 121 TFGGGTKLEIKR 132  
DB 121 TFGGGTKLEIKR 132

RESULT 2  
ADP45549  
ID ADP45549 standard; protein; 238 AA.  
XX  
AC ADP45549;  
XX  
DT 09-SEP-2004 (first entry)  
XX  
DE Mouse binding molecule 11C7 light chain SEQ ID NO:3.  
XX  
KW binding molecule; human; NogoA; NiG; NiG-D20; NogoA\_623-640;  
KW nerve repair; neuroprotective; gene therapy;  
KW central nervous system injury; CNS injury; neurodegenerative disorder;  
KW mouse; antibody.  
XX  
OS Mus musculus.  
XX WO2004052932-A2.  
XX  
XX 24-JUN-2004.  
XX  
XX 09-DEC-2003; 2003WO-EP013960.  
XX  
XX 10-DEC-2002; 2002GB-00028832.  
XX  
XX (NOVS ) NOVARTIS AG.  
XX (NOVS ) NOVARTIS PHARMA GMBH.  
XX (UYZU-) UNIV ZUERICH.  
XX  
XX Barske C, Mir AK, Oertle T, Schnell L, Schwab ME, Vitaliti A;  
XX Zurini M;  
XX WPI; 2004-468818/44.  
XX  
XX New binding molecule that binds to the human NogoA polypeptide, NiG, NiG-D20 or NogoA623-640, useful in preparing a composition for treating CNS injury or neurodegenerative disorders.  
XX  
XX Claim 9; SEQ ID NO 3; 121pp; English.

CC The present invention describes a binding molecule which binds to human  
CC NogoA polypeptide, human NiG, human NiG-D20 or human NogoA\_623-640 with a  
CC dissociation constant of less than 100nM. Also described: (1) a  
CC polynucleotide encoding the binding molecule; (2) an expression vector or  
CC system comprising the polynucleotide; (3) a host cell comprising the  
CC expression system; (4) a pharmaceutical composition comprising the

CC binding molecule and a carrier or diluent; and (5) treating diseases  
CC associated with nerve repair. The binding molecule has neuroprotective  
CC activity, and can be used in gene therapy. The binding molecule is useful  
CC in preparing a composition for treating central nervous system (CNS)  
CC injury or neurodegenerative disorders. The present sequence represents a  
CC mouse binding molecule 11C7 light chain, which is used in the  
CC exemplification of the present invention.  
XX  
SQ Sequence 238 AA;

Query Match 93.6%; Score 644; DB 8; Length 238;  
Best Local Similarity 92.4%; Pred. No. 7.8e-51;  
Matches 122; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLIWQETNGDVVMTQPLTLSTVIGQPASISCKSSQSLYSNGKTYLNL 60  
DB 1 MSPAQFLFLVLIWQETNGDVVMTQPLTLSTVIGQPASISCKSSQSLYSNGKTYLNL 60  
QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTFFPH 120  
DB 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTFFPH 120  
QY 121 TFGGGTKLEIKR 132  
DB 121 TFGGGTKLEIKR 132

RESULT 3  
ADM72033  
ID ADM72033 standard; protein; 238 AA.  
XX  
AC ADM72033;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Chimeric mouse-human antibody M3C11 light chain.  
XX  
KW GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer;  
KW cytostatic; M3C11.  
XX  
OS Mus sp.  
OS Homo sapiens.  
OS Chimeric.  
XX WO2004022739-A1.  
XX  
XX 18-MAR-2004.  
XX  
XX 04-SEP-2003; 2003WO-JP011318.  
XX  
XX 04-SEP-2002; 2002WO-JP008999.  
XX  
XX (CHUS ) CHUGAI SEIYAKU KK.  
XX  
XX Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y, Tokita S;  
XX WPI; 2004-269573/25.  
XX N-PSDB; ADM72032.  
XX  
XX Antibody against the N terminus of glypican 3 (GPC3) causes cell  
XX disruption and is useful as an anticancer agent.  
XX  
XX Example 4; SEQ ID NO 18; 122pp; Japanese.

CC The invention relates to an antibody against the N terminus of glypican 3  
CC (GPC3). The antibody can be used for causing cell disruption and can be  
CC used as an anti-cancer agent. The present sequence represents a chimeric  
CC mouse-human antibody M3C11 light chain.  
XX  
SQ Sequence 238 AA;

Query Match 92.7%; Score 638; DB 8; Length 238;  
Best Local Similarity 93.2%; Pred. No. 2.8e-50;



Matches 123; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MSPAQFLLLVLMWIOETNGDVVMTQPTLTLSTVIGQPASISCKSSQSLYNGKTYLNWL 60  
DDB 1 MSPAQFLLLVLMWIRETNGYVMTQPTLTLSTVIGQPASISCKSSQSLDSDGKTYLNWL 61  
QY 61 LORPQSPKRLIYLVSKLDGVPDRFTGSGSGTDTLTKISRVEADLGYYVCVQGTTHPPH 120  
DDB 61 LORPQSPKRLIYLVSKLDGAPDRFTGSGSGTDTLTKISRVEADLGYYVCVQGTTHPPH 120  
QY 121 TFGGKLEIKR 132  
DDB 121 TFGAGTKLEIKR 132

RESULT 4  
ABG76923  
ID ABG76923 standard; protein; 132 AA.  
AC ABG76923;  
XX  
DT 05-NOV-2002 (first entry)  
XX  
XX Mouse 3D6 VL protein.  
DE Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;  
XX variable region complementarity determining region; 3D6; 10D5;  
KW variable framework region; amyloidogenic disease; Alzheimer's disease;  
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;  
KW nototropic; neuroprotective; inhibitor of beta amyloid accumulation;  
KW Abeta.  
XX  
XX Mus musculus.  
OS  
XX WO200246237-A2.  
PN  
XX 13-JUN-2002.  
PD  
XX 06-DEC-2001; 2001WO-US046587.  
XX  
XX 06-DEC-2000; 2000US-0251892P.  
XX  
XX (NEUR-) NEURALAB LTD.  
PA (AMHP ) WYETH.  
XX  
XX Basi G, Saldanha J, Yednock T;  
PI  
XX WPI; 2002-519658/55.  
DR N-PSDB; ABS59426.  
XX  
XX Novel light/heavy chain of humanized immunoglobulin for treating  
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity  
PT determining regions and variable framework region from human acceptor  
PT immunoglobulin.  
XX  
XX  
PS Claim 67; Fig 1; 17ipp; English.  
XX  
XX The present invention relates to new humanized immunoglobulin (Ig) light  
CC chain (LC) or heavy chain (HC) comprising variable region complementarity  
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,  
CC and variable framework region from human acceptor Ig LC or HC sequence.  
CC The invention is useful for preventing or treating an amyloidogenic  
CC disease or Alzheimer's disease in a patient. The invention is also useful  
CC for in vivo imaging amyloid deposits in a patient. The present amino acid  
CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or  
CC variable heavy (VH) chain protein of the invention  
XX  
SQ Sequence 132 AA;

Query Match 92.4%; Score 636; DB 5; Length 132;  
Best Local Similarity 93.9%; Pred. NO. 2.2e-50;  
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSPAQFLLLVLMWIOETNGDVVMTQPTLTLSTVIGQPASISCKSSQSLYNGKTYLNWL 60  
DDB 2 MSPAQFLLLVLMWIRETNGYVMTQPTLTLSTVIGQPASISCKSSQSLDSDGKTYLNWL 61  
QY 61 LORPQSPKRLIYLVSKLDGVPDRFTGSGSGTDTLTKISRVEADLGYYVCVQGTTHPPH 120  
DDB 62 LORPQSPKRLIYLVSKLDGVPDRFTGSGSGTDTLTKISRVEADLGYYVCVQGTTHPPH 121  
QY 121 TFGGKLEIK 131  
DDB 122 TFGGKLEIK 132

RESULT 5  
ADR88406  
ID ADR88406 standard; protein; 132 AA.  
XX  
AC ADR88406;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Murine 3D6 immunoglobulin light chain variable region SEQ ID NO:2.  
XX  
XX 3D6; light chain variable region; immunoglobulin;  
KW complementarity determining region; CDR; 10D5; variable framework region;  
KW neuroprotective; nototropic; gene therapy; amyloidogenic disease;  
KW Alzheimer's disease.  
XX  
OS Mus musculus.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..20  
FT /label= signal peptide  
FT Protein 21..132  
FT /label= mature protein  
XX  
XX WO2004080419-A2.  
PN  
XX 23-SEP-2004.  
XX  
XX 12-MAR-2004; 2004WO-US007503.  
XX  
XX 12-MAR-2003; 2003US-00388389.  
XX (NEUR-) NEURALAB LTD.  
PA (AMHP ) WYETH.  
XX  
XX Basi G, Saldanha JW, Yednock T;  
PI  
XX WPI; 2004-668880/65.  
DR N-PSDB; ADR88405.  
XX  
XX New humanized antibodies that recognize beta amyloid peptides, useful for  
PT preventing or treating amyloidogenic diseases, such as Alzheimer's  
PT disease.  
XX  
XX Claim 1; SEQ ID NO 2; 176pp; English.  
XX  
XX The invention relates to a novel humanised immunoglobulin light or heavy  
CC chain. The humanised immunoglobulin light or heavy chain comprises:  
CC variable region complementarity determining regions (CDR's) from the 3D6  
CC immunoglobulin light chain variable region sequence of 132 amino acids  
CC fully defined in the specification (ADR88406), or heavy chain variable  
CC region sequence of 138 amino acids fully defined in the specification  
CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region  
CC sequence of 131 amino acids given in the specification (ADR88418) or  
CC heavy chain variable region sequence of 142 amino acids fully defined in  
CC the specification (ADR88420); and a variable framework region from a  
CC human acceptor immunoglobulin light or heavy chain sequence, provided  
CC that at least one framework residue is substituted with the corresponding  
CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain  
CC variable region sequence, where the framework residue is a residue that  
CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR

CC -interacting residue or a residue participating in the VL-VH interface.  
CC An antibody of the invention has neuroprotective and neurotropic activity,  
CC and may have a use in gene therapy. The composition and methods are  
CC useful for preventing or treating an amyloidogenic disease, such as  
CC Alzheimer's disease. The variable region sequence is useful in producing  
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin  
CC chain, or its domain. The present sequence represents the murine 3D6  
CC immunoglobulin light chain variable region.  
XX  
XX  
SQ Sequence 132 AA;

Query Match 92.4%; Score 636; DB 8; Length 132;  
Best Local Similarity 93.9%; Pred. No. 2.2e-50;  
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MSPAQFLFLVLWIQTNGDVVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNL 60  
DB 2 MSPAQFLFLVLWIQTNGDVVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNL 61  
QY 61 LORPGOSPKRLIYLVSKLDSGVPDRTGSGSGTDFTLKISRVEADLGVYVCVQGTTHPPH 120  
DB 62 LORPGOSPKRLIYLVSKLDSGVPDRTGSGSGTDFTLKISRVEADLGVYVCVQGTTHPPH 121  
QY 121 TFGGGTKLEIK 131  
DB 122 TFGGGTKLEIK 132

RESULT 6  
ABB79729  
ID ABB79729 standard; protein; 135 AA.  
XX  
AC ABB79729;  
XX  
DT 29-OCT-2002 (first entry)  
XX  
DE Anti-Streptococcus mutans surface antigen MAB SWLA3 VL.  
XX  
KW Streptococcus mutans; monoclonal antibody; MAB; mouse; chimeric antibody;  
KW antibody; anticaries; transgenic plant; transgenic animal; caries;  
KW immunotherapy; therapy.  
XX  
OS Mus musculus.  
XX  
PN US2002068066-A1.  
XX  
PD 06-JUN-2002.  
XX  
PF 15-JUN-2001; 2001US-00881823.  
XX  
PR 20-AUG-1999; 99US-00378577.  
XX  
PA (SHIW/) SHI W.  
PA (MORR/) MORRISON S L.  
PA (TRIN/) TRINH K.  
PA (WIMS/) WIMS L.  
PA (CHEN/) CHEN L.  
PA (ANDE/) ANDERSON M H.  
XX  
PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;  
XX  
XX WPI: 2002-565838/60.  
DR N-PSDB; ABR84610.  
XX  
XX Treatment and prevention of dental caries in mammals, in particular  
PT humans by orally administering genetically engineered or purified  
PT antibodies that bind to surface antigens of carcinogenic organisms.  
XX  
XX Claim 13; Fig 3A; 30pp; English.  
PS  
XX The present sequence is the protein sequence of the light chain variable  
CC region (VL) of the murine monoclonal antibody SWLA3 (IGG), which binds  
CC specifically to the surface antigens of cariogenic type c Streptococcus  
CC

CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC  
CC HB 12558) hybridoma cells. In an example from the invention, chimeric  
CC monoclonal antibody TEFE was produced comprising SWLA3 variable regions  
CC and human antibody constant regions. Such chimeric monoclonal antibodies  
CC can be used to prevent or treat dental caries in humans. The antibodies  
CC engage the effector apparatus of the human immune system when they bind  
CC cariogenic organisms, resulting in their destruction. The chimeric  
CC antibodies may be produced in edible plants, in transgenic animals, or in  
CC chicken eggs for oral ingestion  
XX  
XX  
SQ Sequence 135 AA;

Query Match 91.6%; Score 630; DB 5; Length 135;  
Best Local Similarity 92.4%; Pred. No. 7.9e-50;  
Matches 122; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MSPAQFLFLVLWIQTNGDVVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNL 60  
DB 2 MSPAQFLFLVLWIQTNGDVVMTQPLTSLVTIGQPASISCKSSQSLDSDGKTYLNL 61  
QY 61 LORPGOSPKRLIYLVSKLDSGVPDRTGSGSGTDFTLKISRVEADLGVYVCVQGTTHPPH 120  
DB 62 LORPGOSPKRLIYLVSKLDSGVPDRTGSGSGTDFTLKISRVEADLGVYVCVQGTTHPPH 121  
QY 121 TFGGGTKLEIKR 132  
DB 122 TFGGGTKLEIKR 133

RESULT 7  
ADO00819  
ID ADO00819 standard; protein; 133 AA.  
XX  
AC ADO00819;  
XX  
DT 01-JUL-2004 (first entry)  
XX  
DE Antibody JRF/cAbeta40/10 light chain variable region, SEQ ID 6.  
XX  
KW Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;  
KW beta-amyloid-related disease; Alzheimer's disease; Abeta secretase;  
KW cleavage site; immunogen; murine; antibody; light chain; variable region;  
KW JRF/cAbeta40/10.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Domain 44..59  
FT /note= "CDR1"  
FT Domain 75..81  
FT /note= "CDR2"  
FT Domain 114..122  
FT /note= "CDR3"  
XX  
PN WO2004029629-A1.  
XX  
PD 08-APR-2004.  
XX  
PF 27-SEP-2002; 2002WO-EP011062.  
XX  
PR 27-SEP-2002; 2002WO-EP011062.  
XX  
PA (JANC ) JANSSEN PHARM NV.  
XX  
XX Mercken MH, Vandermeeren MMP;  
PI  
XX WPI: 2004-316180/29.  
XX  
PT New N-11 truncated amyloid-beta monoclonal antibodies specific for human  
PT Amyloid-beta 11 N-terminal site (A-beta11-x peptides), useful for  
PT diagnosing or treating beta-amyloid-related diseases e.g. Alzheimer's  
PT disease.  
XX

PS Disclosure; SEQ ID NO 6; 42pp; English.

XX The present invention relates to an antibody expressed by the hybridoma  
 CC cells J6JPRD/hAbeta1/1 and J6JPRD/hAbeta1/2, which is capable of  
 CC specifically recognizing human Amyloid-beta 11 N-terminal site (i.e.,  
 CC Abeta11-x peptides). The antibody is useful for diagnosing beta-amyloid-  
 CC related diseases. It is particularly useful for prognosing and monitoring  
 CC response to therapy of Alzheimer's disease and other beta-amyloid related  
 CC diseases and in passive immunization as a method for treating such  
 CC diseases. A humanized form of the antibody is useful for manufacturing a  
 CC medicament for treating, preventing or reversing cognitive decline in  
 CC clinical or pre-clinical Alzheimer's Disease, Down's syndrome, Hereditary  
 CC Cerebral Hemorrhage with Amyloidosis of the Dutch Type, cerebral amyloid  
 CC angiopathy or other beta-amyloid-related diseases, or to inhibit the  
 CC formation of amyloid plaques or the effects of toxic soluble Amyloid-beta  
 CC ; species in humans. It can also be used in assay systems such as  
 CC competitive methods and nephelometry. The present sequence was used to  
 CC illustrate the invention.

XX  
 CC Sequence 133 AA;

Query Match 91.0%; Score 626; DB 8; Length 133;  
 Best Local Similarity 90.9%; Pred. No. 1.8e-49;  
 Matches 120; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSQSLYNGKTYLNL 60  
 DB 2 MSPAQFLFLVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSQSLYNGKTYLNL 61

QY 61 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDTPLKISRVEADLGVYVCVQGTTHPPH 120  
 DB 62 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDTPLKISRVEADLGVYVCVQGTTHPPH 121

QY 121 TFGGGTKLEIKR 132  
 DB 122 TFGGGTKLEIKR 133

RESULT 8  
 ADO43845  
 ID ADO43845 standard; protein; 133 AA.

XX ADO43845;

XX 15-JUL-2004 (first entry)

XX Light chain variable region of anti-amyloid-beta antibody.

XX antibody; Amyloid-beta1-x peptide; BACE-1; amyloid-beta; beta-secretase;  
 KW beta-amyloid precursor protein; beta-amyloid-related disease;  
 KW Alzheimer's disease; vaccine; Down's syndrome;  
 KW hereditary cerebral haemorrhage; amyloidosis;  
 KW cerebral amyloid angiopathy; amyloid plaque.

XX Mus sp.

XX Key Location/Qualifiers  
 FT Region 44..59  
 FT /note= "CDR1"  
 FT Region 75..81  
 FT /note= "CDR2"  
 FT Region 114..122  
 FT /note= "CDR3"

XX WO2004029630-A1.

XX 08-APR-2004.

XX 09-SEP-2003; 2003WO-EP010092.

XX 27-SEP-2002; 2002WO-EP011062.

XX (JANC ) JANSSEN PHARM NV.

XX  
 PI Mercken MH, Vandermeeren MMPF;  
 XX WPI; 2004-316181/29.

XX New N-11 truncated amyloid-beta monoclonal antibodies specific for human  
 PT Amyloid-beta 11-x peptides (A-beta11-x peptides), useful for diagnosing  
 PT or treating beta-amyloid-related diseases e.g., Alzheimer's disease.

XX Disclosure; Page 38-39; 50pp; English.

XX The specification describes a monoclonal antibody which specifically  
 CC recognizes human Amyloid-beta1-x peptides. These peptides result from  
 CC overexpression of BACE-1 which causes additional cleavage at the +11 site  
 CC of amyloid-beta, generating shorter fragments known as Amyloid-beta11-x  
 CC peptides. BACE-1 is the major beta-secretase required for cleavage of  
 CC beta-amyloid precursor protein. The antibody is useful for detecting the  
 CC presence of amyloid-beta peptides in a tissue or fluid sample and for  
 CC diagnosing beta-amyloid-related diseases. It is particularly useful for  
 CC prognosing and monitoring response to therapy of Alzheimer's disease and  
 CC other beta-amyloid related diseases and in passive immunization as a  
 CC method for treating such diseases. A humanized form of the antibody is  
 CC useful for manufacturing a medicament for treating, preventing or  
 CC reversing cognitive decline in clinical or pre-clinical Alzheimer's  
 CC Disease, Down's syndrome, Hereditary Cerebral Haemorrhage with  
 CC Amyloidosis of the Dutch type, cerebral amyloid angiopathy or other beta-  
 CC amyloid-related diseases, or to inhibit the formation of amyloid plaques  
 CC or the effects of toxic soluble Amyloid-beta species in humans. The  
 CC present sequence represents the light chain variable region of an  
 CC antibody that recognises amyloid-beta-40 and amyloid-beta11-x peptide  
 CC amyloid-beta11-40.

XX  
 CC Sequence 133 AA;

Query Match 91.0%; Score 626; DB 8; Length 133;  
 Best Local Similarity 90.9%; Pred. No. 1.8e-49;  
 Matches 120; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSQSLYNGKTYLNL 60  
 DB 2 MSPAQFLFLVLWIQTNGDVVMTQTPLTSLVTIGQPASISCKSQSLYNGKTYLNL 61

QY 61 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDTPLKISRVEADLGVYVCVQGTTHPPH 120  
 DB 62 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDTPLKISRVEADLGVYVCVQGTTHPPH 121

QY 121 TFGGGTKLEIKR 132  
 DB 122 TFGGGTKLEIKR 133

RESULT 9  
 ABP58274  
 ID ABP58274 standard; protein; 239 AA.

XX ABP58274;

XX 23-OCT-2003 (revised)  
 DT 31-MAR-2003 (first entry)

XX Humanised 3D6 antibody light chain.

XX Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;  
 KW human; humanised antibody; antibody; Alzheimer's disease;  
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.

XX Mus sp.  
 OS Homo sapiens.  
 OS Chimeric.

XX Key Location/Qualifiers  
 FT Peptide 1..20  
 FT /label= Signal\_peptide

FT Protein 21..239  
 FT /label= "Mature\_peptide"  
 FT /notes= "the mature light chain is claimed in Claim 5"  
 FT Region 21..133  
 FT /notes= "light chain variable region, claimed in Claim 4"  
 FT Region 44..59  
 FT /note= "CDR1"  
 FT Region 75..81  
 FT /note= "CDR2"  
 FT Region 114..122  
 FT /note= "CDR3"  
 XX WO200288306-A2.  
 XX  
 XX 07-NOV-2002.  
 XX  
 XX 26-APR-2002; 2002WO-US011853.  
 XX  
 XX 30-APR-2001; 2001US-0287539P.  
 XX  
 XX (ELIL ) LILLY & CO ELI.  
 XX  
 XX Tsurushita N, Vasquez M;  
 PI  
 XX WPI: 2003-183835/18.  
 XX  
 XX N-PSDB; AB224632, AB224634.  
 XX  
 XX New humanized forms of mouse 3D6 antibodies, useful for treating Down's,  
 FT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral  
 FT amyloid angiopathy, or for inhibiting formation of or reducing Abeta  
 FT plaque in the brain.  
 XX  
 XX Disclosure; Page 12-13; 54pp; English.  
 XX  
 XX The present sequence is that of a preferred light chain of a humanised  
 CC antibody of the present invention. In the variable region of this  
 CC sequence, the complementarity determining regions (CDRs) originate from  
 CC murine monoclonal antibody 3D6 and the framework region from human  
 CC germline V $\kappa$  segment DPK19 and J segment JK4. Novel humanised antibodies  
 CC of the invention have CDRs from 3D6 and human framework sequences. These  
 CC humanised antibodies have binding affinities (affinity and epitope  
 CC location) approximately the same as those of the mouse 3D6 antibody. The  
 CC invention includes antibodies, single chain antibodies, and their  
 CC fragments, as well as nucleotide sequences, vectors, transformed host  
 CC cells, and methods of using the humanised antibody to treat, prevent,  
 CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology  
 CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or  
 CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation of  
 CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise  
 CC OS field)  
 XX  
 XX Sequence 239 AA;  
 SQ  
 Query Match 90.1%; Score 620; DB 6; Length 239;  
 Best Local Similarity 89.4%; Pred. No. 1.2e-48;  
 Matches 118; Conservative 9; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 MSPAQFLFLVLMIQETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLYSNGKTYLNL 60  
 Db 2 MSPAQFLFLVLMIQETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLYSNGKTYLNL 61  
 QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEADLVGYVCQGTFFPH 120  
 Db 62 QRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEADLVGYVCQGTFFPH 121  
 QY 121 TFGGGTKLEIKR 132  
 Db 122 TFGGGTKLEIKR 133  
 QY  
 Db  
 RESULT 10  
 AAR12361  
 ID AAR12361 standard; protein; 132 AA.

XX AAR12361;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 15-AUG-1991 (first entry)  
 XX  
 XX Light (kappa) chain variable region of murine 4D12 immunoglobulin.  
 DE  
 XX Chimeric antibodies; immunoconjugates; HIV; AIDS.  
 KW  
 XX Mus musculus.  
 OS  
 XX WO9107493-A.  
 PN  
 XX 30-MAY-1991.  
 PD  
 XX  
 XX 13-NOV-1989; 89US-00433730.  
 PF  
 XX 13-NOV-1989; 89US-00433730.  
 PR  
 XX (XOMA ) XOMA CORP.  
 XX (GREC ) GREEN CROSS CORP.  
 PA  
 XX Better MD, Horwitz AH, Ghoshdasti P, Robinson R;  
 PI  
 XX WPI: 1991-178105/24.  
 DR N-PSDB; AAQ12063.  
 XX  
 XX New chimeric mouse-human antibodies - used to detect, kill and remove HIV  
 FT -1 antigen from sample.  
 PT  
 XX Disclosure; Fig 18; 107pp; English.  
 PS  
 XX This is the light (kappa) - chain variable (V) region of a mouse  
 CC monoclonal antibody (MAB), 4D12, and is specific for an HIV-1 viral  
 CC antigen. It is used in the construction of a chimeric MAB comprising  
 CC heavy and light chains having murine V regions and human C regions. The  
 CC chimeric MABs are more effective than murine MAB 4D12 since they have an  
 CC increased compatibility in humans. The heavy and light chain V-regions  
 CC are joined by manipulating their respective joining (J) regions, to  
 CC generate restriction enzyme recognition sites. The chimeric MABs can be  
 CC used as immunoconjugates, in association with e.g. toxins for HIV  
 CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-  
 CC 62. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003  
 CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)  
 XX  
 XX Sequence 132 AA;  
 SQ  
 Query Match 89.7%; Score 617; DB 2; Length 132;  
 Best Local Similarity 90.1%; Pred. No. 1.2e-48;  
 Matches 118; Conservative 7; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MSPAQFLFLVLMIQETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLYSNGKTYLNL 60  
 Db 2 MSPAQFLFLVLMIQETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLYSNGKTYLNL 61  
 QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEADLVGYVCQGTFFPH 120  
 Db 62 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVEADLVGYVCQGTFFPH 121  
 QY 121 TFGGGTKLEIKR 131  
 Db 122 TFGAGTKLELR 132  
 QY  
 Db  
 RESULT 11  
 ADD47025  
 ID ADD47025 standard; protein; 239 AA.  
 XX  
 AC ADD47025;  
 XX  
 DT 02-DEC-2004 (revised)  
 DT 29-JAN-2004 (first entry)

XX Rat Protein L22655, SEQ ID NO 12711.  
 XX DE  
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 XX OS  
 XX Rattus norvegicus.  
 XX OS Unidentified.  
 XX PN WO2003016475-A2.  
 XX XX  
 XX PD 27-FEB-2003.  
 XX XX  
 XX PF 14-AUG-2002; 2002WO-US025765.  
 XX XX  
 XX PR 14-AUG-2001; 2001US-0312147P.  
 XX PR 01-NOV-2001; 2001US-0346382P.  
 XX PR 26-NOV-2001; 2001US-0333347P.  
 XX XX  
 XX (GEHO ) GEN HOSPITAL CORP.  
 XX PA (FARB ) BAYER AG.  
 XX PA  
 XX PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX DR WPI; 2003-268312/26.  
 XX DR GENBANK; L22655.  
 XX XX  
 XX PT New composition comprising two or more isolated polypeptides, useful for  
 XX PT preparing a medicament for treating pain in an animal.  
 XX XX  
 XX PS Example 1; Page; 1017pp; English.  
 XX XX  
 XX The invention discloses a composition comprising two or more isolated rat  
 XX CC or human polynucleotides or a polynucleotide which represents a fragment,  
 XX CC derivative or allelic variation of the nucleic acid sequence. Also  
 XX CC claimed are a vector comprising the novel polynucleotide, a host cell  
 XX CC comprising the vector, a method for identifying a nucleotide sequence  
 XX CC which is differentially regulated in an animal subjected to pain and a  
 XX CC kit to perform the method, an array, a method for identifying an agent  
 XX CC that increases or decreases the expression of the polynucleotide sequence  
 XX CC that is differentially expressed in neuronal tissue of a first animal  
 XX CC subjected to pain, a method for identifying a compound which regulates  
 XX CC the expression of a polynucleotide sequence which is differentially  
 XX CC expressed in an animal subjected to pain, a method for identifying a  
 XX CC compound that regulates the activity of one or more of the  
 XX CC polynucleotides, a method for producing a pharmaceutical composition, a  
 XX CC method for identifying a compound or small molecule that regulates the  
 XX CC activity in an animal of one or more of the polypeptides given in the  
 XX CC specification, a method for identifying a compound useful in treating  
 XX CC pain and a pharmaceutical composition comprising the one or more  
 XX CC polypeptides or their antibodies. The polynucleotide or the compound that  
 XX CC modulates its activity is useful for preparing a medicament for treating  
 XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 XX CC therapy). The sequence presented is a rat protein (described in Table 3  
 XX CC of the specification) which is differentially expressed during pain.  
 XX CC Note: The sequence data for this patent did not form part of the printed  
 XX CC specification, but was obtained in electronic form directly from WIPO at  
 XX CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX SQ Sequence 239 AA;  
 Query Match 89.5%; Score 616; DB 7; Length 239;  
 Best Local Similarity 88.6%; Pred. No. 2.9e-48;  
 Matches 117; Conservative 10; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 MSPAQFLFLVLVLTQETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLLYSNGKTYLNWL 60  
 DB 1 MSPAQFLFLVLVLTQETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLLYSNGKTYLNWL 60  
 QY 61 LQRPQSPKRLIYLVSCLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPPH 120  
 DB 61 LQRPQSPKRLIYLVSCLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPPH 120

QY 121 TFGGTTKLEIKR 132  
 DB 121 TFGGTTKLEIKR 132  
 RESULT 12  
 AAR12239  
 ID AAR12239 standard; protein; 131 AA.  
 XX AC AAR12239;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 19-AUG-1991 (first entry)  
 XX DE Mouse MAb 4D12 L chain V region.  
 XX KW HIV-1; chimera.  
 XX OS Mus sp.  
 XX PN WO9107494-A.  
 XX PD 30-MAY-1991.  
 XX PF 13-NOV-1989; 89US-00433703.  
 XX PR 13-NOV-1989; 89US-00433703.  
 XX PA (XOMA ) XOMA CORP.  
 XX PA (GREC ) GREEN CROSS CORP.  
 XX PA (ZOMA-) ZOMA CORP.  
 XX PI Better MD, Horwitz AH, Ghoshdaeti P, Robinson RR;  
 XX WPI; 1991-178106/24.  
 XX DR N-PSDB; AAQ12019.  
 XX PT New chimeric mouse human antibodies - used in treatment, diagnosis and  
 XX PT prophylaxis of HIV infections.  
 XX PS Disclosure; Fig 18; 108pp; English.  
 XX CC The mouse VL gene product may be used to produce chimeric mouse- human  
 XX CC Abs against HIV-1 comprising human Ig constant regions and murine  
 XX CC variable regions. These novel sequence are useful in treatment, diagnosis  
 XX CC and prophylaxis of HIV infections, and may be produced by a bacterial,  
 XX CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct  
 XX CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)  
 XX SQ Sequence 131 AA;  
 Query Match 89.4%; Score 615; DB 2; Length 131;  
 Best Local Similarity 90.8%; Pred. No. 1.8e-48;  
 Matches 118; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MSPAQFLFLVLVLTQETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLLYSNGKTYLNWL 60  
 DB 2 MSPAQFLFLVLVLTQETNGDVVMTQTPLTSLVITIGQPASISCKSSQSLLYSNGKTYLNWL 61  
 QY 61 LQRPQSPKRLIYLVSCLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPPH 120  
 DB 62 LQRPQSPKRLIYLVSCLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYVCVQGTTHPPH 121  
 QY 121 TFGGTTKLEI 130  
 DB 122 TFGGTTKLEI 131  
 RESULT 13  
 AAR24712  
 ID AAR24712 standard; protein; 132 AA.  
 XX

```

AC AAR24712;
XX 25-MAR-2003 (revised)
DT '28-DEC-1992 (first entry)
XX
XX Sequence encoded by the genomic FIB1-11 kappa chain variable (VFK) gene.
XX
XX Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
KW antithrombotic agent; myocardial infarction therapy.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
FH Peptide 1..20
FT /label= leader
FT Region 21..43
FT /label= Framework Region (FR) 1
FT Region 44..59
FT /label= complementarity determining region(CDR)1
FT Region 60..74
FT /label= FR-2
FT Region 75..81
FT /label= CDR-2
FT Region 82..112
FT /label= FR-3
FT Region 113..122
FT /label= CDR-3
FT Region 123..132
FT /label= FR-4
XX
XX EP491351-A2.
XX
XX 24-JUN-1992.
XX
XX 17-DEC-1991; 91EP-00121591.
XX
XX 18-DEC-1990; 90JP-00413829.
XX 11-NOV-1991; 91JP-00294464.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Iwasa S, Tada H, Watanabe T;
XX
XX WPI; 1992-209528/26.
XX N-PSDB; AAQ25665.
XX
XX Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
PT and heavy chain variable and constant for treating thrombotic conditions
PT e.g. myocardial infarction.
XX
XX Example; Fig 1; 87pp; English.
XX
XX A genomic DNA library was prepd. from mouse anti-human fibrin specific
CC antibody producer hybrid FIB1-11. Screening using a 32P- labeled mouse
CC JK4-5 gene fragment as a hybridisation probe gave three positive
CC recombinant phage clones. Phage clone KE14 was identified as a clone
CC contg. a 15kb fragment coding for the VFK gene. The phage clone KE14 was
CC subcloned in the plasmid vector pUC119 and sequenced. VFK was a
CC functional VK gene formed by recombination between the VK gene belonging
CC to the Subgroup II (VKII) and the JK2 gene (see AAQ25665). (Updated on 25
CC -MAR-2003 to correct PN field.)
XX
XX Sequence 132 AA;
SQ
Query Match 88.4%; Score 608; DB 2; Length 132;
Best Local Similarity 90.8%; Pred. No. 8e-48;
Matches 119; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
QY 1 MSPAQFLFLVLWIOETNGDVVMTOTPLTSLVTIGOPASTISCKSSQSLLYSNGKTYLNLW 60
DB 2 MSPAQFLFLVLWIOETNGDVVMTOTPLTSLVTIGOPASTISCKSSQSLLYSNGKTYLNLW 61
QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGYYVCQGTTHFP 120

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Db 62 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGYYVCQGTTHFP 121
QY 121 TFGGGTKLEIK 131
Db 122 TFGGGTKLEIK 132
XX
XX RESULT 14
XX ABG76931
ID ABG76931 standard; protein; 132 AA.
XX
XX AC ABG76931;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE Humanised 3D6 light chain variable region #2.
XX
XX KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
XX variable region complementarity determining region; 3D6; 10D5;
XX variable framework region; amyloidogenic disease; Alzheimer's disease;
XX amyloid deposit; variable light chain; VL; variable heavy chain; VH;
XX notropic; neuroprotective; inhibitor of beta amyloid accumulation;
XX Abeta.
XX
XX OS Homo sapiens.
XX OS Mus musculus.
XX OS Synthetic.
XX
XX FN WO200246237-A2.
XX
XX PD 13-JUN-2002.
XX
XX PF 06-DEC-2001; 2001WO-US046587.
XX
XX PR 06-DEC-2000; 2000US-0251892P.
XX
XX PA (NEUR-) NEURALAB LTD.
XX
XX PA (AMHP ) WYETH.
XX
XX PI Basi G, Saldanha J, Yednock T;
XX
XX WPI; 2002-519658/55.
XX
XX Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
XX Claim 55; Page 157; 171pp; English.
XX
XX The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a humanized 3D6 variable light (VL) chain or variable
CC heavy (VH) chain protein of the invention
XX
XX Sequence 132 AA;
SQ
Query Match 87.4%; Score 601; DB 5; Length 132;
Best Local Similarity 87.8%; Pred. No. 3.5e-47;
Matches 115; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 1 MSPAQFLFLVLWIOETNGDVVMTOTPLTSLVTIGOPASTISCKSSQSLLYSNGKTYLNLW 60
DB 2 MSPAQFLFLVLWIOETNGDVVMTOTPLTSLVTIGOPASTISCKSSQSLLYSNGKTYLNLW 61
QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGDTFTLKISRVEAEDLGYYVCQGTTHFP 120

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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 16.454 Seconds  
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6: /cgn2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	631	91.7	131	4	US-09-647-468-163
2	628	91.3	131	4	US-09-647-468-164
3	596	86.6	142	4	US-09-840-459-102
4	596	86.6	142	4	US-09-497-625A-102
5	555	80.7	132	1	US-08-477-877B-91
6	555	80.7	132	2	US-08-472-281A-91
7	555	80.7	132	2	US-08-477-989B-91
8	555	80.7	257	4	US-09-419-788-113
9	553	80.4	113	4	US-09-698-705-7
10	553	80.4	218	4	US-09-698-705-12
11	546	79.4	112	4	US-09-809-739-11
12	546	79.4	112	4	US-09-840-459-9
13	546	79.4	112	4	US-09-497-625A-9
14	542	78.8	112	4	US-09-647-468-149
15	542	78.8	112	4	US-09-647-468-150
16	541	78.6	353	4	US-09-203-958A-4
17	537	78.1	112	4	US-09-840-459-54
18	537	78.1	112	4	US-09-497-625A-54
19	536	77.9	132	1	US-08-477-877B-84
20	536	77.9	132	2	US-08-472-281A-84
21	536	77.9	132	2	US-08-477-989B-84
22	534	77.6	535	3	US-08-983-035A-38
23	527	76.6	112	2	US-08-678-194-6
24	527	76.6	112	3	US-08-890-011-6
25	527	76.6	112	3	US-09-262-724-6
26	524	76.2	112	3	US-09-184-658-49
27	524	76.2	112	4	US-09-504-262D-49

28	524	76.2	112	4	US-09-809-739-16	Sequence 16, Appl
29	524	76.2	112	4	US-09-840-459-14	Sequence 14, Appl
30	524	76.2	112	4	US-09-497-625A-14	Sequence 14, Appl
31	524	76.2	242	4	US-09-479-614-20	Sequence 20, Appl
32	522	75.9	135	1	US-08-259-372A-12	Sequence 12, Appl
33	522	75.9	135	1	US-08-468-671-12	Sequence 12, Appl
34	521	75.7	289	3	US-09-184-658-63	Sequence 63, Appl
35	521	75.7	289	4	US-09-504-262D-63	Sequence 63, Appl
36	520	75.6	113	3	US-09-214-095D-116	Sequence 116, App
37	519	75.4	100	4	US-09-840-459-23	Sequence 23, Appl
38	519	75.4	100	4	US-09-497-625A-23	Sequence 23, Appl
39	519	75.4	112	4	US-09-809-739-17	Sequence 17, Appl
40	519	75.4	112	4	US-09-840-459-15	Sequence 15, Appl
41	519	75.4	112	4	US-09-497-625A-15	Sequence 15, Appl
42	516	75.0	112	4	US-09-809-739-15	Sequence 15, Appl
43	516	75.0	112	4	US-09-840-459-13	Sequence 13, Appl
44	516	75.0	112	4	US-09-497-625A-13	Sequence 13, Appl
45	511	74.3	112	4	US-09-809-739-18	Sequence 18, Appl

## ALIGNMENTS

## RESULT 1

US-09-647-468-163  
; Sequence 163, Application US/09647468  
; Patent No. 6677436  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: ADACHI, HIDEKI  
; APPLICANT: YABUTA, NAHITO  
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND  
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY  
; FILE REFERENCE: 053466/0289  
; CURRENT APPLICATION NUMBER: US/09/647,468  
; CURRENT FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: PCT/JP99/01768  
; PRIOR FILING DATE: 1999-04-02  
; PRIOR APPLICATION NUMBER: JP 10-91850  
; PRIOR FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 183  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 163  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF  
; OTHER INFORMATION: mouse monoclonal antibody ATR-7  
US-09-647-468-163

Query Match 91.7%; Score 631; DB 4; Length 131;  
Best Local Similarity 93.1%; Pred. No. 2.8e-53;  
Matches 122; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MSPAQFLFLVLVLTQETNGDVMVTQPLTTSVTIGQPASISCKSSQSLYNGKTYLNLW 60  
DB 1 MSPAQFLFLVLVLTQETNGDVMVTQPLTTSVTIGQPASISCKSSQSLYNGKTYLNLW 60  
QY 61 LQRPQSPKRLIYLVSKLDSCVPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTFFPH 120  
DB 61 LQRPQSPKRLIYLVSKLDSCVPDRFTGSGSGDTFTLKISRVEADLGYYVCVQGTFFPD 120  
QY 121 TFGGTYKLEIK 131  
DB 121 TFGGTYKLEIK 131

## RESULT 2

US-09-647-468-164  
; Sequence 164, Application US/09647468  
; Patent No. 6677436

GENERAL INFORMATION:  
APPLICANT: SATO, KOH  
APPLICANT: ADACHI, HIDEKI  
APPLICANT: YABUTA, NAOKIHO  
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND  
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY  
FILE REFERENCE: 053466/0289  
CURRENT APPLICATION NUMBER: US/09/647,468  
CURRENT FILING DATE: 2000-09-29  
PRIOR APPLICATION NUMBER: PCT/JP99/01768  
PRIOR FILING DATE: 1999-04-02  
PRIOR APPLICATION NUMBER: JP 10-91850  
PRIOR FILING DATE: 1998-04-03  
NUMBER OF SEQ ID NOS: 183  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 164  
LENGTH: 131  
TYPE: PRT  
ORGANISM: Mus sp.  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Amino acid  
OTHER INFORMATION: sequence coding for L chain V region of ant-TF  
OTHER INFORMATION: mouse monoclonal antibody AIR-8  
US-09-647-468-164

Query Match 91.3%; Score 628; DB 4; Length 131;  
Best Local Similarity 92.4%; Pred. No. 5.4e-53;  
Matches 121; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MSPAQFLFLVLMQETNGDVMTQTPLTSLVITGQPASISCKSSQSLLYSNGKTYLNWL 60  
DB 1 MSPAQFLFLVLMQETNGDVMTQTPLTSLVITGQPASISCKSSQSLLYSNGKTYLNWL 60  
QY 61 LQPPGSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTTHFP 120  
DB 61 LQPPGSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTTHFP 120  
QY 121 TFGGGTKLEIK 131  
DB 121 TFGGGTKLEIK 131

RESULT 3  
US-09-840-459-102  
Sequence 102, Application US/09840459  
Patent No. 6696550

GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-012  
CURRENT APPLICATION NUMBER: US/09/840,459  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: PCT/US01/03537  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/497,625  
PRIOR FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 107  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 102  
LENGTH: 142  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-840-459-102

Query Match 86.6%; Score 596; DB 4; Length 142;  
Best Local Similarity 92.7%; Pred. No. 7e-50;  
Matches 115; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 9 LVLVMIQETNGDVMTQTPLTSLVITGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSP 68  
DB 7 LVLVMIQETNGDVMTQTPLTSLVITGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSP 66  
QY 69 KRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTTHFP 128  
DB 67 KRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTTHFP 126  
QY 129 EIKR 132  
DB 127 EIKR 130

RESULT 4  
US-09-497-625A-102  
Sequence 102, Application US/09497625A  
Patent No. 6727349

GENERAL INFORMATION:  
APPLICANT: LaRosa, Gregory J.  
APPLICANT: Horvath, Christopher  
APPLICANT: Newman, Walter  
APPLICANT: Jones, S. Tarran  
APPLICANT: O'Brien, Siobhan H.  
APPLICANT: O'Keefe, Theresa  
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND  
TITLE OF INVENTION: METHODS OF USE THEREFOR  
FILE REFERENCE: 1855.1052-004  
CURRENT APPLICATION NUMBER: US/09/497,625A  
CURRENT FILING DATE: 2000-02-03  
PRIOR APPLICATION NUMBER: 09/359,193  
PRIOR FILING DATE: 1999-07-22  
PRIOR APPLICATION NUMBER: 09/121,781  
PRIOR FILING DATE: 1998-07-23  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 102  
LENGTH: 142  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-497-625A-102

Query Match 86.6%; Score 596; DB 4; Length 142;  
Best Local Similarity 92.7%; Pred. No. 7e-50;  
Matches 115; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
QY 9 LVLVMIQETNGDVMTQTPLTSLVITGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSP 68  
DB 7 LVLVMIQETNGDVMTQTPLTSLVITGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSP 66  
QY 69 KRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTTHFP 128  
DB 67 KRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYCVQGTTHFP 126  
QY 129 EIKR 132  
DB 127 EIKR 130

RESULT 5  
US-08-477-877B-91  
Sequence 91, Application US/0847787B  
Patent No. 5730979

GENERAL INFORMATION:  
APPLICANT: Bazin, Herv  
APPLICANT: Latime, Dominique  
TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-Cell Activ  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:

```

; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Humanized LO-CD2a light chain variable region.
; US-08-472-281A-91

Query Match 80.7%; Score 555; DB 2; Length 132;
Best Local Similarity 80.9%; Pred. No. 5.5e-46;
Matches 106; Conservative 14; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOETNGDVVMTPTLTLSVTIGOPASISCKSSOSLLVYSGKTYLNL 60
DB 2 MSPVQSLFLULLWLIGTNGDVVMTQPPSLVLTLGQPASISCKSSOSLLHSSGTYLNL 61
QY 61 LQRPQSPKRLVLYLSKLDGVPDRFTGSGSGTDTFLKISRVEADLVGYVCVQGTFFPH 120
DB 62 LQRPQSPQLVLYLSKLESGVPDRFTGSGSGTDTFLKISGVEADLVGYVCVQGTFFPY 121
QY 121 TFGGGTKLEIK 131
DB 122 TFGQGTKEIK 132

RESULT 7
US-08-477-989B-91
; Sequence 91, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road

```

; CITY: Roseland  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,989B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/407,009  
; FILING DATE: 29-MAR-1995  
; APPLICATION NUMBER: 08/119,032  
; FILING DATE: 09-SEP-1993  
; APPLICATION NUMBER: 08/027,008  
; FILING DATE: 05-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Olstein, Elliot M.  
; REGISTRATION NUMBER: 24,025  
; REFERENCE/DOCKET NUMBER: 61750-147  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 132 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: polypeptide  
; FEATURE:  
; NAME/KEY: Humanized LO-CD2a light chain  
; NAME/KEY: variable region.  
US-08-477-989B-91

Query Match 80.7%; Score 555; DB 2; Length 132;  
Best Local Similarity 80.9%; Pred. No. 5.5e-46;  
Matches 106; Conservative 14; Mismatches 11; Indels 0; Gaps 0;  
  
QY 1 MSPAQFLFLVLIQFTNGDVVMTQPTLTLSVTIGQPASISCKSSQSLLYSNGKTYLNLW 60  
Db 2 MSPVQSLFLULLILGTNGDVVMTQPSLLVTLGQPASISCKSSQSLHSSGNTYLNWL 61  
  
QY 61 LQRPQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVIYVCVQGTFFPH 120  
Db 62 LQRPQSPQLIYLVSKLDSGVPDRFTGSGSGTDFTLKISGVEAEDVGVIYVCVQGTFFPY 121  
  
QY 121 TFGGTTKLEIK 131  
Db 122 TFGGTTKLEIK 132

RESULT 8  
US-09-419-788-113  
; Sequence 113, Application US/09419788  
; Patent No. 6825325  
; GENERAL INFORMATION:  
; APPLICANT: FISCHER, Rainer  
; APPLICANT: SCHILLBERG, Stefan  
; APPLICANT: NAHRING, Jorg  
; APPLICANT: SACK, Markus  
; APPLICANT: MONECKE, Michael  
; APPLICANT: LIAO, Yu-Cai  
; APPLICANT: SPIEGEL, Holger  
; APPLICANT: ZIMMERMAN, Sabine  
; APPLICANT: EMANS, Neil  
; TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease  
; TITLE OF INVENTION: Resistance  
; FILE REFERENCE: 0147-0189P

; CURRENT APPLICATION NUMBER: US/09/419,788  
; CURRENT FILING DATE: 1999-10-18  
; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP  
; EARLIER FILING DATE: 1998-10-16  
; EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA  
; EARLIER FILING DATE: 1998-10-16  
; NUMBER OF SEQ ID NOS: 163  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 113  
; LENGTH: 257  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no  
; OTHER INFORMATION: natural origin  
US-09-419-788-113  
  
Query Match 80.7%; Score 555; DB 4; Length 257;  
Best Local Similarity 94.7%; Pred. No. 1.2e-45;  
Matches 107; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 20 DVVMTQTPLTSLVTTIGQPASISCKSSQSLLYSNGKTYLNLWLRFGQSPKRLIYLVSKLD 79  
Db 137 DVIMTQAPLTLSVTIGQPASISCKSSQSLDGDGKTYLNLWLRFGQSPKRLIYLVSKLD 196  
  
QY 80 SGVPRFTGSGSGTDFTLKISRVEAEDLGVIYVCVQGTFFPHFTGGTTKLEIKR 132  
Db 197 SGVPRFTGSGSGTDFTLKISRVEAEDLGVIYVCVQGTFFPHFTGGTTKLEIKR 249

RESULT 9  
US-09-698-705-7  
; Sequence 7, Application US/09698705  
; Patent No. 6824780  
; GENERAL INFORMATION:  
; APPLICANT: Devaux, B.  
; APPLICANT: Keller, G.  
; APPLICANT: Koepfen, H.  
; APPLICANT: Lasky, L.  
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use  
; FILE REFERENCE: P177R1  
; CURRENT APPLICATION NUMBER: US/09/698,705  
; CURRENT FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/162,558  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: US 60/182,872  
; PRIOR FILING DATE: 2000-02-16  
; NUMBER OF SEQ ID NOS: 25  
; SEQ ID NO 7  
; LENGTH: 113  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-698-705-7

Query Match 80.4%; Score 553; DB 4; Length 113;  
Best Local Similarity 95.6%; Pred. No. 7.2e-46;  
Matches 108; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 20 DVVMTQTPLTSLVTTIGQPASISCKSSQSLLYSNGKTYLNLWLRFGQSPKRLIYLVSKLD 79  
Db 1 DVVMTQTPLTSLVTTIGQPASISCKSSQSLDSDGKTYLNLWLRFGQSPKRLIYLVSTLD 60  
  
QY 80 SGVPRFTGSGSGTDFTLKISRVEAEDLGVIYVCVQGTFFPHFTGGTTKLEIKR 132  
Db 61 SGVPRFTGSGSGTDFTLKISRVEAEDLGVIYVCVQGTFFPHFTGGTTKLEIKR 113

RESULT 10  
US-09-698-705-12  
; Sequence 12, Application US/09698705  
; Patent No. 6824780  
; GENERAL INFORMATION:  
; APPLICANT: Devaux, B.

```
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P177781
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-12

Query Match      80.4%; Score 553; DB 4; Length 218;
Best Local Similarity 95.6%; Pred. No. 1.6e-45;
Matches 108; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 20 DVVMTQTPLTSLVITIGQPASISCKSSQSLLSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVVMTQTPLTSLVITIGQPASISCKSSQSLLSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60

Qy 80 SGVPDRFTGSGGTDFTLKISRVEAEDLGVVYCVQGTFFPHTFGGTTKLEIKR 132
Db 61 SGVPDRFTGSGGTDFTLKISRVEAEDLGVVYCVQGTFFPHTFGGTTKLEIKR 113

RESULT 11
US-09-809-739-11
; Sequence 11, Application US/09809739
; Patent No. 666383
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
; NAME/KEY: SITE
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (55)...(61)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (94)...(102)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-11

Query Match      79.4%; Score 546; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.3e-45;
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 20 DVVMTQTPLTSLVITIGQPASISCKSSQSLLSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVVMTQTPLTSLVITIGQPASISCKSSQSLLSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60

Qy 80 SGVPDRFTGSGGTDFTLKISRVEAEDLGVVYCVQGTFFPHTFGGTTKLEIKR 131
Db 61 SGVPDRFTGSGGTDFTLKISRVEAEDLGVVYCVQGTFFPHTFGGTTKLEIKR 112

RESULT 12
US-09-840-459-9
; Sequence 9, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-9

Query Match      79.4%; Score 546; DB 4; Length 112;
Best Local Similarity 93.8%; Pred. No. 3.3e-45;
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 20 DVVMTQTPLTSLVITIGQPASISCKSSQSLLSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
Db 1 DVVMTQTPLTSLVITIGQPASISCKSSQSLLSNGKTYLNWLLQRPQSPKRLIYLVSKLD 60

Qy 80 SGVPDRFTGSGGTDFTLKISRVEAEDLGVVYCVQGTFFPHTFGGTTKLEIKR 131
Db 61 SGVPDRFTGSGGTDFTLKISRVEAEDLGVVYCVQGTFFPHTFGGTTKLEIKR 112

RESULT 13
US-09-497-625A-9
; Sequence 9, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-004
; CURRENT APPLICATION NUMBER: US/09/497,625A
; CURRENT FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 60.9042 Seconds  
(without alignments)  
724.991 Million cell updates/sec

Title: US-10-006-773A-11  
Perfect score: 688  
Sequence: 1 MSPAQFLFLVLWLTQETNGD.....VQGTHTFHTFGGTTKLEIKR 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
  - 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
  - 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
  - 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
  - 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
  - 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	688	100.0	132	13	US-10-006-773-11
2	636	92.4	132	14	US-10-010-942B-2
3	636	92.4	132	15	US-10-388-389-2
4	636	92.4	132	16	US-10-703-713-2
5	636	92.4	132	16	US-10-704-070-2
6	636	92.4	132	17	US-10-232-030-2
7	631	91.7	131	15	US-10-462-062-163
8	630	91.6	135	9	US-09-881-823-10
9	628	91.3	131	15	US-10-462-062-164
10	620	90.1	239	17	US-10-476-265-19
11	606	88.1	145	17	US-10-861-662-52
12	606	88.1	145	17	US-10-861-662-58
13	606	88.1	145	17	US-10-861-662-61

14	601	87.4	132	14	US-10-010-942B-11	Sequence 11, Appl
15	601	87.4	132	15	US-10-388-389-11	Sequence 11, Appl
16	601	87.4	132	16	US-10-703-713-11	Sequence 11, Appl
17	601	87.4	132	16	US-10-704-070-11	Sequence 11, Appl
18	601	87.4	132	17	US-10-232-030-11	Sequence 11, Appl
19	596	86.6	142	9	US-09-840-459-102	Sequence 102, App
20	596	86.6	142	16	US-10-766-773-102	Sequence 102, App
21	596	86.6	142	16	US-10-766-610-102	Sequence 102, App
22	596	86.6	142	16	US-10-733-563-102	Sequence 102, App
23	592	86.0	132	14	US-10-010-942B-5	Sequence 5, Appli
24	592	86.0	132	15	US-10-388-389-5	Sequence 5, Appli
25	592	86.0	132	15	US-10-703-713-5	Sequence 5, Appli
26	592	86.0	132	16	US-10-704-070-5	Sequence 5, Appli
27	592	86.0	132	17	US-10-232-030-5	Sequence 5, Appli
28	553	80.4	113	17	US-10-937-046-7	Sequence 7, Appli
29	553	80.4	218	17	US-10-937-046-12	Sequence 12, Appl
30	552	80.2	122	15	US-10-272-899A-86	Sequence 86, Appl
31	552	80.2	130	15	US-10-272-899A-88	Sequence 88, Appl
32	546	79.4	112	9	US-09-835-087-1	Sequence 1, Appli
33	546	79.4	112	9	US-09-809-739-11	Sequence 11, Appl
34	546	79.4	112	9	US-09-840-459-9	Sequence 9, Appli
35	546	79.4	112	16	US-10-766-773-9	Sequence 9, Appli
36	546	79.4	112	16	US-10-766-610-9	Sequence 9, Appli
37	546	79.4	112	16	US-10-733-563-9	Sequence 9, Appli
38	542	78.8	112	15	US-10-462-062-149	Sequence 149, App
39	542	78.8	112	15	US-10-462-062-150	Sequence 150, App
40	541	78.6	112	17	US-10-855-013-12	Sequence 12, Appl
41	541	78.6	353	10	US-09-203-958A-4	Sequence 4, Appli
42	539	78.3	162	15	US-10-410-907A-30	Sequence 30, Appl
43	539	78.3	500	14	US-10-168-809-22	Sequence 22, Appl
44	537	78.1	112	9	US-09-840-459-54	Sequence 54, Appl
45	537	78.1	112	16	US-10-766-773-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1  
US-10-006-773-11  
; Sequence 11, Application US/10006773  
; Publication No. US20020132983A1  
; GENERAL INFORMATION:  
; APPLICANT: Junghans, Richard P.  
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Ant  
; FILE REFERENCE: 003  
; CURRENT APPLICATION NUMBER: US/10/006,773  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/250,089  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-006-773-11

Query Match	100.0%	Score 688;	DB 13;	Length 132;
Best Local Similarity	100.0%	Pred. No. 1.6e-54;		
Matches 132;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MSPAQFLFLVLWLTQETNGDVVMTQPTLTSVTIGQPASISCKSSQSLLYNGKTYLNLW	60	
Db	1	MSPAQFLFLVLWLTQETNGDVVMTQPTLTSVTIGQPASISCKSSQSLLYNGKTYLNLW	60	
Qy	61	LQRQSPKRLIYLVSKLDCVDPFRFTGSGSGTFTLKISRVEADLGVYVCVQGTTHPPH	120	
Db	61	LQRQSPKRLIYLVSKLDCVDPFRFTGSGSGTFTLKISRVEADLGVYVCVQGTTHPPH	120	
Qy	121	TFGGGTLEIKR	132	
Db	121	TFGGGTLEIKR	132	

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RESULT 2
US-10-010-942B-2
; Sequence 2, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus. musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-010-942B-2

Query Match          92.4%; Score 636; DB 14; Length 132;
Best Local Similarity 93.9%; Pred. No. 8e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOTETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNWL 60
DB 2 MSPAQFLFLVLWIOTETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNWL 61

QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGVVYCVQGTFFPH 120
DB 62 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGVVYCVQGTFFPH 121

QY 121 TFGGGTKLEIK 131
DB 122 TFGGGTKLEIK 132

RESULT 3
US-10-388-389-2
; Sequence 2, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-388-389-2

Query Match          92.4%; Score 636; DB 15; Length 132;
Best Local Similarity 93.9%; Pred. No. 8e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOTETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNWL 60
DB 2 MSPAQFLFLVLWIOTETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNWL 61

QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGVVYCVQGTFFPH 120
DB 62 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGVVYCVQGTFFPH 121

QY 121 TFGGGTKLEIK 131
DB 122 TFGGGTKLEIK 132

RESULT 4
US-10-703-713-2
; Sequence 2, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-703-713-2

Query Match          92.4%; Score 636; DB 16; Length 132;
Best Local Similarity 93.9%; Pred. No. 8e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOTETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNWL 60
DB 2 MSPAQFLFLVLWIOTETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNWL 61

QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGVVYCVQGTFFPH 120
DB 62 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGVVYCVQGTFFPH 121

QY 121 TFGGGTKLEIK 131
DB 122 TFGGGTKLEIK 132

RESULT 5
US-10-704-070-2
; Sequence 2, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-704-070-2

Query Match          92.4%; Score 636; DB 15; Length 132;
Best Local Similarity 93.9%; Pred. No. 8e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSPAQFLFLVLWIOTETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNWL 60
DB 2 MSPAQFLFLVLWIOTETNGDVVMTQPTLTLSVTIGOPASISCKSSQSLYSNGKTYLNWL 61

QY 61 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGVVYCVQGTFFPH 120
DB 62 LQRPQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEADLGVVYCVQGTFFPH 121

QY 121 TFGGGTKLEIK 131
DB 122 TFGGGTKLEIK 132
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; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-704-070-2

Query Match          92.4%; Score 636; DB 16; Length 132;
Best Local Similarity 93.9%; Pred. No. 8e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MSPAQFLFLVLVIQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLLYSGKTYLNL 60
Db 2 MSPAQFLFLVLVIQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLLYSGKTYLNL 61
Qy 61 LORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYCVQGTTHPPH 120
Db 62 LORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYCVQGTTHPPR 121
Qy 121 TFGGGTKLEIK 131
Db 122 TFGGGTKLEIK 132

RESULT 7
US-10-462-062-163
; Sequence 163, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for L chain V region of anti-Tf mouse monoclonal
; OTHER INFORMATION: antibody ATR-7
US-10-462-062-163

Query Match          91.7%; Score 631; DB 15; Length 131;
Best Local Similarity 93.1%; Pred. No. 2.2e-49;
Matches 122; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MSPAQFLFLVLVIQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLLYSGKTYLNL 60
Db 1 MSPAQFLFLVLVIQETNGDVVMTQPTLTLSVTIGQPASISCKSSQSLLYSGKTYLNL 60
Qy 61 LORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYCVQGTTHPPH 120
Db 61 LORPGQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDFTLKISRVEAEDLGVYCVQGTTHPPD 120
Qy 121 TFGGGTKLEIK 131
Db 121 TFGGGTKLEIK 131

RESULT 8
US-09-881-823-10
; Sequence 10, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-662-52

Query Match      88.1%; Score 606; DB 17; Length 145;
Best Local Similarity 95.2%; Pred. No. 4.6e-47;
Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 LVLWIQETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNMLLQRPQSP 68
Db 14 LVLWIRETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNMLLQRPQSP 73

QY 69 KRLIYLVSKLDGVPDRFTGSGGDTFTLKISRVEAEDLGYYVCQGTTHPFTFGGTKL 128
Db 74 KRLIYLVSKLDGVPDRFTGSGGDTFTLKISRVEAEDLGYYVCQGTTHPFTFGGTKL 133

QY 129 EIKR 132
Db 134 EIKR 137

RESULT 12
US-10-861-662-58
; Sequence 58, Application US/10861662
; Publication No. US20050086707A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Etessami, Soudabeh
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Perez-Villar, Juan
; APPLICANT: Meyrick Morrison, Karen Jane
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Paris, Mary
; APPLICANT: Gudas, Jean
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: Antibodies and Molecules Derived
; FILE REFERENCE: 51158-20016.26
; CURRENT APPLICATION NUMBER: US/10/861,662
; PRIOR FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 10/010,667
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/011,095
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/236,878
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-662-61

Query Match      88.1%; Score 606; DB 17; Length 145;
Best Local Similarity 95.2%; Pred. No. 4.6e-47;
Matches 118; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 LVLWIQETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNMLLQRPQSP 68
Db 14 LVLWIRETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLLYSNGKTYLNMLLQRPQSP 73

QY 69 KRLIYLVSKLDGVPDRFTGSGGDTFTLKISRVEAEDLGYYVCQGTTHPFTFGGTKL 128
Db 74 KRLIYLVSKLDGVPDRFTGSGGDTFTLKISRVEAEDLGYYVCQGTTHPFTFGGTKL 133

QY 129 EIKR 132
Db 134 EIKR 137

RESULT 14
US-10-010-942B-11
; Sequence 11, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
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; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 396 light chain
US-10-010-942B-11

```

[illegible]

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RESULT 15
US-10-388-389-11
; Sequence 11, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saidanha, Jose
; APPLICANT: yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELM-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable
US-10-388-389-11

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Query Match	87.4%;	Score 601;	DB 15;	Length 132;
Best Local Similarity	87.8%;	Pred. No. 1.2e-46;		
Matches \115; Conservative	10;	Mismatches 6;	Indels 0;	Gaps 0;
Qy	1	MSPAQFLFLVLWLTQETNGDVVMTQTPLTLSVTIGQPASISCKSQSLLYNGKTYLNLW	60	
Db	2	MSPAQFLFLVLWLTQETNGDVVMTQTPLTLSVTIGQPASISCKSQSLLYNGKTYLNLW	61	
Qy	61	LQREGQPKRLIYLVSKLDSVDPDRFTGSGSGTDFTLKISRVEADLGVYCVGTGPH	120	
Db	62	LQREGQPKRLIYLVSKLDSVDPDRFTGSGSGTDFTLKISRVEADLGVYCVGTGPH	121	
Qy	121	TFGGGTGLEIK	131	

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 18.6642 Seconds  
(without alignments)  
680.480 Million cell updates/sec

Title: US-10-006-773A-11  
Perfect score: 688  
Sequence: 1 MSPAQFLFLVLVWVQETNGD.....VQGTHTFPGGTTKLEIKR 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649	94.3	132	2 C32513	Ig kappa chain pre
2	603	87.6	131	2 S31577	Ig kappa chain - m
3	569	82.7	112	2 P10273	Ig kappa chain V r
4	561	81.5	113	2 P30560	Ig kappa chain V r
5	547	79.5	112	2 A5491	proteolytic antibo
6	543	78.9	133	2 S23230	Ig kappa chain pre
7	540	78.5	111	2 S20709	Ig kappa chain V r
8	538	78.2	133	2 S40324	Ig kappa chain V r
9	533	77.5	133	1 K2HURP	Ig kappa chain pre
10	532	77.3	133	2 S42611	HUNK protein prec
11	531	77.2	112	2 A36259	Ig kappa chain V r
12	527	76.6	142	2 S22902	Ig kappa chain V r
13	521	75.7	133	1 A24452	Ig kappa chain pre
14	515	74.9	132	2 S40322	Ig kappa chain - h
15	513.5	74.6	140	2 S22658	Ig kappa chain pre
16	505	73.4	101	2 A33730	Ig kappa chain V r
17	501	72.8	103	2 P10555	Ig light chain V r
18	492	71.5	120	2 S42267	Ig kappa chain V r
19	492	71.5	120	2 S42267	Ig kappa chain V r
20	489	71.1	103	2 P10556	Ig light chain V r
21	488	70.9	128	2 S40373	Ig kappa chain - h
22	486.5	70.7	114	2 S49572	Ig kappa chain pre
23	486	70.6	126	2 S40312	Ig kappa chain - h
24	486	70.6	131	2 D29380	Ig kappa chain pre
25	486	70.6	136	2 S40357	Ig kappa chain V-J
26	485	70.5	118	2 S40374	Ig kappa chain - h
27	483	70.2	132	2 S26882	Ig kappa chain V r
28	482	70.1	131	2 B34904	Ig kappa chain pre
29	481	69.9	131	2 S09259	Ig kappa chain pre

ALIGNMENTS

RESULT 1

C32513

Ig kappa chain precursor V region (BXW14) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000

C:Accession: C32513

R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;

J. Clin. Invest. 82, 852-860, 1988

A:Title: Immunoglobulin kappa light chain variable region gene complex organization and

A:Reference number: A94689; MUID:88331394; PMID:3138286

A:Accession: C32513

A:Molecule type: DNA

A:Residues: 1-132 <KOF>

A:Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 94.3%; Score 649; DB 2; Length 132;  
Best Local Similarity 96.2%; Pred. No. 2.2e-48;  
Matches 126; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MSPAQFLFLVLVWVQETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLNSKGYLWNL 60  
Db |||||  
2 MSPAQFLFLVLVWVQETNGDVVMTQTPLTSLVTIGQPASISCKSSQSLNSKGYLWNL 61  
|||

Qy 61 LQRFQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVAEADLGYYVCVQGTTHPPH 120  
Db |||||  
62 LQRFQSPKRLIYLVSKLDSGVDPDRFTGSGSGTDTLTKISRVAEADLGYYVCVQGTTHPPR 121  
|||

Qy 121 TFGGTTKLEIK 131  
Db |||||  
122 TFGGTTKLEIK 132  
|||

RESULT 2

S31577

Ig kappa chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000

C:Accession: S31577

R:Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.

submitted to the EMBL Data Library, January 1993

A:Description: Immunoglobulin variable heavy and light chain cDNA sequences for two anti

A:Reference number: S31577

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-131 <REC>

A:Cross-references: EMBL:Z19575; NID:g53983; PIDN:CNA79627.1; PID:g53984

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin



QY	3	PAQFLFLVLWIQETNGDVVMTQPTLTSLVTICQPASISCKSSQSLLSYNGKTYLNLWLO	62
DB	4	PAQLGLLMLWPGSSGVVMTQPSLPTVLTLGPASISCRSSQSLVSYDGNTHLWVQQ	63
QY	63	RPQSPKRLIYLVSKLDSGVDPDRFTSGSGTDTFTLKISRVEADLGVYVCQGTPEPHTF	122
DB	64	RPQSPKRLIYKVNRDSDGVDPDRFSGSGTDTFTLKISRVEADVGYYVCQGTHTWPTF	123
QY	123	GGGTKLEIKR	132
DB	124	GGGTKLEIKR	133

RESULT 7  
 S20709  
 IG kappa chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S20709  
 R:Brennan, D.M.; Hands, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osb  
 submitted to the EMBL Data Library, April 1992  
 A:Description: Binding specificity and variable region sequences of two monoclonal anti  
 A:Reference number: S20706  
 A:Accession: S20709  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-111 <BRE>  
 A:Cross-references: EMBL:Z11917; NID:g52655; PIDN:CAA7975.1; PID:g52656  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-95/Domain: immunoglobulin homology <IMM>

Query Match	78.5%;	Score 540;	DB 2;	Length 111;
Best Local Similarity	92.8%;	Pred. No. 3.5e-39;		
Matches 103;	Conservative 5;	Mismatches 3;	Indels 0;	Gaps 0;

QY	20	DVVMQTPTLTSLVTICQPASISCKSSQSLLSYNGKTYLNLWLLQRPQSPKRLIYLVSKLD	79
DB	1	DIQLTQSLTSLVTICQPASISCKSSQSLLHSGKTYLNLWLLQRPQSPKRLIYLVSKLD	60
QY	80	SGVPDRFTSGSGTDTFTLKISRVEADLGVYVCQGTPEPHTFGGTTKLEI	130
DB	61	SGVPDRFTSGSGTDTFTLKISRVEADLGVYVCQGTPEPHTFGGTTKLEI	111

RESULT 8  
 S40324  
 IG kappa chain V region - human  
 C:Species: Homo sapiens (man)  
 C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
 C:Accession: S40324  
 R:Klein, R.; Jaenisch, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40312; MUID:9408091; PMID:8258341  
 A:Accession: S40324  
 A>Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-133 <KLE>  
 A:Cross-references: UNIPROT:Q8TCD0; EMBL:X72434  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:33-112/Domain: immunoglobulin homology <IMM>

Query Match	78.2%;	Score 538;	DB 2;	Length 133;
Best Local Similarity	76.9%;	Pred. No. 6.2e-39;		
Matches 100;	Conservative 17;	Mismatches 13;	Indels 0;	Gaps 0;

QY	3	PAQFLFLVLWIQETNGDVVMTQPTLTSLVTICQPASISCKSSQSLLSYNGKTYLNLWLO	62
DB	1	PAQLGLLMLWPGSSGVVLTQPSLPTVLTLGPASISCRSDQSLVSYDGKTYLWVYQQ	60





Search completed: May 25, 2005, 16:48:39  
Job time : 19.6642 secg



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 64.3423 Seconds  
(without alignments)  
1050.544 Million cell updates/sec

Title: US-10-006-773A-11

Perfect score: 688

Sequence: 1 MSPAQFLFLVLIWQETNGD.....VOGTHPHTFGGTYKLEIKR 132

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	535	77.8	239	2 Q8TCD0	Q8tcd0 homo sapien
2	533	77.5	133	1 KV2F HUMAN	P06310 homo sapien
3	495	71.9	239	2 Q6P491	Q6p491 homo sapien
4	485	70.5	239	2 Q8NEK0	Q8nek0 homo sapien
5	472.5	68.7	240	2 Q6PIH6	Q6pih6 homo sapien
6	466.5	67.8	114	2 Q9UL80	Q9ul80 homo sapien
7	456	66.3	113	1 KV2G MOUSE	P01631 mus musculus
8	450	65.4	219	2 Q65ZC0	Q65zc0 mus musculus
9	444	64.5	113	1 KV2B HUMAN	P01615 homo sapien
10	444	64.5	117	1 KV2E HUMAN	P06309 homo sapien
11	443	64.4	248	2 Q65Z07	Q65z07 mus sp. b3(
12	430	62.5	113	1 KV2D HUMAN	P01617 homo sapien
13	421.5	61.3	115	1 KV2A HUMAN	P01630 mus musculus
14	417	60.6	113	1 KV2F MOUSE	P01614 mus musculus
15	412	59.9	112	2 Q6LEM8	Q6lem8 mus musculus
16	410	59.6	113	1 KV2E MOUSE	P03976 mus musculus
17	401.5	58.4	112	1 KV2C HUMAN	P01616 homo sapien
18	399	58.0	133	1 KV4B HUMAN	P06313 homo sapien
19	397.5	57.8	134	1 KV4C HUMAN	P06314 homo sapien
20	392	57.0	113	1 KV2C MOUSE	P01628 mus musculus
21	392	57.0	120	1 KV2B MOUSE	P01627 mus musculus
22	391	56.8	112	1 KV2D MOUSE	P01629 mus musculus
23	389	56.5	129	1 KV3L HUMAN	P18135 homo sapien
24	385.5	56.0	236	2 Q6PIL8	Q6pil8 homo sapien
25	383	55.7	112	1 KV2A MOUSE	P01626 mus musculus
26	382	55.5	129	1 KV3M HUMAN	P18136 homo sapien
27	380	55.2	235	2 Q6GMV9	Q6gmv9 homo sapien
28	375.5	54.6	108	1 KV1 CANFA	P01618 canis famil
29	374.5	54.4	236	2 Q6P5S8	Q6p5s8 homo sapien
30	372.5	54.1	114	1 KV4A HUMAN	P01625 homo sapien
31	371.5	54.0	111	1 KV3L MOUSE	P01664 mus musculus

#### RESULT 1

ID	Q8TCD0	PRELIMINARY;	PRT;	239 AA.
AC	Q8TCD0;			
DT	01-JUN-2002 (Tremblrel. 21, Created)			
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
EX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RL	[2]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RA	Strausberg R.			
RL	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC022362; AAH22362.1; -			
DR	PIR; S22658; S22658.			
DR	PIR; S24095; S24095.			
DR	PIR; S40324; S40324.			
DR	PIR; S40374; S40374.			
DR	PIR; S42267; S42267.			
DR	PIR; S42268; S42268.			
DR	HSSP; P01834; I172.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig_cl.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF07654; C1-set; I.			

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_unknwn_1.
SQ SEQUENCE 239 AA; 26234 MW; 3ACEDCA3B03871D CRC64;

Query Match 77.8%; Score 535; DB 2; Length 239;
Best Local Similarity 76.2%; Pred. No. 2.5e-44;
Matches 99; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 3 PAQFLFLVLVLTQETNGDVVMTQPTLTSVTIGQPASISCKSSQSLYNGKTYLNWLLQ 62
DB 4 PAQLGLLMLWVPGSGDVVMTQSPSLPVTIGQPASISCRSQSLVSDGTYLNWFFQ 63
QY 63 RPOQSPKRLIYLVSKLDGVPDRFTGSGGTDTFTLKISRVEADLGVYCVQGTTHPPHF 122
DB 64 RPOQSPRLIYKVNRDVGVPDRFSGSGGTDTFTLKISRVEADLGVYCMQGTHTWSPF 123
QY 123 GGGTKLEIKR 132
DB 124 GGGTKLEIKR 133

RESULT 2
KV2F HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Kloback H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513 (1985).
CC -----
CC This 'SWISS-PROT' entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; Z00020; CAA77315.1; -.
DR FIR; A01890; K2HURP.
DR HSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-II region RPMI 6410.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 59 Complementarity-determining-1.
FT DOMAIN 60 74 Framework-2.
FT DOMAIN 75 81 Complementarity-determining-2.
FT DOMAIN 82 113 Framework-3.
FT DOMAIN 114 122 Complementarity-determining-3.
FT DOMAIN 123 132 Framework-4.
FT DISULFID 43 113 By similarity.
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FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 77.5%; Score 533; DB 1; Length 133;
Best Local Similarity 76.9%; Pred. No. 2e-44;
Matches 100; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 3 PAQFLFLVLVLTQETNGDVVMTQPTLTSVTIGQPASISCKSSQSLYNGKTYLNWLLQ 62
DB 4 PAQLGLLMLWVPGSGDVVMTQSPSLPVTIGQPASISCRSQSLVSDGTYLNWFFQ 63
QY 63 RPOQSPKRLIYLVSKLDGVPDRFTGSGGTDTFTLKISRVEADLGVYCVQGTTHPPHF 122
DB 64 RPOQSPRLIYKVNRDVGVPDRFSGSGGTDTFTLKISRVEADLGVYCMQGTHTWSPF 123
QY 123 GGGTKLEIKR 132
DB 124 GGGTKVEIKR 133

RESULT 3
Q6P491 PRELIMINARY; PRT; 239 AA.
AC Q6P491;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063599; AAH63599.1; -.
DR HSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
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DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;  
 Query Match 71.9%; Score 495; DB 2; Length 239;  
 Best Local Similarity 71.3%; Pred. No. 2,1e-40;  
 Matches 92; Conservative 20; Mismatches 17; Indels 0; Gaps 0;  
 QY 4 AQFLFLVLWIQTNGDVVMTQPLTSLVITIGOPASISCKSSQSLLSNGKTYLWLLQ 63  
 Db 5 AQLGLMLWVPGSGDIVMTQPLSPVTLGQPASISCRSSLLSHNSGNTYLSWLHOR 64  
 QY 64 PGQSPKRLIYLVSKLSDGVDPDRFTGSGGTDFTLKISRVEADLGVYVCQGTTHPFTF 123  
 Db 65 PGQPPRLIYKISNRPSGVDPDRFSGSGAGTDFTLKISRVEADLGVYVCQGTTHPFTF 124  
 QY 124 GGTGKLEIKR 132  
 Db 125 GGTGKLEIKR 133  
 RESULT 4  
 Q8NEKO PRELIMINARY; PRT; 239 AA.  
 ID Q8NEKO  
 AC Q8NEKO  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 DE Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalka U., Smillius D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RC Strausberg R.;  
 RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC030814; AAH30814.1; -;  
 DR PIR; S23638; S23638.  
 DR PIR; S40342; S40342.  
 DR PIR; S40357; S40357.  
 DR HSSP; P01834; 1172.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig.cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR SMART; SM00409; IG; 2.



```

RT allergen Chi t I.";
RL Int. Arch. Allergy Immunol. 110:348-353(1996).
DR EMBL; Z37499; CAA85724.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match 65.4%; Score 450; DB 2; Length 219;
Best Local Similarity 75.2%; Pred. No. 5.1e-36;
Matches 85; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 20 DVVMTQPLTSLVITIGQPASISCKSSQSLLYSNKTYLWLLQRPQSPKRLIYLVSKLD 79
DB 1 ELVMTQSPLSVSLGDAQSISCRSSQSLVHTNGNTYLFHWLQKPLGLSPKLLIYVSNRF 60
QY 80 SGVPDRFTGSGSGDTFTLKISRVEADLGVCYVCGVTHPHTFGGKTLEIKR 132
DB 61 SGVPDRFSGSGSGDTFTLKISRVEADLGVCYVCGVTHPHTFGGKTLEIKR 113

RESULT 9
KV2B HUMAN
ID KV2B HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -I- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin that binds phosphorylcholine.
DR PIR; A01886; K2HUFH.
DR HSSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113

allergen Chi t I.";
RL Int. Arch. Allergy Immunol. 110:348-353(1996).
DR EMBL; Z37499; CAA85724.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match 65.4%; Score 450; DB 2; Length 219;
Best Local Similarity 75.2%; Pred. No. 5.1e-36;
Matches 85; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 20 DVVMTQPLTSLVITIGQPASISCKSSQSLLYSNKTYLWLLQRPQSPKRLIYLVSKLD 79
DB 1 ELVMTQSPLSVSLGDAQSISCRSSQSLVHTNGNTYLFHWLQKPLGLSPKLLIYVSNRF 60
QY 80 SGVPDRFTGSGSGDTFTLKISRVEADLGVCYVCGVTHPHTFGGKTLEIKR 132
DB 61 SGVPDRFSGSGSGDTFTLKISRVEADLGVCYVCGVTHPHTFGGKTLEIKR 113

RESULT 10
KV2E HUMAN
ID KV2E HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RL Nature 303:73-76(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00009; -; NOT ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117
FT DOMAIN 5 27
FT DOMAIN 28 43
FT DOMAIN 44 58
FT DOMAIN 59 65
FT DOMAIN 66 97
FT DOMAIN 98 106
FT DOMAIN 107 116
FT DISULFID 27 97
FT NON_TER 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 64.5%; Score 444; DB 1; Length 117;
Best Local Similarity 73.3%; Pred. No. 9.8e-36;
Matches 85; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

```





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RL  Naturwissenschaften 56:195-205(1969).
CC  -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC  -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR  HSP; B91639; K2HUCM.
DR  PIR; P01751; INOB.
DR  GO; GO:0005576; C:extracellular; NAS.
DR  GO; GO:0003823; F:antigen binding; NAS.
DR  GO; GO:0006955; P:immune response; NAS.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003596; Ig_v.
DR  Pfam; PF00047; Ig; 1.
DR  SMART; SM00406; Igv; 1.
DR  PROSITE; PS50835; IG_LIKE; 1.
KW  Bence-Jones protein; Direct protein sequencing;
KW  Immunoglobulin V region.
FT  DISULFID 24 95
FT  NON_TER 115 115
SQ  SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 61.3%; Score 421.5; DB 1; Length 115;
Best Local Similarity 72.8%; Pred. No. 1.6e-33;
Matches 83; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

QY 20 DVVMTQTPLTSLVITIGQPASISCKSSQSLLYS-NKTYLNWLLQRPQSPKRLIYLVSKL 78
DB 2 DIVMTQTPLSLPVTGPEPASISCKSSQSLDSDGNTYLNWYLOKAGSQPLLIIYLSYR 61

QY 79 DSGVDRFTGSGSGDFTLKISRVEAEDLGVVYCVQGHFPHFTFGGTTKLEIKR 132
DB 62 ASGVDRFTGSGSGDFTLKISRVAEDVGVYCMQRIEIPYTFGGGTTKLEIR 115

RESULT 14
KV2F MOUSE
ID KV2F MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoazobenzene isothiocyanate technique
RT for the isolation of peptides."
RL Biochem. J. 211:173-180(1983).
CC -!- MISCELLANEOUS: This chain is from a hybridoma-derived monoclonal
CC antibody against the streptococcal group A polysaccharide.
DR PIR; A01913; KVMS7S.
DR HSP; Q99M37; I191.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;
KW Monoclonal antibody.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.

FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 60.6%; Score 417; DB 1; Length 113;
Best Local Similarity 70.8%; Pred. No. 4.2e-33;
Matches 80; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 20 DVVMTQTPLTSLVITIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
DB 1 DIVMTQTAPSAVTPGESVSIKSSKSLLSNGNTLYWFLQRPQSPQLLIYRMSNLA 60

QY 80 SGVDRFTGSGSGDFTLKISRVEAEDLGVVYCVQGHFPHFTFGGTTKLEIKR 132
DB 61 SGVDRFTGSGSGDFTLKISRVAEDVGVYCMQREYPTFTFGGTTKLEIKR 113

RESULT 15
Q6LEM8
ID Q6LEM8 PRELIMINARY; PRT; 112 AA.
AC Q6LEM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22267451; PubMed=12379368; DOI=10.1016/S0022-1759(02)00242-9;
RA Hifumi E., Mitsuda Y., Ohara K., Uda T.;
RT "Targeted destruction of the HIV-1 coat protein gp41 by a catalytic
RT antibody light chain."
RL J. Immunol. Methods 269:283-298(2002).
DR EMBL; D85104; BAD00151.1; -.
DR HSSP; P01820; I1A70.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12443 MW; BAD3E14B90BCF122 CRC64;

Query Match 59.9%; Score 412; DB 2; Length 112;
Best Local Similarity 70.5%; Pred. No. 1.3e-32;
Matches 79; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 20 DVVMTQTPLTSLVITIGQPASISCKSSQSLLYSNGKTYLNWLLQRPQSPKRLIYLVSKLD 79
DB 1 DIVMTQTAPSVTPGESVFISCKSSKSLLSNGNTLYWFLQRPQSPQLLIYRLFLHA 60

QY 80 SGVDRFTGSGSGDFTLKISRVEAEDLGVVYCVQGHFPHFTFGGTTKLEIK 131
DB 61 SGVDRFTGSGSGDFTLKISRVAEDVGVYCMQHLEYPYTFGGGTTKLEIK 112

Search completed: May 25, 2005, 15:56:05
Job time : 65.3423 secs

```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 65.427 Seconds  
(without alignments)  
821.675 Million cell updates/sec

Title: US-10-006-773A-13  
Perfect score: 756  
Sequence: 1 MGWRWIFLLSGTAGVHCQ.....NFPYAMDYWGQTSVTVSS 139

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980a:\*
- 2: geneseqp1990a:\*
- 3: geneseqp2000a:\*
- 4: geneseqp2001a:\*
- 5: geneseqp2002a:\*
- 6: geneseqp2003a:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	756	100.0	139	6	ABG74245 Mouse ant
2	678.5	89.7	138	8	ADI26639 Mouse ant
3	613	81.1	469	2	AAR40384 Monoclonal
4	602	79.6	138	3	AAV56873 MAB CT-M-
5	600	79.4	139	2	AAW29750 Anti-HMPG
6	597	79.0	139	2	AAR33950 CTMO1 VH.
7	593.5	78.5	140	2	AAW06213 MAB Co-1
8	593.5	78.5	140	2	AAW85061 Mouse Co-
9	593.5	78.5	140	6	ABU58895 Mouse ant
10	587.5	77.7	140	6	ABU58895 Mouse ant
11	587.5	77.7	140	8	ADM79825 Co-1 Heav
12	587.5	77.7	253	8	ADM79825 Mouse IgG
13	585	77.4	116	2	AAW79241 Heavy cha
14	577	76.3	135	2	AAW60866 Variable
15	577	76.3	135	3	AAV80293 Igm chime
16	577	76.3	590	2	AAW31751 H chain s
17	577	76.3	590	2	AAW71888 Anti-huma
18	577	76.3	590	3	AAAB12308 Anti-huma
19	574.5	76.0	140	2	AAR55554 DREG-200
20	569	75.3	135	2	AAW68548 Anti-CD33
21	569	75.3	135	4	AAW68548 Anti-CD33
22	569	75.3	135	8	ADO47773 Murine M19
23	565.5	74.8	138	2	AAW50218 Amino aci
24	563.5	74.5	136	3	AAAB23815 Plasmid p
25	563.5	74.5	136	4	AAW67491 Amino aci

26	563.5	74.5	136	5	AAW47629 Murine MA
27	563.5	74.5	136	5	ABG97806 Mouse MAB
28	563.5	74.5	136	5	ABG35309 Thrombopo
29	561.5	74.3	136	3	AAAB23813 Plasmid p
30	561.5	74.3	136	4	AAW67489 Amino aci
31	561.5	74.3	136	5	AAW47627 Murine MA
32	561.5	74.3	136	5	ABG97804 Mouse MAB
33	561.5	74.3	136	5	ABG35307 Thrombopo
34	561.5	74.3	138	4	AAW69688 Murine CM
35	561.5	74.3	138	8	ADO47789 Mouse CM
36	559	73.9	137	2	AAR05090 Heavy cha
37	559	73.9	137	3	AAV99845 Mouse par
38	559	73.9	139	2	AAR29009 p64-h2 pr
39	559	73.9	139	2	AAV53328 KM-796 he
40	559	73.9	139	2	AAV28356 Antibody
41	559	73.9	139	2	AAV28384 Anti-GM2
42	558	73.8	118	3	AAAB11391 Murine II
43	557	73.7	137	2	AAW62445 81C6 heav
44	555.5	73.5	140	2	AAW21843 Heavy cha
45	555	73.4	561	2	AAV17415 Mouse imm

ALIGNMENTS

RESULT 1  
ABG74245  
ID ABG74245 standard; protein; 139 AA.

XX AC ABG74245;  
XX DT 22-APR-2003 (first entry)  
XX DE Mouse antibody 4D4 heavy chain variable region.

XX KW T-cell receptor; cytostatic; dermatological; neuroprotective;  
immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;  
3E11; prostate-specific membrane antigen; zeta signalling chain;  
XX KW CDalpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;  
small cell lung cancer; heavy chain variable region; mouse.

XX OS Mus sp.

XX PN US2002132983-A1.

XX PD 19-SEP-2002.

XX PF 10-DEC-2001; 2001US-00006773.

XX PR 30-NOV-2000; 2000US-0250087P.

XX PR 30-NOV-2000; 2000US-0250089P.

XX PA (JUNG/) JUNGHANS R P.

XX PI Junghans RP;

XX PI WPI; 2003-208946/20.

XX DR N-PSDB; ABX16571.

XX PT New chimeric molecule useful in treating patients with disorders, such as

XX PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer

XX PT comprises GD3 and/or PSMA binding domains of antibody.

XX PS Disclosure; Page 14-15; 35pp; English.

XX CC The invention relates to a chimaeric molecule comprising the GD3  
(ganglioside antigen) binding domain of antibody MB3.6, with any of 3  
variable gene sequences, or the PSMA (prostate-specific membrane antigen)  
binding domain of antibody 3D8, 4D4 and 3E11, with variable gene  
sequences, the zeta signalling chain of the T cell receptor and an  
intervening CD8alpha hinge in which cysteine residues have been mutated.  
XX CC The chimaeric molecules expressed in T cells or NK cells or other  
effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),  
 CC and/or together with each other or with heterologous constructs to engage  
 CC additional stimulatory and functional properties of the effector cells to  
 CC enhance the antitumour therapeutic efficacy (claimed). They are  
 CC particularly useful in disorders including melanoma, neuroendocrine  
 CC tumours and prostate and small cell lung cancer. The present sequence  
 CC represents the mouse antibody 4D4 heavy chain variable region  
 XX  
 SQ Sequence 139 AA;

Query Match 100.0%; Score 756; DB 6; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-58;  
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
 DB 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
 QY 61 GQGLEWIGWIYPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120  
 DB 61 GQGLEWIGWIYPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120  
 QY 121 FPSYAMDYWGQGSTVTSS 139  
 DB 121 FPSYAMDYWGQGSTVTSS 139

RESULT 2  
 ADI26639  
 ID ADI26639 standard; protein; 138 AA.

AC ADI26639;  
 XX  
 DT 15-APR-2004 (first entry)  
 XX  
 DE Mouse anti-IgM antibody O1/A1/A4 JH protein.  
 XX  
 KW Mouse; antibody; IgM; remyelination; neuronal growth; autoantibody;  
 KW demyelination disease; multiple sclerosis; central nervous system; CNS;  
 KW axon; glial cell proliferation;  
 KW Theiler's murine encephalomyelitis virus infection; CNS injury;  
 KW spinal cord injury.  
 XX  
 OS Mus sp.

PN US2003185827-A1.  
 XX  
 PD 02-OCT-2003..  
 XX  
 PF 13-NOV-2001; 2001US-00010729.  
 XX  
 PR 29-APR-1994; 94US-00236520.  
 PR 08-AUG-1996; 96US-00692084.  
 PR 07-JAN-1997; 97US-00779784.  
 PR 28-MAY-1999; 99US-00322862.  
 PR 30-MAY-2000; 2000US-00580787.  
 PR 05-DEC-2000; 2000US-00730473.  
 XX

(MAYO-) MAYO FOUND.  
 XX  
 XX Rodriguez M, Miller DJ, Pease LR;  
 XX  
 XX WPI; 2004-119219/12.  
 XX  
 XX New human immunoglobulin M antibody for treating or preventing a  
 PT demyelinating disease of the central nervous system in a human or  
 PT domestic animal, such as multiple sclerosis.  
 XX  
 XX Example 4; Fig 12; 159pp; English.

XX The invention relates to an antibody (I) produced by injecting an  
 CC immunocompetent host with an antibody peptide, and harvesting the  
 CC antibody, where the peptide comprises a human anti-IgM antibody fragment

CC given in the specification, or active fragments. Also included are  
 CC stimulating remyelination of central nervous system (CNS) axons in a  
 CC mammal (comprising administering a monoclonal antibody, or mixtures,  
 CC monomers, active fragments, or recombinant antibodies derived from it,  
 CC characterised by their ability to bind structures and cells within the  
 CC CNS, including oligodendrocytes), stimulating the proliferation of glial  
 CC cells in CNS axons in a mammal (comprising administering a monoclonal  
 CC antibody, or mixtures, monomers, active fragments, or recombinant  
 CC antibodies derived from it, characterised by their ability to bind  
 CC structures and cells within the CNS), treating or preventing a  
 CC demyelinating disease of the CNS in a mammal (comprising administering a  
 CC monoclonal antibody, or mixtures, monomers, active fragments, or  
 CC recombinant antibodies derived from it, characterised by their ability to  
 CC bind structures and cells within the CNS, and to stimulate remyelination  
 CC of axons of the CNS), stimulating, in vitro, the proliferation of glial  
 CC cells from mixed cell culture, stimulating remyelination of CNS axons in  
 CC a mammal, a DNA sequence (or degenerate variant of it) which encodes an  
 CC antibody (or a peptide analogue, hapten, or active fragment of it, where  
 CC the DNA sequence consists of a sequence encoding an anti IgM antibody), a  
 CC probe capable of screening for the antibody, an assay for screening drugs  
 CC and other agents for the ability to modulate the production or mimic the  
 CC activities of mAb SHGM22, SHGM46, or combinations of them, a  
 CC recombinant virus transformed with recombinant antibody nucleic acids or  
 CC vector, imaging a portion of the CNS using the antibody and diagnosing or  
 CC monitoring demyelination and/or remyelination of the CNS comprising using  
 CC CNS image. The antibody is used to stimulate remyelination of CNS axons,  
 CC and to stimulate the proliferation of glial cells in CNS axons,  
 CC optionally in vitro. The antibody is used to treat or prevent a  
 CC demyelinating disease of the CNS in a human or domestic animal, such as  
 CC multiple sclerosis, or a disease, other injury or dysfunction of the CNS,  
 CC preferably the mammal is a mouse infected with Strain DA of Theiler's  
 CC murine encephalomyelitis virus. The antibody is used to treat a spinal  
 CC cord injury and used to screen drugs and other agents for the ability to  
 CC modulate the production or mimic the activities of the antibody. The  
 CC antibody can be used to image a portion of the CNS which can be used to  
 CC diagnose or monitor demyelination and/or remyelination of the CNS. The  
 CC present sequence is a variable region of a mouse anti-IgM antibody (or  
 CC fragment).  
 XX  
 SQ Sequence 138 AA;

Query Match 89.7%; Score 678.5; DB 8; Length 138;  
 Best Local Similarity 92.1%; Pred. No. 2.7e-51;  
 Matches 128; Conservative 1; Mismatches 9; Indels 1; Gaps 1;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
 DB 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
 QY 61 GQGLEWIGWIYPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120  
 DB 61 GQGLEWIGWIYPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120  
 QY 121 FPSYAMDYWGQGSTVTSS 139  
 DB 121 FYWY-FDVWAGTFTVTSS 138

RESULT 3  
 AAR40384  
 ID AAR40384 standard; protein; 469 AA.  
 XX  
 AC AAR40384;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 10-MAR-2003 (revised)  
 DT 08-FEB-1994 (first entry)  
 XX  
 DE Monoclonal antibody M(alpha)2-3 Heavy-chain.

anti-snake small neurotoxin antibody; heavy chain; IgG2; immunoglobulin;  
 bispecific bivalent antibody; cell-targeting; cytotoxic agent.

OS Unidentified.

XX Key Location/Qualifiers

FT Peptide 1..19

FT Region /label= signal\_peptide

FT Region 20..139

FT Region /label= variable

FT Region 140..236

FT Region /label= constant

FT Region 237..252

FT Region /label= joining

FT Region 253..362

FT Region /label= constant

FT Region 363..469

FT Region /label= constant

XX EP556111-A1.

PN XX

XX 18-AUG-1993.

PD XX

XX 09-FEB-1993; 93EP-00400323.

PF XX

XX 11-FEB-1992; 92FR-00001505.

PR XX

XX (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.

PA XX

XX Boulain J, Ducancel F, Gillet D, Menez A;

PI XX

XX WPI; 1993-260351/33.

DR XX

XX N-PSDB; AAQ48037.

DR XX

XX New immunoglobulin hybrid proteins - with immunoglobulin fragments linked to dimeric protein, for diagnostic or therapeutic use.

PT XX

XX Example 1; Fig 3A; 37pp; French.

PS XX

XX A fragment of the heavy chain (VH + CH1) from the anti-snake small neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from hybridoma-derived cDNA using primers AAQ48039 and AAQ48040. A light chain fragment (VL + CL) was amplified from the same source using primers AAQ48041 and AAQ48042. The two amplified fragments were inserted into the same vector; the H-chain fragment was inserted (in-frame) between codons 6-7 of the phoA coding sequence and the L-chain fragment was inserted into a cassette which contained a phoA S-D sequence, a signal peptide and the first 6 codons of phoA. The cassette was positioned between the termination codon and the transcription termination sequence of phoA. The fusion construct is expected to encode a hybrid protein comprising two identical Ab-derived units. The invention also covers hybrid proteins containing two different Ab-derived units (i.e. to produce bispecific antibodies). When a toxic protein is used in place of phoA, the hybrid molecules can be used as cell-targeting therapeutic agents. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct CC PN field.)

XX SQ Sequence 469 AA;

Query Match 81.1%; Score 613; DB 2; Length 469;

Best Local Similarity 80.6%; Pred. No. 5e-45;

Matches 112; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKQRP 60

DB 1 MGWSWIFLLSGTAGVHCQVLOQSGPELVKPGASVKISKASGYTFTDYVINWVKQRP 60

QY 61 GQGLEWIGWIYPGCGTNNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120

DB 61 GQGLEWIGWIYPASGNTKYNENFKGKATLTVDTSSTAYMQLSSLTSEDVAVYFCARANG 120

QY 121 FPSYAMDYWGQGTSTVTVSS 139

DB 121 ATATLLDYWGQGTSTVTVSS 139

RESULT 4

AA56873

ID AAY56873 standard; protein; 138 AA.

XX AC AAY56873;

XX DT 14-APR-2000 (first entry)

XX DE MAb CT-M-01 heavy chain VH domain.

XX KW Cytotoxic; drug conjugate; humanized; monoclonal antibody; CT-M-01; human milk fat globule; growth inhibition.

XX OS Homo sapiens.

XX PN US6015562-A.

XX PD 18-JAN-2000.

XX PF 16-FEB-1996; 96US-00603024.

XX PR 22-SEP-1992; 92US-00948277.

XX PR 06-OCT-1993; 93US-00132725.

XX PR 31-OCT-1994; 94US-00332025.

XX PA (AMCY ) AMERICAN CYANAMID CO.

XX PI Hamann PR, Hinman LM;

XX DR WPI; 2000-126309/11.

XX DR N-PSDB; AAZ46912.

XX DT New cytotoxic drug conjugates are useful for inhibiting the growth of unwanted cells.

PT XX

PT Disclosure; Col 21-22; 37pp; English.

PS XX

XX The invention relates to cytotoxic drug conjugates of a specified formula. The conjugate comprise a humanized monoclonal antibody (Mab) hu:CT-M-01 reactive to human milk fat globule, its antigen-recognizing fragments, or chemically manipulated counterparts. The cytotoxic drug conjugates are useful for inhibiting the growth of unwanted cells. The present sequence represents the Mab CT-M-01 heavy chain VH domain

XX SQ Sequence 138 AA;

Query Match 79.6%; Score 602; DB 3; Length 138;

Best Local Similarity 81.2%; Pred. No. 1.2e-44;

Matches 112; Conservative 6; Mismatches 20; Indels 0; Gaps 0;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKQRP 60

DB 1 MGWSWIFLLSVTTGVHCQVLOQSGPELVKPGASVKISKASGYTFTDYVINWVKQRP 60

QY 61 GQGLEWIGWIYPGCGTNNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120

DB 61 GQGLEWIGWIDPGSGNTKYNENFKGKATLTVDTSSTAYMQLSSLTSEDVAVYFCAREKT 120

QY 121 FPSYAMDYWGQGTSTVTVSS 138

DB 121 TTYVAMDYWGQGTSTVTVSS 138

RESULT 5

AAW29750

ID AAW29750 standard; protein; 139 AA.

XX AC AAW29750;

XX DT 25-MAR-2003 (revised)

XX DT 14-JAN-1998 (first entry)

XX DE Anti-HMFG Mab CTMO1 heavy chain variable region.

XX Humanised antibody; CDR-grafted antibody; chimeric antibody; CTMO1;  
 KW complementarity determining region; human milk fat globule; HMFG;  
 KW monoclonal antibody; MAb; mouse; cancer; breast cancer; ovary carcinoma;  
 KW lung cancer; uterus cancer; diagnosis; therapy.  
 XX Mus musculus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /label= Leader\_peptide  
 FT Misc-difference 344  
 FT /note= "encoded by ACG"  
 XX  
 XX EP781845-A2.  
 XX  
 XX  
 XX 02-JUL-1997.  
 XX  
 XX 24-SEP-1992; 97EP-00200482.  
 XX  
 XX 26-SEP-1991; 91GB-00020467.  
 PR  
 PR 24-SEP-1992; 92EP-00308680.  
 XX  
 XX (CLLT ) CELLTECH THERAPEUTICS LTD.  
 XX  
 XX Hamann PR, Adair JR, Owens RJ, Baker TS, Lyons AH, Hinman LM;  
 PI Menendez AT;  
 PI  
 XX WPI; 1997-334902/31.  
 DR N-PSDB; AAT85854.  
 XX  
 XX DNA encoding composite heavy and light chains of humanised antibody -  
 PT specific for human milk fat globule, useful in cancer diagnosis or  
 PT therapy.  
 PT  
 XX  
 PS Claim 1; Page 17-18; 53pp; English.  
 XX  
 XX This polypeptide sequence comprises the heavy chain variable region VH of  
 CC murine anti-human milk fat globule (HMFG) monoclonal antibody CTMO1. The  
 CC sequence was deduced from an isolated cDNA clone (see AAT85854). CTMO1  
 CC recognises a polymorphic epithelial mucin of HMFG. The CTMO1 VH region  
 CC can be used in the design of chimeric humanised antibodies or CDR-grafted  
 CC humanised anti-HMFG antibodies. Preferred humanised antibody heavy chains  
 CC include residues 2, 26-35, 37, 50-65, 71, 73, 95-105 and 107 (Kabab  
 CC numbering) of murine CTMO1 VH, and may also include residues 6, 23, 49,  
 CC 76, 78, 80, 88 and 91, in a human LAY POM, TUR, TEI, KOL, NEWN, REI or EU  
 CC framework. The recombinant VH can be expressed in transformed host cells.  
 CC Humanised antibodies may be conjugated with labels or drugs (especially  
 CC methylthio antitumour agents) and used for diagnosis or therapy of  
 CC human carcinomas, e.g. of the ovary, breast, uterus and lung. (Updated on  
 CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR  
 CC field.)  
 XX  
 XX Sequence 139 AA;  
 SQ  
 Query Match 79.4%; Score 600; DB 2; Length 139;  
 Best Local Similarity 80.8%; Pred. No. 1.8e-44;  
 Matches 112; Conservative 7; Mismatches 20; Indels 0; Gaps 0;  
 QY 1 MGRWRIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
 Db 1 MEWSWVFLFSLVTTGVHCQIQIQQQSGPELVKPGASVKISCKASGYTFTDYINWVKQRP 60  
 QY 61 GQGLEWIGWYIPDGGTNYNEKFKGKATLTADKSSSTAYWQLSSLTSSENSAVYFCARGN 120  
 Db 61 GQGLEWIGWIDPGSGNTKYNEKFKGKATLTVDTSSTAYWQLSSLTSEDVAVYFCAREKI 120  
 QY 121 FPSYANDYWGQGSTVTSS 139  
 Db 121 TTYIAMDYWGQGSTVTSSA 139

RESULT 6

AAR33950  
 ID AAR33950 standard; protein; 139 AA.  
 XX  
 AC AAR33950;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 16-JUL-1993 (first entry)  
 XX  
 XX CTMO1 VH.  
 XX  
 XX Heavy; light; chain; variable; domain; CTMO1; PCR; primer; carcinoma;  
 KW immunoglobulin; murine; monoclonal; antibody; MAB; IGG-kappa; ovary;  
 KW humanised; diagnosis; therapy; breast; uterus; lung.  
 XX  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..19  
 FT /note= "Signal peptide"  
 FT Protein 20..139  
 FT /note= "Mature protein"  
 XX  
 XX EP534742-A1.  
 XX  
 XX 31-MAR-1993.  
 XX  
 XX 24-SEP-1992; 92EP-00308680.  
 XX  
 XX 26-SEP-1991; 91GB-00020467.  
 XX  
 XX (CLLT ) CELLTECH LTD.  
 PA (CLLT ) CELLTECH THERAPEUTICS LTD.  
 XX  
 XX Adair JR, Hamann PR, Owens RJ, Baker TS, Lyons AH, Hinman LM;  
 PI Menendez AT;  
 PI  
 XX WPI; 1993-102837/13.  
 DR N-PSDB; AAQ38877.  
 XX  
 XX Anti-human milk fat globule humanised antibodies - useful as conjugate  
 PT for in-vivo diagnosis and therapy of e.g. ovarian or breast cancer.  
 XX  
 XX Disclosure; Page 17-18; 57pp; English.  
 XX  
 XX The sequences given in AAR33950-51 represent the heavy and light chain  
 CC variable domains of CTMO1 respectively. The DNA encoding these peptides  
 CC was isolated by PCR using the primer sequences given in AAQ38879-80.  
 CC Examination of these amino acid sequences revealed considerable homology  
 CC with other characterised immunoglobulin genes. The murine monoclonal  
 CC antibody (MAB), CTMO1, was confirmed to be an IGG-kappa antibody. CTMO1  
 CC was used in the production of a humanised antibody for in vivo diagnosis  
 CC and therapy of carcinomas of ovary, breast, uterus and lung. (Updated on  
 CC 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA  
 CC field.)  
 XX  
 XX Sequence 139 AA;  
 SQ  
 Query Match 79.0%; Score 597; DB 2; Length 139;  
 Best Local Similarity 79.9%; Pred. No. 3.4e-44;  
 Matches 111; Conservative 7; Mismatches 21; Indels 0; Gaps 0;  
 QY 1 MGRWRIFLLSGTAGVHCQVQLQQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
 Db 1 MEWSWVFLFSLVTTGVHCQIQIQQQSGPELVKPGASVKISCKASGYTFTDYINWVKQRP 60  
 QY 61 GQGLEWIGWYIPDGGTNYNEKFKGKATLTADKSSSTAYWQLSSLTSSENSAVYFCARGN 120  
 Db 61 GQGLEWIGWIDPGSGNTKYNEKFKGKATLTVDTSSTAYWQLSSLTSEDVAVYFCAREKT 120  
 QY 121 FPSYANDYWGQGSTVTSS 139  
 Db 121 TTYIAMDYWGQGSTVTSSA 139

## RESULT 7

AAW06213  
 ID AAW06213 standard; protein; 140 AA.  
 XX AC AAW06213;  
 XX DT 25-MAR-2003 (revised)  
 DT 13-FEB-1997 (first entry)  
 XX DE MAb Co-1 heavy chain variable region.  
 XX KW Chimeric antibody; monoclonal antibody; Co-1; antibody engineering;  
 KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;  
 KW ovary carcinoma; cancer; diagnosis; therapy; heavy chain.  
 XX OS Mus sp.  
 XX PN US5576184-A.  
 XX PD 19-NOV-1996.  
 XX PF 27-DEC-1994; 94US-00364001.  
 XX PR 06-SEP-1988; 88US-00240624.  
 PR 08-SEP-1988; 88US-00241744.  
 PR 13-SEP-1988; 88US-00243739.  
 PR 04-OCT-1988; 88US-00253002.  
 PR 19-JUN-1989; 89US-00367641.  
 PR 21-JUL-1989; 89US-00382768.  
 PR 06-MAY-1991; 91US-00659401.  
 XX PA (XOMA) XOMA CORP.  
 XX PI Chang CP, Lei S, Better MD, Robinson RR, Horwitz AH;  
 XX WPI; 1997-011249/01.  
 DR N-PSDB; AAT43438.  
 XX Chimeric mouse-human antibodies - recognise a human tumour antigen, used  
 PT for the treatment and diagnosis of human cancers.  
 XX Example 3; Fig 22; 102pp; English.

PS The heavy chain variable region (AAW06213) of mouse monoclonal antibody  
 CC Co-1 is the product of a cDNA clone (AAT43438) isolated from a Co-1  
 CC hybridoma cDNA library. MAb Co-1 (IgG1) binds to an antigen that is  
 CC expressed on the surface of human lung, breast, colon and ovary  
 CC carcinomas, but not on most normal adult tissues. The heavy chain and  
 CC light chain variable regions (see also AAW06214) of Co-1 can be linked to  
 CC human constant regions and expressed in transformed host cells. Novel  
 CC mouse-human chimeric antibodies (see also AAW06209-12 and AAW06215-18)  
 CC can be produced that have specificity to human tumour antigens and can be  
 CC used for the treatment and diagnosis of human cancer. (Updated on 25-MAR-  
 CC 2003 to correct PF field.)  
 XX SQ Sequence 140 AA;

Query Match 78.5%; Score 593.5; DB 2; Length 140;  
 Best Local Similarity 81.4%; Pred. No. 6.8e-44;  
 Matches 114; Conservative 12; Mismatches 13; Indels 1; Gaps 1;  
 Qy 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTTSYDINWVKQRP 60  
 Db 1 MEWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKMSCKASGYTTSYMHVWKQRP 60  
 Qy 61 GQGLEWIGWIYPGOGGTNYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGN 120  
 Db 61 GQGLEWIGWIYPNDGTSYNEKFKGKATLTSDKSSSTAYMELSLTSDSAVYFCARRIY 120  
 Qy 121 FDSYVMDYWGQGTSTVTVSS 139  
 Db 121 FDSYVMDYWGQGTSTVTVSS 140

## RESULT 8

AAW85061  
 ID AAW85061 standard; protein; 140 AA.  
 XX AC AAW85061;  
 XX DT 20-MAR-2003 (revised)  
 DT 16-APR-1999 (first entry)  
 XX DE Mouse Co-1 heavy chain variable region.  
 XX KW Heavy chain variable region; murine antibody Co-1; antibody ING-1;  
 KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;  
 KW treatment; human cancer.  
 XX OS Mus sp.  
 XX PN US5843685-A.  
 XX PD 01-DEC-1998.  
 XX PF 06-JUN-1995; 95US-00466034.  
 XX PR 06-SEP-1988; 88US-00240624.  
 PR 08-SEP-1988; 88US-00241744.  
 PR 13-SEP-1988; 88US-00243739.  
 PR 04-OCT-1988; 88US-00253002.  
 PR 19-JUN-1989; 89US-00367641.  
 PR 21-JUL-1989; 89US-00382768.  
 PR 06-SEP-1989; 89WO-US003852.  
 PR 06-MAY-1991; 91US-00659401.  
 PR 27-DEC-1994; 94US-00364001.  
 XX PA (XOMA) XOMA CORP.  
 XX PI Horwitz AH, Lei S, Chang CP, Better MD, Robinson RR;  
 XX WPI; 1999-044574/04.  
 DR N-PSDB; AAW71157.  
 XX Chimeric antibody specific for human tumour antigen - useful as  
 PT immunosassay, imaging or antitumour agent.  
 XX Example 3; Fig 22; 92pp; English.  
 XX The present sequence represents the heavy chain variable region of murine  
 CC antibody Co-1. The sequence was used to create chimeric mouse-human  
 CC immunoglobulins which recognise the human tumour antigen bound by  
 CC antibody ING-1 (produced by hybridoma cell line ATCC HB 9812). The  
 CC chimeric antibodies also have an antigen-binding site that competitively  
 CC inhibits the binding of antibody ING-1, and mediate complement-dependent  
 CC cytotoxicity of target cells or antibody-dependent cellular cytotoxicity to  
 CC target cells. The chimeric antibodies can be used for therapeutic  
 CC purposes in the treatment of human cancer. (Updated on 20-MAR-2003 to  
 CC correct PR field.)  
 XX SQ Sequence 140 AA;

Query Match 78.5%; Score 593.5; DB 2; Length 140;  
 Best Local Similarity 81.4%; Pred. No. 6.8e-44;  
 Matches 114; Conservative 12; Mismatches 13; Indels 1; Gaps 1;  
 Qy 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTTSYDINWVKQRP 60  
 Db 1 MEWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKMSCKASGYTTSYMHVWKQRP 60  
 Qy 61 GQGLEWIGWIYPGOGGTNYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGN 120  
 Db 61 GQGLEWIGWIYPNDGTSYNEKFKGKATLTSDKSSSTAYMELSLTSDSAVYFCARRIY 120  
 Qy 121 FDSYVMDYWGQGTSTVTVSS 139

121 FDYSYVMDYWGQGTSTVTSS 140

| | | | | | | | | | | | | | | |

Db

## RESULT 9

ABU58895  
ID ABU58895 standard; protein; 140 AA.

XX

AC ABU58895;

XX

DT 16-APR-2003 (first entry)

XX

DE Mouse antibody heavy chain variable region #3.

XX

KW Mouse; human tumour antigen; anti-human tumour antigen-antibody;

KW

KW ING-1 antibody; cell line H9812; immunoassay; imaging; tumour diagnosis;

KW

XX tumour therapy; cytostatic; heavy chain variable region.

XX

OS Mus sp.

XX

XX US6461824-B1.

XX

XX 08-OCT-2002.

XX

XX 06-JUN-1995; 95US-00467142.

XX

XX 06-SEP-1988; 88US-00240624.

XX

XX 08-SEP-1988; 88US-00241744.

XX

XX 13-SEP-1988; 88US-00243739.

XX

XX 04-OCT-1988; 88US-00253002.

XX

XX 19-JUN-1989; 89US-00367641.

XX

XX 21-JUL-1989; 89US-00382768.

XX

XX 06-SEP-1989; 89WO-US003852.

XX

XX 06-MAY-1991; 91US-00659401.

XX

XX 27-DEC-1994; 94US-00364001.

XX

XX (XOMA ) XOMA TECHNOLOGY LTD.

XX

XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;

XX

XX WPI; 2003-196707/19.

XX

XX N-PSDB; ABK79237.

XX

XX Antibody for detecting antigen in animal or killing cells carrying

XX

XX antigen comprises human constant region and variable region having

XX

XX specificity for human tumor antigen bound by ING-1 antibody.

XX

XX Example 3; Fig 22; 101pp; English.

XX

XX The invention describes an antibody comprising a human constant region

XX

XX and a variable region having specificity for the human tumour antigen

XX

XX bound by the ING-1 antibody, where the ING-1 is produced by cell line

XX

XX HB9812 as deposited with ATCC, and the antibody has the same affinity as

XX

XX the ING-1 for the human tumour antigen. The antibody is useful in an

XX

XX immunoassay method for detecting an antigen in a sample by contacting a

XX

XX label-detectable antigen in the sample with the antibody, detecting the

XX

XX label and relating the detected label to the presence of the antigen; for

XX

XX use in an imaging method for revealing the presence of a label-detectable

XX

XX antigen in an animal by contacting the antibody with a part of the animal

CC antibodies, as well as their derivatives, in tumour diagnosis and  
CC therapy. This is the amino acid sequence of a mouse antibody heavy chain  
CC variable region used in the creation of an anti-human tumour antigen-  
CC antibody  
CC

XX Sequence 140 AA;  
SQ

Query Match 78.5%; Score 593.5; DB 6; Length 140;

Best Local Similarity 81.4%; Pred. No. 6.8e-44;

Matches 114; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 1 MGRWIFLLSGTAGVHCQVQLQDSGPELVKPGALVKISKASGYTFTSYDINWVKQRP 60

Db 1 MEWSNIFLLSGTAGVHSEVQLQDSGPELVKPGASVKMSCKASGYTFTSYVHWVKQRP 60

QY 61 GQGLEWIGHIYPDGDTNNEKFKGKATLTADKSSSTAYMQLSSLTSENNAVYFCARGN 120

Db 61 GQGLEWIGVINPDGDTNNEKFKGKATLTADKSSSTAYMQLSSLTSENNAVYFCARRI 120

QY 121 FFSYVMDYWGQGTSTVTSS 139

Db 121 FFSYVMDYWGQGTSTVTSS 140

RESULT 10

AAR09425

ID AAR09425 standard; protein; 140 AA.

XX

AC AAR09425;

XX

DT 25-MAR-2003 (revised)

XX

DT 04-MAR-1993 (first entry)

XX

DE Co-1 Heavy Chain V Region (mouse).

XX

KW Monoclonal antibody; chimera; light; heavy; chain; constant; variable;

XX

KW antigen; diagnosis; cancer; tumour.

XX

OS Mus musculus.

XX

XX WO9002569-A.

XX

XX 22-MAR-1990.

XX

XX 08-SEP-1988; 88US-00241744.

XX

XX 08-SEP-1988; 88US-00241744.

XX

XX 13-SEP-1988; 88US-00243739.

XX

XX 04-OCT-1988; 88US-00253002.

XX

XX 19-JUN-1989; 89US-00367641.

XX

XX 21-JUL-1989; 89US-00382768.

XX

XX (ITGE-) INT GENETIC ENG INC.

XX

XX (INGE-) INGENE INT GENETIC.

XX

XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;

XX

XX WPI; 1990-115825/15.

XX

XX N-PSDB; AAQ08607.

XX

XX Chimeric mouse-human antibodies - prepd. using genes coding for constant  
XX human region murine variable region, esp. to 3 tumour antigen.

XX

XX Claim 13; Page 123 + Fig 22; 173pp; English.

XX

XX The sequence is used in the prodn. of a chimeric antibody mol. comprising  
XX two light chains and two heavy chains, each having a constant region  
XX (human) and a variable region (murine) having specificity to an antigen  
XX bound by murine monoclonal antibody (MAB) Co-1. The chimeric antibodies  
XX can be used for any purpose for which the original murine MABs can be  
XX used, with the advantage that they are more compatible with the human  
XX body. They are esp. used for the diagnosis and treatment of cancer.  
XX (Updated on 25-MAR-2003 to correct PA field.)



XX Sequence 140 AA;  
 SQ Query Match 77.7%; Score 587.5; DB 2; Length 140;  
 Best Local Similarity 80.7%; Pred. No. 2.3e-43;  
 Matches 113; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 MGNRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSDINWVKORP 60  
 DB 1 MGNRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSDINWVKORP 60  
 QY 61 GQGLEWIGWIPVGGTNYNEKFKGKATLTADKSSSTAYMOLSSITSENSAVYFCARGN 120  
 DB 61 GQGLEWIGWIPVGGTNYNEKFKGKATLTADKSSSTAYMOLSSITSENSAVYFCARGN 120  
 QY 121 FSYVMDYWGQGTSTVTVSS 139  
 DB 121 FSYVMDYWGQGTSTVTVSS 140  
 RESULT 11  
 ADM79825  
 ID ADM79825 standard; protein; 148 AA.  
 XX  
 AC ADM79825;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Mouse IgG2b heavy chain protein SEQ ID NO:2.  
 XX  
 KW cell death-inducing agent; human leukocyte antigen; HLA; antibody;  
 KW 2D7 antibody; 2D7 antibody degradation product;  
 KW cell proliferation inhibition; antitumor; autoimmune disease;  
 KW cytostatic; immunosuppressive; antiinflammatory; dermatological; cancer;  
 KW Crohn's disease; systemic lupus erythematosus; mouse; IgG2b heavy chain.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2004033499-A1.  
 XX  
 PD 22-APR-2004.  
 XX  
 PF 10-OCT-2003; 2003WO-JP013063.  
 XX  
 PR 11-OCT-2002; 2002JP-00299289.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PA (OZAK/) OZAKI S.  
 PA (ABEM/) ABE M.  
 XX  
 PI Ozaki S, Abe M, Tsuchiya M, Kimura N, Kawai S;  
 XX  
 DR WPI; 2004-330447/30.  
 DR N-PSDB; ADM79824.  
 XX  
 PT Cell death-inducing agents containing degradation product of antibody  
 PT particularly diabody recognizing human leukocyte antigen (HLA),  
 PT applicable in antitumor agents and remedies for autoimmune diseases for  
 PT treating e.g. cancer.  
 XX  
 FS Claim 6; SEQ ID NO 2; 106pp; Japanese.  
 XX  
 CC The present invention describes cell death-inducing agents containing the  
 CC degradation product of an antibody which can recognise human leukocyte  
 CC antigen (HLA). Also described: (1) a degradation product of the 2D7  
 CC antibody; (2) a similar degradation product of an antibody which is: (a)  
 CC one containing an amino acid sequence of (SEQ ID NO:6) with 253 amino  
 CC acids; (b) one based on the sequence of (SEQ ID NO:6) but with some amino  
 CC acids substituted, deleted, inserted and/or added and being functionally  
 CC equivalent to the parent; (c) one containing the CDR amino-acid sequences  
 CC of (SEQ ID NO:2) and (SEQ ID NO:4) with 148 and 144 amino acids  
 CC respectively; or (d) one based on the sequence of (SEQ ID NO:2) and (SEQ  
 CC ID NO:4) but with some amino acids substituted, deleted, inserted and/or

CC added and being functionally equivalent to the parent; (3) a process for  
 CC producing an antibody with an increase of activity by degrading a HLA-  
 CC recognising antibody, or by degrading 2D7 antibody; (4) cell death-  
 CC inducing agents containing the degradation products of antibody,  
 CC comprising the produced antibodies or 2D7 antibody as active ingredient;  
 CC (5) agents for inhibiting cell proliferation containing the degradation  
 CC products of antibody, comprising the produced antibodies or 2D7 antibody;  
 CC (6) antitumor agents containing the degradation products of antibody,  
 CC comprising the produced antibodies or 2D7 antibody; and (7) remedies for  
 CC autoimmune diseases containing the degradation products of antibody,  
 CC comprising the produced antibodies or 2D7 antibody. The 2D7 antibody has  
 CC cytostatic, immunosuppressive, antiinflammatory and dermatological  
 CC activities. The cell death-inducing agents are applicable in antitumor  
 CC agents and remedies for autoimmune diseases for treating e.g. cancer,  
 CC Crohn's disease and systemic lupus erythematosus. The present sequence  
 CC represents a mouse IgG2b heavy chain, which is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 148 AA;  
 Query Match 77.7%; Score 587.5; DB 8; Length 148;  
 Best Local Similarity 79.1%; Pred. No. 2.4e-43;  
 Matches 110; Conservative 11; Mismatches 13; Indels 5; Gaps 1;  
 QY 1 MGNRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSDINWVKORP 60  
 DB 1 MGNRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSDINWVKORP 60  
 QY 61 GQGLEWIGWIPVGGTNYNEKFKGKATLTADKSSSTAYMOLSSITSENSAVYFCARGN 120  
 DB 61 GQGLEWIGWIPVGGTNYNEKFKGKATLTADKSSSTAYMOLSSITSENSAVYFCARGN 120  
 QY 121 FSYVMDYWGQGTSTVTVSS 139  
 DB 121 FSYVMDYWGQGTSTVTVSS 134  
 RESULT 12  
 ADM79829  
 ID ADM79829 standard; protein; 253 AA.  
 XX  
 AC ADM79829;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE 2D7 diabody (2D7DB) protein SEQ ID NO:6.  
 XX  
 KW cell death-inducing agent; human leukocyte antigen; HLA; antibody;  
 KW 2D7 antibody; 2D7 antibody degradation product;  
 KW cell proliferation inhibition; antitumor; autoimmune disease;  
 KW cytostatic; immunosuppressive; antiinflammatory; dermatological; cancer;  
 KW Crohn's disease; systemic lupus erythematosus; 2D7 diabody; 2D7DB.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2004033499-A1.  
 XX  
 PD 22-APR-2004.  
 XX  
 PF 10-OCT-2003; 2003WO-JP013063.  
 XX  
 PR 11-OCT-2002; 2002JP-00299289.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 PA (OZAK/) OZAKI S.  
 PA (ABEM/) ABE M.  
 XX  
 PI Ozaki S, Abe M, Tsuchiya M, Kimura N, Kawai S;  
 XX  
 DR WPI; 2004-330447/30.  
 DR N-PSDB; ADM79828.  
 XX  
 PT Cell death-inducing agents containing degradation product of antibody

PT particularly diabody recognizing human leukocyte antigen (HLA),  
 PT applicable in antitumor agents and remedies for autoimmune diseases for  
 PT treating e.g. cancer.

XX Claim 6; SEQ ID NO 6; 106pp; Japanese.

XX The present invention describes cell death-inducing agents containing the  
 CC degradation product of an antibody which can recognise human leukocyte  
 CC antigen (HLA). Also described: (1) a degradation product of the 2D7  
 CC antibody; (2) a similar degradation product of an antibody which is: (a)  
 CC one containing an amino acid sequence of (SEQ ID NO:6) with 253 amino  
 CC acids; (b) one based on the sequence of (SEQ ID NO:6) but with some amino  
 CC acids substituted, deleted, inserted and/or added and being functionally  
 CC equivalent to the parent; (c) one containing the CDR amino-acid sequences  
 CC of (SEQ ID NO:2) and (SEQ ID NO:4) with 148 and 144 amino acids  
 CC respectively; or (d) one based on the sequence of (SEQ ID NO:2) and (SEQ  
 CC ID NO:4) but with some amino acids substituted, deleted, inserted and/or  
 CC added and being functionally equivalent to the parent; (3) a process for  
 CC producing an antibody with an increase of activity by degrading a HLA-  
 CC recognising antibody, or by degrading 2D7 antibody; (4) cell death-  
 CC inducing agents containing the degradation products of antibody,  
 CC comprising the produced antibodies or 2D7 antibody as active ingredient;  
 CC (5) agents for inhibiting cell proliferation containing the degradation  
 CC products of antibody, comprising the produced antibodies or 2D7 antibody;  
 CC (6) antitumor agents containing the degradation products of antibody,  
 CC comprising the produced antibodies or 2D7 antibody; and (7) remedies for  
 CC autoimmune diseases containing the degradation products of antibody,  
 CC comprising the produced antibodies or 2D7 antibody. The 2D7 antibody has  
 CC cytostatic, immunosuppressive, antiinflammatory and dermatological  
 CC activities. The cell death-inducing agents are applicable in antitumor  
 CC agents and remedies for autoimmune diseases for treating e.g. cancer.  
 CC Crohn's disease and systemic lupus erythematosus. The present sequence  
 CC represents a 2D7 dabody (2D7DB), which is used in the exemplification of  
 CC the present invention.

XX Sequence 253 AA;

Query Match 77.7%; Score 587.5; DB 8; Length 253;  
 Best Local Similarity 79.4%; Pred. No. 4.3e-43;  
 Matches 110; Conservative 11; Mismatches 13; Indels 5; Gaps 1;

QY 1 MGRWIFLLSITAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
 DB 1 MRWSIFLLSITAGVHCQVQLQSGPELVKPGASVMSCKASGYTFTDIFHWVKQRP 60  
 QY 61 GQGLEWIGWYIPGDDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGN 120  
 DB 61 GQGLEWIGWYIPGDDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCVRSD 120  
 QY 121 FPSYANDYWGQTSVTSS 139  
 DB 121 F-----DYWGQGTTLTVSS 134

RESULT 13

AAR79241  
 ID AAR79241 standard; protein; 116 AA.

XX AAR79241;

XX 25-MAR-2003 (revised)

DT 21-DEC-1995 (first entry)

XX Heavy chain variable region for monoclonal antibody 4A10.

XX Monoclonal antibody; heavy metal; mercury; variable region; heavy chain.

XX Synthetic.

XX W09520607-A1.

XX 03-AUG-1995.

PF 27-JAN-1995; 95WO-US001195.

XX 27-JAN-1994; 94US-00187407.

XX (BION-) BIONEERASKA INC.

PI Lopez O, Wylie DE, Wagner F;

DR WPI; 1995-275415/36.

DR N-PSDB; AAQ97498.

XX New polypeptide(s) which bind heavy metals, esp. mercury - derived from  
 PT monoclonal antibodies, used for detecting, removing, adding or  
 PT neutralising heavy metals.

XX Claim 13; Page 54; 106pp; English.

XX Hybridoma antibodies have been produced with the spleen cells of BALB/c  
 CC mouse that had received multiple injections of mercuric ions reacted with  
 CC glutathione to produce a mercuric ion coordinate covalent compound which  
 CC was covalently bound to keyhole limpet hemocyanin (KLH). Eight hybridomas  
 CC (1F10, 4A10, 1C11, 5G4, 23P8, 2D5, 5B6 and 3E8) were producing MAb's that  
 CC were strongly positive against glutathione-mercuric ions but negative  
 CC against glutathione without mercuric ions. RNA was isolated from  
 CC hybridoma cells with guanidine isothiocyanate. First strand cDNA  
 CC synthesis was catalysed by MuLV reverse transcriptase. The primers used  
 CC for cDNA synthesis were complementary to the 5' end of the CH1 domain of  
 CC the heavy chain expressed by the hybridoma of interest, or to the 5' and  
 CC of the C kappa domain. Some of the primers used for cDNA synthesis are  
 CC shown in AAQ97511-Q97518. The primer used for cDNA synthesis of the  
 CC variable region of a particular antibody polypeptide was also used for  
 CC PCR amplification of that variable region, in conjunction with an  
 CC appropriate V-region primer. In addition, the VH primer AAQ97518 was used  
 CC to amplify the MAb 2D5 and 5B6 heavy chains. The sequences of the PCR  
 CC amplified nucleotides were determined. These are given in AAQ97498-Q97510  
 CC and the deduced AA sequences in AAR79241-R79250 & AAR78970-R78971. The  
 CC descriptions of the SEQ ID nos given on pp 44-45 and in the claims are  
 CC different from the descriptions in the sequence listings. The  
 CC descriptions in the sequence listings are used here. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX Sequence 116 AA;

Query Match 77.4%; Score 585; DB 2; Length 116;  
 Best Local Similarity 93.3%; Pred. No. 3.1e-43;  
 Matches 112; Conservative 1; Mismatches 3; Indels 4; Gaps 1;

QY 20 QVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPQGLEWIGWYIPGDDGNTY 79  
 DB 1 EVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRPQGLEWIGWYIPGDDGNTY 60  
 QY 80 NEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGNPFPSYANDYWGQTSVTSS 139  
 DB 61 NEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGNPFPSYANDYWGQTSVTSS 116

RESULT 14

AAW60866

ID AAW60866 standard; protein; 135 AA.

XX AAW60866;

XX 10-SEP-1998 (first entry)

XX Variable region of an anti-Fas antibody heavy chain.

XX Variable region; heavy chain; anti-Fas antibody; human; mouse;

XX immunoglobulin G; IgG; light chain; treatment; diagnosis;

XX autoimmune disease.

XX Mus sp.

XX JP10165178-A.

```

XX 23-JUN-1998.
PD
XX
XX PF 01-JUL-1997; 97JP-00191769.
XX
XX PR 02-JUL-1996; 96JP-00172228.
XX PR 09-OCT-1996; 96JP-00268737.
XX
XX PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX
XX DR WPI; 1998-406105/35.
XX DR N-PSDB; AAV37264.
XX
XX PT DNA encoding, e.g. variable region of anti-Fas antibody - useful for,
XX e.g. diagnosis and treatment of auto-immune diseases.
XX
XX PS Claim 7; Page 13; 16pp; Japanese.
XX
XX CC The present sequence represents a variable region of the heavy chain of
XX an anti-Fas antibody. The constant region of the heavy chain is derived
XX from human immunoglobulin G (IgG). The anti-Fas antibody can be used for
XX the treatment and diagnosis of autoimmune diseases
XX
XX SQ Sequence 135 AA;

Query Match 76.3%; Score 577; DB 2; Length 135;
Best Local Similarity 78.4%; Pred. No. 1.8e-42;
Matches 109; Conservative 11; Mismatches 15; Indels 4; Gaps 1;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKCKASGYTFTSYDINWVKQRP 60
DB 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKCKASGYTFTDYNMHWKQSH 60

QY 61 GQGLEWIGWIYPGDTGTYNNEKFKGKATLTADKSSSTAYMQLSSLTSNSAVYFCARGN 120
DB 61 GKSLEWIGVIYPYNGGTGYNQKFKSKATLTVDNSSLSTAYMELRLSLTSDSAVYICARS-- 118

QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --YYAMDYWGQGTSTVTVSS 135

RESULT 15
AA80293
ID AAY80293 standard; protein; 135 AA.
XX
XX AC AAY80293;
XX
XX DT 30-MAY-2000 (first entry)
XX
XX DE IgM chimeric antibody heavy chain variable region SEQ ID NO:1.
XX
XX KW Humanised; anti-Fas antibody; mouse hybridoma; autoimmune disease;
XX KW diagnosis; CDR; complementarity determining region; apoptosis;
XX KW immunosuppressive.
XX
XX OS Mus sp.
XX OS Synthetic.
XX
XX PN JP2000014383-A.
XX
XX PD 18-JAN-2000.
XX
XX PF 03-JUL-1998; 98JP-00204318.
XX
XX PR 03-JUL-1998; 98JP-00204318.
XX
XX PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX
XX DR WPI; 2000-199626/18.
XX DR N-PSDB; AAZ95282.
XX
XX PT Novel recombinant antibody used for treating and diagnosing autoimmune

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PT diseases - is humanized anti-Fas antibody which controls and induces
PT apoptosis in cells expressing fas antigen.
XX
XX PS Example 1; Page 9-10; 25pp; Japanese.
XX
XX CC The present invention describes a recombinant antibody (A) which binds to
XX fas antigen, and controls and induces apoptosis in cells which expressed
XX fas antigen. The complementarity determining regions (CDR) of (A) contain
XX amino acid sequences obtained from a mammal other than human, other
XX regions contain amino acid sequences from human and they partly contain
XX modified amino acids. (A) has immunosuppressive activity. (A) is used for
XX treating and/or diagnosing autoimmune diseases. The present sequence
XX represents an immunoglobulin M chimeric antibody heavy chain variable
XX region from an example from the present invention
XX
XX SQ Sequence 135 AA;

Query Match 76.3%; Score 577; DB 3; Length 135;
Best Local Similarity 78.4%; Pred. No. 1.8e-42;
Matches 109; Conservative 11; Mismatches 15; Indels 4; Gaps 1;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKCKASGYTFTSYDINWVKQRP 60
DB 1 MGWSWIFLLSGTAGVHSEVLOQSGPELVKPGASVKISKCKASGYTFTDYNMHWKQSH 60

QY 61 GQGLEWIGWIYPGDTGTYNNEKFKGKATLTADKSSSTAYMQLSSLTSNSAVYFCARGN 120
DB 61 GKSLEWIGVIYPYNGGTGYNQKFKSKATLTVDNSSLSTAYMELRLSLTSDSAVYICARS-- 118

QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --YYAMDYWGQGTSTVTVSS 135

Search completed: May 25, 2005, 15:47:20
Job time : 67.427 secs

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Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 17.3265 Seconds  
(without alignments)  
598.864 Million cell updates/sec

Title: US-10-006-773A-13  
Perfect score: 756  
Sequence: 1 MGWRWFLFLSLGTAGVHCQ.....NPPSYAMDYWGQTSVTVSS 139

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	603	79.8	139	1	US-08-253-877C-8
2	603	79.8	139	2	US-08-452-164A-8
3	602	79.6	138	3	US-08-603-024-2
4	585	77.4	116	2	US-08-888-366-2
5	574.5	76.0	140	5	PCT-US93-11612-4
6	569	75.3	135	1	US-07-634-278-69
7	569	75.3	135	1	US-08-477-728-69
8	569	75.3	135	1	US-08-474-040-69
9	569	75.3	135	1	US-08-487-200-69
10	569	75.3	135	3	US-08-484-537-69
11	565.5	74.8	138	4	US-09-254-180C-143
12	565.5	74.8	140	3	US-08-579-378A-4
13	561.5	74.3	138	1	US-07-634-278-85
14	561.5	74.3	138	1	US-08-477-728-85
15	561.5	74.3	138	1	US-08-474-040-85
16	561.5	74.3	138	1	US-08-487-200-85
17	561.5	74.3	138	3	US-08-484-537-85
18	559	73.9	139	1	US-08-137-117D-35
19	559	73.9	139	2	US-08-436-717-35
20	559	73.9	139	2	US-08-116-778E-1
21	559	73.9	139	2	US-08-438-562-1
22	559	73.9	139	2	US-08-483-528B-91
23	557	73.7	137	1	US-08-392-419-2
24	556	73.5	151	3	US-08-513-968-34
25	555.5	73.5	140	3	US-08-836-561-27
26	555.5	73.5	140	4	US-09-434-122-27
27	555	73.4	561	3	US-09-192-545-2

28	552	73.0	137	2	US-08-116-778E-3	Sequence 3, Appli
29	552	73.0	137	2	US-08-438-562-3	Sequence 3, Appli
30	552	73.0	137	2	US-08-483-528B-93	Sequence 93, Appl
31	550	72.8	135	1	US-08-137-117D-27	Sequence 27, Appl
32	550	72.8	135	2	US-08-436-717-27	Sequence 27, Appl
33	548	72.5	137	4	US-09-647-468-153	Sequence 153, App
34	548	72.5	137	4	US-09-647-468-154	Sequence 154, App
35	537.5	71.1	138	1	US-08-458-516-7	Sequence 7, Appli
36	536.5	71.0	136	5	PCT-US93-11611-4	Sequence 4, Appli
37	536	70.9	135	1	US-07-634-278-19	Sequence 19, Appl
38	536	70.9	135	1	US-08-477-728-19	Sequence 19, Appl
39	536	70.9	135	1	US-08-474-040-19	Sequence 19, Appl
40	536	70.9	135	1	US-08-487-200-19	Sequence 19, Appl
41	536	70.9	135	2	US-08-303-569B-31	Sequence 31, Appl
42	536	70.9	135	3	US-08-484-537-19	Sequence 19, Appl
43	534	70.6	233	3	US-08-444-644-33	Sequence 33, Appl
44	534	70.6	233	3	US-08-232-246A-33	Sequence 33, Appl
45	534	70.6	235	3	US-08-444-644-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1  
US-08-253-877C-8  
; Sequence 8, Application US/08253877C  
; Patent No. 5773001  
; GENERAL INFORMATION:  
; APPLICANT: Hamann, Philip R.  
; APPLICANT: Hinman, Lois  
; APPLICANT: Hollander, Irwin  
; APPLICANT: Holcomb, Ryan  
; APPLICANT: Hallett, William  
; APPLICANT: Tsou, Hwei-Ru  
; APPLICANT: Weiss, Martin J.  
; TITLE OF INVENTION: Conjugates of Methylthio Antitumor  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: American Cyanamid Company  
; STREET: One Cyanamid Plaza  
; CITY: Wayne  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07470-8426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/253,877C  
; FILING DATE: 03-JUN-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhard, Elizabeth M.  
; REGISTRATION NUMBER: 31,088  
; REFERENCE/DOCKET NUMBER: 32,368  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-831-3246  
; TELEFAX: 201-831-3305  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 139 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-253-877C-8

Query Match 79.8%; Score 603; DB 1; Length 139;  
Best Local Similarity 80.6%; Pred. No. 1.7e-49;  
Matches 112; Conservative 7; Mismatches 20; Indels 0; Gaps 0;



;; ADDRESSSE: Merchant & Gould  
;; STREET: 90 South 7th Street, 3100 No. 5972656west Ctr.  
;; CITY: Minneapolis  
;; STATE: MN  
;; COUNTRY: USA  
;; ZIP: 55402  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/888,366  
;; FILING DATE: 03-JUL-1997  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/187,407  
;; FILING DATE: 27-JAN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/990,542  
;; FILING DATE: 14-DEC-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/493,299  
;; FILING DATE: 14-MAR-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/324,392  
;; FILING DATE: 14-MAR-1989  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Carter, Charles G.  
;; REGISTRATION NUMBER: 35,093  
;; REFERENCE/DOCKET NUMBER: 8648.39USC1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 612-332-5300  
;; TELEFAX: 612-332-9081  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 116 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
;; US-08-888-366-2

Query Match 77.4%; Score 585; DB 2; Length 116;  
Best Local Similarity 93.3%; Pred. No. 6.7e-48;  
Matches 112; Conservative 1; Mismatches 3; Indels 4; Gaps 1;  
  
Qy 20 QVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKRPGQGLEWIGWIYPGCGGTNY 79  
Db 1 EVLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKRPGQGLEWIGWIYPGCGSTKY 60  
  
Qy 80 NEKFKGKATLTADKSSSTAYMQLSLTSENSAVYFCARGGNFPPSYAMDYWGQGTSTVTVSS 139  
Db 61 NEKFKGKATLTADKSSSTAYMQLSLTSENSAVYFCARGG----YAMDYWGQGTSTVTVSS 116

RESULT 5  
PCT-US93-11612-4  
;; Sequence 4, Application PC/TUS9311612  
;; GENERAL INFORMATION:  
;; APPLICANT: Co, Man Sung  
;; TITLE OF INVENTION: Humanized Antibodies Reactive with  
;; TITLE OF INVENTION: L-Selectin  
;; NUMBER OF SEQUENCES: 12  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend Kourie and Crew  
;; STREET: One Market Plaza, Steuart Tower, Suite 2000  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94105  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US93/11612  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/983,946  
;; FILING DATE: 01-DEC-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Smith, William M.  
;; REGISTRATION NUMBER: 30,223  
;; REFERENCE/DOCKET NUMBER: 11823-22  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-326-2400  
;; TELEFAX: 415-326-2422  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 140 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
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;; PCT-US93-11612-4

Query Match 76.0%; Score 574.5; DB 5; Length 140;  
Best Local Similarity 78.0%; Pred. No. 8.1e-47;  
Matches 110; Conservative 14; Mismatches 14; Indels 3; Gaps 2;  
  
Qy 1 MGFWIFLLSLGTAGVHCVOLOQSGPELVKPGALVKISCKASGYTFTSYDINWVKRKP 60  
Db 1 MENSWIFLLSLGTAGVHSEVLOQSGPDLVKPGASVMSCKASGYTFTSYVMHVKRKP 60  
  
Qy 61 GQGLEWIGWIYPGCGGTNYNEKFKGKATLTADKSSSTAYMQLSLTSENSAVYFCARG-- 118  
Db 61 GQGLEWIGWIYPYNDGTYNEKFKGKATLTADKSSSTAYMQLSLTSENSAVYFCAREY 120  
  
Qy 119 GNFPYAMDYWGQGTSTVTVSS 139  
Db 121 GNVVRY-FDVMGAGTTVTVSS 140

RESULT 6  
US-07-634-278-69  
;; Sequence 69, Application US/07634278  
;; Patent No. 5530101  
;; GENERAL INFORMATION:  
;; APPLICANT: QUEEN, Cary L.  
;; APPLICANT: CO, Man Sung  
;; APPLICANT: SCHNEIDER, William P.  
;; APPLICANT: LANDOLFI, Nicholas F.  
;; APPLICANT: COELINGH, Kathleen L.  
;; APPLICANT: SELICK, Harold E.  
;; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
;; NUMBER OF SEQUENCES: 113  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend Kourie and Crew  
;; STREET: 379 Lytton Avenue  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: US  
;; ZIP: 94301  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/634,278  
;; FILING DATE: 19-DEC-1990  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/590,274  
;; FILING DATE: 28-SEP-1990

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA: US 07/290,975
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-634-278-69

Query Match 75.3%; Score 569; DB 1; Length 135;
Best Local Similarity 77.7%; Pred. No. 2.6e-46;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

QY 1 MGRWIFLLSAGTGVHCVQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKQRP 60
DB 1 MGRWIFLLSAGTGVHCVQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKQSH 60
QY 61 GQGLEWIGWYIPGCGTNTNNEKFKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120
DB 61 GKSLEWIGWYIPYNGGTGYNQKFKATLTVDNSSSTAYMDVRLTSEDSAVYYCARG-- 118
QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --RPAMDYWGQGTSTVTVSS 135

RESULT 7
US-08-477-728-69
; Sequence 69, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
```

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-477-728-69

Query Match 75.3%; Score 569; DB 1; Length 135;
Best Local Similarity 77.7%; Pred. No. 2.6e-46;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

QY 1 MGRWIFLLSAGTGVHCVQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKQRP 60
DB 1 MGRWIFLLSAGTGVHCVQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKQSH 60
QY 61 GQGLEWIGWYIPGCGTNTNNEKFKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120
DB 61 GKSLEWIGWYIPYNGGTGYNQKFKATLTVDNSSSTAYMDVRLTSEDSAVYYCARG-- 118
QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --RPAMDYWGQGTSTVTVSS 135

RESULT 8
US-08-474-040-69
; Sequence 69, Application US/08474040
; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
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; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-484-537-69

Query Match 75.3%; Score 569; DB 3; Length 135;
Best Local Similarity 77.7%; Pred. No. 2.6e-46;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MGWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTDYNHWVKQSH 60

QY 61 GQGLEWIGWITPDGDTGTYNNEKFGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GKSLEWIGWITPDGDTGTYNNEKFGKATLTVDNSSSTAYMQLSSLTSENSAVYFCARG-- 118

QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 119 --RPAMDYWGQGTSTVTVSS 135

RESULT 11
US-09-254-180C-143
; Sequence 143, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
; APPLICANT: OKUMURA, Ko
; APPLICANT: EDA, Yasuyuki
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: USHIO, Yoshitaka
; APPLICANT: HIGUCHI, Hirofumi
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or
; FILE REFERENCE: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US/09/254,180C
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: PCT/JP97/02983
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 271546/1996
; PRIOR FILING DATE: 1996-09-20
; PRIOR APPLICATION NUMBER: 231472/1996
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 143
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-254-180C-143

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Query Match 74.8%; Score 565.5; DB 4; Length 138;
Best Local Similarity 77.0%; Pred. No. 5.6e-46;
Matches 107; Conservative 13; Mismatches 18; Indels 1; Gaps 1;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MEWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWITPDGDTGTYNNEKFGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GKSLEWIGWITPDGDTGTYNNEKFGKATLTVDNSSSTAYMQLSSLTSENSAVYFCARG-- 118

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DB 61 GHGLEWIGLYPGGLYTNNEKFGKATLTADTSSSTAYMQLSSLTSEDSAIYCYARYD 120
QY 121 FPSYAMDYWGQGTSTVTVSS 139
DB 121 Y-DYAMDYWGQGTSTVTVSS 138

RESULT 12
US-08-579-378A-4
; Sequence 4, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: CO, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-579-378A-4

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Query Match 74.8%; Score 565.5; DB 3; Length 140;
Best Local Similarity 76.6%; Pred. No. 5.7e-46;
Matches 108; Conservative 15; Mismatches 15; Indels 3; Gaps 2;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
DB 1 MEWSWIFLLSSTAGVHSEVQLQSGPELVKPGASVKMCKASGYTFTSYVMHWVKQRP 60

QY 61 GQGLEWIGWITPDGDTGTYNNEKFGKATLTADKSSSTAYMQLSSLTSENSAVYFCARG-- 118
DB 61 GQGLEWIGWITPDGDTGTYNNEKFGKATLTADKSSSTAYMQLSSLTSEDSAVYCYAREY 120

QY 119 GNFPYSAMDYWGQGTSTVTVSS 139
DB 119 --RPAMDYWGQGTSTVTVSS 135

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; Patent No. 5693761
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELINGH, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,040
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-474-040-85

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Query Match 74.3%; Score 561.5; DB 1; Length 138;
Best Local Similarity 77.0%; Pred. No. 1.3e-45;
Matches 107; Conservative 12; Mismatches 19; Indels 1; Gaps 1;

Qy 1 MGRWIFLLSCTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKQRP 60
Db 1 MGRWIFLLSCTAGVHCQVQLQSGPELVKPGALVKISKASGYTFTSYDINWVKQSH 60

Qy 61 GQGLEWIGWYIPGDGTYNNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120
Db 61 GQNWLEWIGLINFYNGGTSYNOKEFGKATLTVDKSSNTATWELLSLTSADSANYICTRRG- 119

Qy 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 FRDYSMDYWGQGTSTVTVSS 138

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Job time : 18.3265 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 64.134 Seconds  
(without alignments)  
724.991 Million cell updates/sec

Title: US-10-006-773A-13

Perfect score: 756

Sequence: 1 MGWRWIFLLSGTAGVHCQ.....NPFYAMYDYGQGTSTVTSS 139

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Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	756	100.0	139	13	US-10-006-773-13
2	678.5	89.7	138	8	US-08-779-784-31
3	678.5	89.7	138	14	US-10-010-729-67
4	569	75.3	135	15	US-10-389-155-60
5	569	75.3	135	15	US-10-389-417-60
6	569	75.3	135	15	US-10-452-357-69
7	563.5	74.5	136	14	US-10-138-505-12
8	563.5	74.5	136	15	US-10-257-864A-88
9	563.5	74.5	136	15	US-10-221-131-93
10	563.5	74.5	136	15	US-10-399-518-117
11	561.5	74.3	136	14	US-10-138-505-8
12	561.5	74.3	136	15	US-10-257-864A-86
13	561.5	74.3	136	15	US-10-221-131-91

14	561.5	74.3	136	15	US-10-399-518-115	Sequence 115, Appl
15	561.5	74.3	138	15	US-10-389-155-72	Sequence 72, Appl
16	561.5	74.3	138	15	US-10-389-417-72	Sequence 72, Appl
17	561.5	74.3	138	15	US-10-452-357-85	Sequence 85, Appl
18	558	73.8	118	11	US-09-926-323-2	Sequence 2, Appli
19	555.5	73.5	140	14	US-10-283-349-27	Sequence 27, Appl
20	548	72.5	137	15	US-10-462-062-153	Sequence 153, App
21	548	72.5	137	15	US-10-462-062-154	Sequence 154, App
22	542	71.7	135	14	US-10-244-821-91	Sequence 91, Appl
23	541	71.6	467	17	US-10-500-696-2	Sequence 2, Appli
24	540.5	71.5	438	9	US-09-903-327A-6	Sequence 6, Appli
25	540.5	71.5	456	9	US-09-903-327A-2	Sequence 13, Appl
26	540.5	71.5	493	9	US-09-903-327A-13	Sequence 12, Appl
27	540.5	71.5	510	9	US-09-903-327A-12	Sequence 14, Appl
28	540.5	71.5	597	9	US-09-903-327A-11	Sequence 19, Appl
29	540.5	71.5	613	9	US-10-452-357-19	Sequence 40, Appl
30	540	71.4	135	16	US-10-682-845-40	Sequence 40, Appl
31	538.5	71.2	138	16	US-10-682-845-40	Sequence 40, Appl
32	538.5	71.2	143	14	US-10-010-729-66	Sequence 66, Appl
33	537	71.0	139	17	US-10-687-035-34	Sequence 34, Appl
34	536	70.9	135	15	US-10-389-155-32	Sequence 32, Appl
35	536	70.9	135	15	US-10-389-417-32	Sequence 32, Appl
36	532.5	70.4	138	9	US-09-753-436-78	Sequence 78, Appl
37	532.5	70.4	138	14	US-10-163-942-78	Sequence 7, Appli
38	531.5	70.3	136	16	US-10-768-193-7	Sequence 7, Appli
39	531.5	70.3	468	10	US-09-795-515-7	Sequence 7, Appli
40	531.5	70.3	468	15	US-10-704-352-7	Sequence 7, Appli
41	531.5	70.3	468	15	US-10-704-071-7	Sequence 7, Appli
42	531.5	70.3	468	16	US-10-682-845-38	Sequence 38, Appl
43	529.5	70.0	132	14	US-10-197-080-2	Sequence 2, Appli
44	529.5	70.0	132	17	US-10-484-031-2	Sequence 2, Appli
45	529.5	70.0	140	9	US-09-748-960-4	Sequence 4, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-006-773-13  
; Sequence 13, Application US/10006773  
; Publication No. US20020132983A1  
; GENERAL INFORMATION:  
; APPLICANT: Jughans, Richard P.  
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti  
; FILE REFERENCE: 003  
; CURRENT APPLICATION NUMBER: US/10/006,773  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/250,089  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 139  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-006-773-13

Query Match 100.0%; Score 756; DB 13; Length 139;  
Best Local Similarity 100.0%; Pred. No. 2.5e-59;  
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGWRWIFLLSGTAGVHCQVQLQSGPGLVKKPGALVKISCKASGYTFTSYDINWVKORP	60
Db	1	MGWRWIFLLSGTAGVHCQVQLQSGPGLVKKPGALVKISCKASGYTFTSYDINWVKORP	60
Qy	61	GQGLEWIGWIPYDGGTNYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGCN	120
Db	61	GQGLEWIGWIPYDGGTNYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGCN	120
Qy	121	FPSYAMYDYGQGTSTVTSS	139
Db	121	FPSYAMYDYGQGTSTVTSS	139

RESULT 2  
US-08-779-784-31  
; Sequence 31, Application US/08779784  
; Publication No. US20020164325A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; APPLICANT: Asakura, Kunihiko  
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM  
; TITLE OF INVENTION: REMYLINATION USING MONOCLONAL AUTOANTIBODIES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/779,784  
; FILING DATE: 07-JAN-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/692,084  
; FILING DATE: 08-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/236,520  
; FILING DATE: 29-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 138 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Mus musculus  
US-08-779-784-31

Query Match 89.7%; Score 678.5; DB 8; Length 138;  
Best Local Similarity 92.1%; Pred. No. 1.8e-52;  
Matches 128; Conservative 1; Mismatches 9; Indels 1; Gaps 1;  
QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKRQP 60  
DB 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKRQP 60  
QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120  
DB 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120  
QY 121 FPSYANDYWGQTSVTSS 139  
DB 121 FYWY-FDVWGAGTTVTSS 138

RESULT 3

US-10-010-729-67  
; Sequence 67, Application US/10010729  
; Publication No. US20030185827A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; APPLICANT: Pease, Larry R.  
; TITLE OF INVENTION: Human IGM Antibodies and Diagnostic and  
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous  
; TITLE OF INVENTION: System  
; FILE REFERENCE: 1199-1-005CIP2  
; CURRENT APPLICATION NUMBER: US/10/010,729  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: 09/730,473  
; PRIOR FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: 09/580,787  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: 09/322,862  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 08/779,784  
; PRIOR FILING DATE: 1997-01-07  
; PRIOR APPLICATION NUMBER: 08/692,084  
; PRIOR FILING DATE: 1996-08-08  
; PRIOR APPLICATION NUMBER: 08/236,520  
; PRIOR FILING DATE: 1994-04-29  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 67  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-010-729-67  
Query Match 89.7%; Score 678.5; DB 14; Length 138;  
Best Local Similarity 92.1%; Pred. No. 1.8e-52;  
Matches 128; Conservative 1; Mismatches 9; Indels 1; Gaps 1;  
QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKRQP 60  
DB 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKRQP 60  
QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120  
DB 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120  
QY 121 FPSYANDYWGQTSVTSS 139  
DB 121 FYWY-FDVWGAGTTVTSS 138  
RESULT 4  
US-10-389-155-60  
; Sequence 60, Application US/10389155  
; Publication No. US20030229208A1  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary L.  
; Co, Man Sung  
; Schneider, William P.  
; Landolfi, Nicholas F.  
; Coelingh, Kathleen L.  
; Selick, Harold E.  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/389,417
  FILING DATE: 13-Mar-2003
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/09/325,000
  FILING DATE: 01-JUN-1999
  APPLICATION NUMBER: US 07/290,975
  FILING DATE: 28-DEC-1988
  APPLICATION NUMBER: US 07/310,252
  FILING DATE: 13-FEB-1989
  APPLICATION NUMBER: US 07/590,274
  FILING DATE: 28-SEP-1990
  APPLICATION NUMBER: US 07/634,278
  FILING DATE: 19-DEC-1990
  APPLICATION NUMBER: US 08/484,537
  FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
  NAME: Smith, William M.
  REGISTRATION NUMBER: 30,223
  REFERENCE/DOCKET NUMBER: 011823-002650US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (415) 576-0200
  TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 60:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 135 amino acids
    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:

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US-10-389-417-60
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
Query Match 75.3%; Score 569; DB 15; Length 135;
Best Local Similarity 77.7%; Pred. No. 8.8e-43;
Matches 108; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

QY 1 MGNRWIFLELLSGTAGVHCQVLQSGPGLVPGALVKI SCKASGYTFTSYDINWVKQRP 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MGNRWIFLELLSGTAGVHSEVLQSGPGLVPGASVKI SCKASGYTFTDYNMHVWKQSH 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 61 GGGLEWIGWIYPDGGDTTNYEKFKGKATITADKSSSTAYMQLSSLTSENNAVYFCARGN 120
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 GKSLEWIGWIYPNGGTGYNQFKSKATLTVDNSSSTAIMDKSLTSEDSAVYICARG-- 118
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 121 FFSYAMDYMGQGTSTVTSS 139
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 119 --RPAMDYMGQGTSTVTSS 135
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 6  
US-10-452-357-69  
; Sequence 69, Application US/10452357  
; Publication No. US20040058414A1  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary  
; APPLICANT: Co, Man Sung  
; APPLICANT: Schneider, William  
; APPLICANT: Landolfi, Nicholas  
; APPLICANT: Coelingh, Kathleen  
; APPLICANT: Selick, Harold  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; FILE REFERENCE: 05882.0078.CNUS01  
; CURRENT APPLICATION NUMBER: US/10/452,357  
; CURRENT FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: 09/718,993  
; PRIOR FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: 09/487,200  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 07/634,278





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; PRIOR APPLICATION NUMBER: JP 2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP 2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pGEM-M2H
US-10-221-131-93

Query Match      74.5%; Score 563.5; DB 15; Length 136;
Best Local Similarity 77.0%; Pred. No. 2.7e-42;
Matches 107; Conservative 13; Mismatches 16; Indels 3; Gaps 1;

Qy 1 MGWRWFLFLSLGTAGVHCQVQLQSGPGLVKKPGALVKISKASGYTFTSYDINWVKORP 60
Db 1 MEWSWIFLLSLGTAGVHSGVQLQSGPGLVKKPGASVKMSCKASGYTFANHHVWKQKP 60
Qy 61 GQGLEWIGWYIPDGNGTNYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGN 120
Db 61 GQGLEWIGYIYPYNDGTNYNEKFKDKATLTSDKSSSTAYMDLSSLASDSAVYYCARGG- 119
Qy 121 PPSYAMDYWGQGTSTVTVSS 139
Db 120 --YTYDDWGQGTTLTVSS 136

RESULT 10
US-10-399-518-117
; Sequence 117, Application US/10399518
; Publication No. US20040091475A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OHTOMO, TOSHIOHKO
; APPLICANT: YABUTA, NAOHIRO
; APPLICANT: TSUNODA, HIROYUKI
; APPLICANT: ORITA, TETSURO
; TITLE OF INVENTION: DEGRADED TPO AGONIST ANTIBODY
; FILE REFERENCE: 065678/0111
; CURRENT APPLICATION NUMBER: US/10/399,518
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: PCT/JP01/03288
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: JP 2001-277314
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: JP 2000-321821
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-399-518-117

Query Match      74.5%; Score 563.5; DB 15; Length 136;
Best Local Similarity 77.0%; Pred. No. 2.7e-42;
Matches 107; Conservative 13; Mismatches 16; Indels 3; Gaps 1;

Qy 1 MGWRWFLFLSLGTAGVHCQVQLQSGPGLVKKPGALVKISKASGYTFTSYDINWVKORP 60
Db 1 MEWSWIFLLSLGTAGVHSGVQLQSGPGLVKKPGASVKMSCKASGYTFANHHVWKQKP 60
Qy 61 GQGLEWIGWYIPDGNGTNYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGN 120
Db 61 GQGLEWIGYIYPYNDGTNYNEKFKDKATLTSDKSSSTAYMDLSSLASDSAVYYCARGG- 119
Qy 121 PPSYAMDYWGQGTSTVTVSS 139
Db 120 --YTYDDWGQGTTLTVSS 136

RESULT 11
US-10-138-505-8
; Sequence 8, Application US/10138505
; Publication No. US20030108546A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, Naoshi
; APPLICANT: OH-EDA, Masayoshi
; APPLICANT: KIKUCHI, Yasufumi
; TITLE OF INVENTION: APOPTOSIS-INDUCING SINGLE-CHAIN Fv
; FILE REFERENCE: 065678/0102
; CURRENT APPLICATION NUMBER: US/10/138,505
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/09/523,095
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 11-63557
; PRIOR FILING DATE: 1999-03-10
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-138-505-8

Query Match      74.3%; Score 561.5; DB 14; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

Qy 1 MGWRWFLFLSLGTAGVHCQVQLQSGPGLVKKPGALVKISKASGYTFTSYDINWVKORP 60
Db 1 MEWSWIFLLSLGTAGVHSGVQLQSGPGLVKKPGASVKMSCKASGYTFANHHVWKQKP 60
Qy 61 GQGLEWIGWYIPDGNGTNYNEKFKGKATLTADKSSSTAYMOLSLTSENSAVYFCARGN 120
Db 61 GQGLEWIGYIYPYNDGTNYNEKFKGKATLTSEKSSAAAYMELSLSLASDSAVYYCARGG- 119
Qy 121 PPSYAMDYWGQGTSTVTVSS 139
Db 120 --YTYDDWGQGTTLTVSS 136

RESULT 12
US-10-257-864A-86
; Sequence 86, Application US/10257864A
; Publication No. US20040059393A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, NAOSHI
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OH-EDA, MASAYOSHI
; APPLICANT: UNO, SHINSUKE
; APPLICANT: KIKUCHI, YASUFUMI
; APPLICANT: GOTEMBA-SHI, OHTOMO
; TITLE OF INVENTION: AGONIST ANTIBODIES
; FILE REFERENCE: 065678-0107
; CURRENT APPLICATION NUMBER: US/10/257,864A
; CURRENT FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: PCT/JP01/03288
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: PCT/JP01/01912
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: JP2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP2000-321821
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: JP2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
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; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: amino acid sequence encoded by SEQ ID NO: 6
US-10-257-864A-86

Query Match          74.3%; Score 561.5; DB 15; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEWSWIFLLSSTAGVHSQVQLQSGPDLVPGASVKMSCKASGYTFVNVHWHVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GQGLEWIGWYIPDGGTNNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GQGLEWIGWYIPYNDGTYNEKFKGKATLTSEKSSSAAYMELSSLASEDSAVYFCARGG- 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 --YYSYDDWGQGTTLTVSS 136
   ||:|||||:|||||

RESULT 13
US-10-221-131-91
; Sequence 91, Application US/10221131
; Publication No. US20040073013A1
; GENERAL INFORMATION:
; APPLICANT: FUKUSHIMA, NAOHI
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OH-EDA, MASAYOSHI
; APPLICANT: UNO, SHINSUKE
; APPLICANT: KIKUCHI, YASUFUMI
; TITLE OF INVENTION: POLYPEPTIDE INDUCING APOPTOSIS
; FILE REFERENCE: 065678/0106
; CURRENT APPLICATION NUMBER: US/10/221,131
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: PCT/JP01/01912
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 09/523,095
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: JP 2000-115246
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: JP 2000-321822
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: pGEM-M1H
US-10-221-131-91

Query Match          74.3%; Score 561.5; DB 15; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MEWSWIFLLSSTAGVHSQVQLQSGPDLVPGASVKMSCKASGYTFVNVHWHVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GQGLEWIGWYIPDGGTNNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GQGLEWIGWYIPYNDGTYNEKFKGKATLTSEKSSSAAYMELSSLASEDSAVYFCARGG- 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 --YYSYDDWGQGTTLTVSS 136
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RESULT 14
US-10-399-518-115
; Sequence 115, Application US/10399518
; Publication No. US20040091475A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: YABUTA, NAOHIRO
; APPLICANT: TSUNODA, HIROYUKI
; APPLICANT: ORITA, TETSURO
; TITLE OF INVENTION: DEGRADED TPO AGONIST ANTIBODY
; FILE REFERENCE: 065678/0111
; CURRENT APPLICATION NUMBER: US/10/399,518
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: PCT/JP01/03288
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: JP 2001-277314
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: JP 2000-321821
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 115
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-399-518-115

Query Match          74.3%; Score 561.5; DB 15; Length 136;
Best Local Similarity 75.5%; Pred. No. 4.1e-42;
Matches 105; Conservative 17; Mismatches 14; Indels 3; Gaps 1;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MEWSWIFLLSSTAGVHSQVQLQSGPDLVPGASVKMSCKASGYTFVNVHWHVKQRP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GQGLEWIGWYIPDGGTNNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GQGLEWIGWYIPYNDGTYNEKFKGKATLTSEKSSSAAYMELSSLASEDSAVYFCARGG- 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 FPSYAMDYWGQGTSTVTVSS 139
Db 120 --YYSYDDWGQGTTLTVSS 136
   ||:|||||:|||||

RESULT 15
US-10-389-155-72
; Sequence 72, Application US/10389155
; Publication No. US2003029208A1
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
;               Co, Man Sung
;               Schneider, William P.
;               Landolfi, Nicholas F.
;               Coelingh, Kathleen L.
;               Selick, Harold E.
; TITLE OF INVENTION: Improved Humanized Immunoglobulins
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/389,155
; FILING DATE: 13-Mar-2003
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 19.654 Seconds  
(without alignments)  
680.480 Million cell updates/sec

Title: US-10-006-773A-13  
Perfect score: 756  
Sequence: 1 MGWRWIFLLSGTAGVHCQ.....NFRSYAMDYWGQTSVTSS 139

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	82.3	117	1	HVMSA1
2	613	81.1	469	2	Ig heavy chain pre
3	597.5	79.0	138	2	Ig gamma-2a chain
4	564.5	74.4	140	2	Ig heavy chain v r
5	562.5	74.4	140	1	Ig heavy chain v r
6	560	74.1	139	2	Ig heavy chain pre
7	557.5	73.7	138	2	Ig heavy chain pre
8	547	72.4	474	1	Ig gamma-2b chain
9	544.5	72.0	140	2	Ig heavy chain v r
10	544.5	72.0	246	2	Ig gamma chain - m
11	544.5	72.0	446	2	Ig gamma-2a chain
12	542.5	71.8	140	2	Ig heavy chain v r
13	542.5	71.8	140	2	Ig heavy chain v r
14	539.5	71.4	135	2	Ig heavy chain v r
15	539.5	71.4	135	2	Ig heavy chain v r
16	536.5	71.0	140	2	Ig heavy chain v r
17	536	70.9	139	2	Ig heavy chain pre
18	533	70.5	137	2	Ig heavy chain pre
19	532.5	70.4	140	2	Ig heavy chain v r
20	530.5	70.2	140	2	Ig heavy chain v r
21	529.5	70.0	140	2	Ig heavy chain (my
22	529	70.0	135	2	Ig heavy chain pre
23	526	69.6	139	1	Ig heavy chain pre
24	524.5	69.4	140	2	Ig heavy chain v r
25	524	69.3	140	2	Ig heavy chain pre
26	523	69.2	475	2	Ig gamma-2b chain
27	522.5	69.1	135	2	Ig heavy chain v r
28	522	69.0	141	2	Ig heavy chain pre
29	521	68.9	141	2	Ig heavy chain pre

ALIGNMENTS

RESULT 1

HVMSA1

Ig heavy chain precursor v region (A1/A4) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 09-Jul-2004

C:Accession: A02029

R:Yancopoulos, G.D.; Alt, F.W.

Cell 40, 271-281, 1995

A>Title: Developmentally controlled and tissue-specific expression of unrearranged V-H 9

A:Reference number: A90860; MUID:85099340; PMID:2578321

A:Accession: A02029

A:Molecule type: DNA

A:Residues: 1-117 <YAN>

A:Cross-references: UNIPROT:P06327; GB:M13787; NID:gl96006; PIDN:AAA38499.1; PID:g466291

A>Note: the sequence was determined from the germline gene

C:Superfamily: immunoglobulin v region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain v region (A1/A4) #status predicted <MAT>

F:20-49/Region: framework 1

F:34-117/Domain: immunoglobulin homology <IMM>

F:50-54/Region: complementarity-determining 1

F:55-68/Region: framework 2

F:69-85/Region: complementarity-determining 2

F:86-117/Region: framework 3

F:41-115/Disulfide bonds: #status predicted

Query Match 82.3%; Score 622; DB 1; Length 117;

Best Local Similarity 98.3%; Pred. No. 5.2e-46;

Matches 115; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTTSVDINWKORP 60

Db 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTTSVDINWKORP 60

Qy 61 GQGLEWIGWIYPGGGTNNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCAR 117

Db 61 GQGLEWIGWIYPGGGTNNYNEKFKGKATLTADKSSSTAYMOLSSLTSENSAVYFCAR 117

RESULT 2

S37483

Ig gamma-2a chain - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S37483

R:Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A:Reference number: S37483

A:Accession: S37483

A>Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-469 <DUC>  
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: immunoglobulin  
F;276-345/Domain: immunoglobulin homology <IMM>

Query Match 81.1%; Score 613; DB 2; Length 469;  
Best Local Similarity 80.6%; Pred. No. 1.2e-44;  
Matches 112; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
DB 1 MGMSIFLLSSTAGVHCQVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60  
QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120  
DB 61 GQGLRWIGWYIPASGNTKYNENFKGKATLTVDTSSTAYMQLSSLTSEDTAVYFCARWG 120  
QY 121 FPSYAMDYWGQGTSTVTS 139  
DB 121 ATATLDYWGQGTTLTVSS 139

RESULT 3  
S21810  
Ig heavy chain V region - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999  
C;Accession: S21810  
R;Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.  
submitted to the EMBL Data Library, January 1991  
A;Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy chain  
A;Reference number: S21810  
A;Accession: S21810  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-138 <OST>  
A;Cross-references: EMBL:X56936; NID:g54163; PIDN:CAA40257.1; PID:g54164  
C;Genetics:  
A;Introns: 15/3  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 597.5; DB 2; Length 138;  
Best Local Similarity 83.6%; Pred. No. 7.3e-44;  
Matches 117; Conservative 7; Mismatches 13; Indels 3; Gaps 2;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
DB 1 MGMSIFLLSSTAGVHCQVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60  
QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120  
DB 61 GQGLEWIGWYIPGNVNTKYNENFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAR--N 118

QY 121 FPSYAMDYWGQGTSTVTS 139  
DB 119 YGSSYGLAYWGQTLTVSA 138

RESULT 4  
PH1482  
Ig heavy chain V region (clones 36-35[IG] and X7-TG) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C;Accession: PH1482; PH1495  
R;Giusti, A.M.; Manser, T.  
J. Exp. Med. 177, 797-809, 1993  
A;Title: Hypermutation is observed only in antibody H chain V region transgenes that have a for somatic mutation.  
A;Reference number: PH1482; MUID:93171820; PMID:8436910  
A;Accession: PH1482

A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-140 <GIU>  
A;Experimental source: hybridoma cell  
C;Genetics:  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.7%; Score 564.5; DB 2; Length 140;  
Best Local Similarity 77.6%; Pred. No. 4.7e-41;  
Matches 111; Conservative 10; Mismatches 15; Indels 7; Gaps 2;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
DB 1 MGMSIFLLSSTAGVHCQVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60  
QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 117  
DB 61 GQGLEWIGWYIPNGYTKYNENFKGKATLTVDKSSSTAYMQLSLTSEDSAVYFCARSVY 120

QY 118 -CGNFPYSAMDYWGQGTSTVTS 139  
DB 121 YGG---SYVFDYWGQGTTLTVSS 140

RESULT 5  
HVNMSG7  
Ig heavy chain precursor V region (93G7, 36-65) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 18-Aug-1982 #sequence\_revision 18-Aug-1982 #text\_change 09-Jul-2004  
C;Accession: A94264; A91261; A02028  
R;Sims, J.; Rabbitts, T.H.; Estess, P.; Slaughter, C.; Tucker, P.W.; Capra, J.D.  
Science 216, 309-311, 1982  
A;Title: Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain  
A;Reference number: A94264; MUID:82152818; PMID:6801765  
A;Accession: A94264  
A;Molecule type: mRNA  
A;Residues: 1-140 <SIM>  
A;Cross-references: UNIPROT:P01746; GB:J00493; NID:g195006; PIDN:AAA38128.1; PID:g19500  
A;Experimental source: strain A/J, hybridoma 93G7  
R;Siekevitz, M.; Geffer, M.L.; Brodeur, P.; Riblet, R.; Marshak-Rothstein, A.  
Eur. J. Immunol. 12, 1023-1032, 1982  
A;Title: The genetic basis of antibody production: the dominant anti-arsenate idiotype  
A;Reference number: A91261; MUID:83131846; PMID:6186498  
A;Accession: A91261  
A;Molecule type: DNA  
A;Residues: 20-76, 'TK', 79-118, 'V', 120-125, 'Y', 127-134, 'T', 136-140 <SIE>  
A;Cross-references: GB:M19292; NID:g196201; PIDN:AAA38625.1; PID:g196202  
A;Experimental source: strain A/J, hybridoma 36-65  
A;Note: the sequence was determined from the differentiated gene  
A;Note: from analysis of the sizes of several other differentiated genes that hybridize  
C;Genetics:  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; hybridoma; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-140/Product: Ig heavy chain V region (93G7) #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>  
F;41-115/Disulfide bonds: #status predicted

Query Match 74.4%; Score 562.5; DB 1; Length 140;  
Best Local Similarity 77.6%; Pred. No. 6.9e-41;  
Matches 111; Conservative 9; Mismatches 16; Indels 7; Gaps 2;

QY 1 MGRWIFLLSSTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
DB 1 MGMSIFLLSSTAGVHCQVQLQSGPELVKPGASVKISCKASGYTFTSYDINWVKQRP 60  
QY 61 GQGLEWIGWYIPGDGNTYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 117  
DB 61 GQGLEWIGWYIPNGYTKYNENFKGKATLTVDKSSSTAYMQLSLTSEDSAVYFCARSHY 120

QY 118 -GGNPPSYAMDYWGQGTSTVTSS 139  
 DB 121 YGG---SYDFDYWGQGTSTVTSS 140

RESULT 6  
 A27609  
 Ig heavy chain precursor V region (I29) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 15-Dec-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
 C:Accession: A27609  
 R:Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.  
 J. Immunol. 140, 1676-1684, 1988  
 A:Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch  
 A:Reference number: A27609; MUID:88154467; PMID:3126234  
 A:Accession: A27609  
 A:Molecule type: DNA  
 A:Residues: 1-139 <KLB>  
 A:CROSS-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g553992  
 C:Genetics:  
 A:Introns: 16/1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 560; DB 2; Length 139;  
 Best Local Similarity 77.0%; Pred. No. 1.1e-40;  
 Matches 107; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

QY 1 MGWRWIFLLSGTAGVHCQVQLQSGPELVPKPGALVKISKASGYTFTSYDINWVKQRP 60  
 DB 1 MGWSWIFLLSGTAGVLSEVQLQSGPELVPKPGASVRMSCKASGYTFTDYVHWVKQSN 60

QY 61 CQGLEWIGWIPDGGTNNYNEKFKATLTVDTSSTAYMQLSSLTSSNSAVYFCARGN 120  
 DB 61 GKSLEWIGYINPDYTSYNKFKATLTVDKSSSTAYMQLSSLTSSNSAVYFCARYS 120

QY 121 FPSYAMDYWGQGTSTVTSS 139  
 DB 121 YSYAMDYWGQGTSTVTSS 139

RESULT 7  
 E32513  
 Ig heavy chain precursor V region (WRL22) - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 23-Jul-1999  
 C:Accession: E32513  
 R:Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;  
 J. Clin. Invest. 82, 852-860, 1988  
 A:Title: Immunoglobulin kappa light chain variable region gene complex organization and  
 A:Reference number: A94689; MUID:88331394; PMID:3138286  
 A:Accession: E32513  
 A:Molecule type: DNA  
 A:Residues: 1-138 <KOP>  
 A:CROSS-references: GB:M20835; NID:g196945; PIDN:AAA38847.1; PID:g196946  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.7%; Score 557.5; DB 2; Length 138;  
 Best Local Similarity 78.4%; Pred. No. 1.8e-40;  
 Matches 109; Conservative 7; Mismatches 22; Indels 1; Gaps 1;

QY 1 MGWRWIFLLSGTAGVHCQVQLQSGPELVPKPGALVKISKASGYTFTSYDINWVKQRP 60  
 DB 1 MGWSWIFLLVAATGVHSQVQLQSGPELVPKPGASVKLSCKASGYTFTSYDINWVKQRP 60

QY 61 CQGLEWIGWIPDGGTNNYNEKFKATLTVDKSSSTAYMQLSSLTSSNSAVYFCARGN 120  
 DB 61 GKSLEWIGYINPDYTSYNKFKATLTVDKSSSTAYMQLSSLTSSNSAVYFCARYS 120

Db 61 CQGLEWIGWIPGSSSTNNYNEKFKATLTVDTSSTAYMQLSSLTSSNSAVYFCAR-RL 119

QY 121 FPSYAMDYWGQGTSTVTSS 139  
 DB 120 YRYAMDYWGQGTSTVTSS 138

RESULT 8  
 G2MS11  
 Ig gamma-2b chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C:Accession: S25057; A02157; A26232; A26233; A53598  
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
 submitted to the EMBL Data Library, July 1992  
 A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific  
 A:Reference number: S25057  
 A:Accession: S25057  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-474 <FIS>  
 A:CROSS-references: UNIPROT:P01866; EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827  
 R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
 Nature 283, 786-789, 1980  
 A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from  
 A:Reference number: A02157; MUID:80120716; PMID:6766534  
 A:Contents: a allele  
 A:Accession: A02157  
 A:Molecule type: DNA  
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>  
 A:CROSS-references: GB:J00461  
 A:Note: the sequence was determined from the germline gene  
 R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
 Science 206, 1299-1303, 1979  
 A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea  
 A:Reference number: A26235; MUID:80081501; PMID:117548  
 A:Contents: MPC 11  
 A:Accession: A26235  
 A:Molecule type: mRNA  
 A:Residues: 138-172, 'P', 174-189, 'PP', 193-376, 'T', 378-474 <TUI>  
 A:Note: Lys-474 is probably removed posttranslationally  
 R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
 Science 206, 1303-1306, 1979  
 A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob  
 A:Reference number: A26232; MUID:80081502; PMID:117549  
 A:Accession: A26232  
 A:Molecule type: DNA  
 A:Residues: 138-172, 'P', 174-189, 'PP', 193-376, 'T', 378-474 <TU2>  
 R:Ollo, R.; Rougeon, F.  
 Nature 296, 761-763, 1982  
 A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm  
 A:Reference number: A26233; MUID:82173203; PMID:6803173  
 A:Contents: b allele  
 A:Accession: A26233  
 A:Molecule type: DNA  
 A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLI>  
 A:CROSS-references: GB:J00461  
 R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash  
 J. Biol. Chem. 269, 12345-12350, 1994  
 A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
 A:Reference number: A53598; MUID:94216359; PMID:7512967  
 A:Accession: A53598  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 234-251 <KIM>  
 C:Comment: The a allele sequence is shown.  
 C:Genetics:  
 A:Introns: 138/1; 236/1; 258/1; 368/1  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
 main disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob  
 F:157-222/Domain: immunoglobulin homology <IM1>

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A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match      72.0%; Score 544.5; DB 2; Length 246;
Best Local Similarity 85.8%; Pred. No. 4e-39;
Matches 103; Conservative 5; Mismatches 9; Indels 3; Gaps 1

Qy      20  QVQLQSGPELVKPGALVKISCRASGYTFTSYDINHWVKRPGQGLEWIGTWIPGDSGTTY 79
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1  QIQLQSGPELVKPGASVKISCRASGYTFTDYIHWVKRPGEGLEWIGTWIPGDSGNTKY 60

Qy      80  NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGNFPFAYAMDYWGQGSVTYVSS 139
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61  NEKFKGKATLTDTSSSTAYMQLSSLTSEDSAVYFCARGGKF---AMDYWGQGSVTYVSS 117
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 09-Jul-2004  
C;Accession: S40295  
A;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber,  
R.; Klebert, S. submitted to the EMBL Data Library, January 1993  
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb73595  
A;Reference number: S40295  
A;Accession: S40295  
A;Molecule type: protein  
A;Residues: 1-446 <KLE>  
A;Cross-references: UNIPROT:Q99L25  
C;Genetics:

```

F;341-446/Domain: immunoglobulin homology <IMM>
F;360-427/Domain: pyrrolidone carboxylic acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;237/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 72.0% Score 544.5 DB 2 Length 446;

```

Db 61 NEXFKGKATLTVDTSSTAYMQLSLTSEDSAVYFCARGKF---AMDYMGQGTSVTYSS 117

RESULT 12

PH1486

IG heavy chain V region (clone X7-3D12) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

C:Accession: PH1486

R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993



A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1486

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-140 <GIU>

A:Experimental source: hybridoma cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 542.5; DB 2; Length 140;

Best Local Similarity 76.2%; Pred. No. 3.4e-39;

Matches 109; Conservative 9; Mismatches 18; Indels 7; Gaps 2;

Qy 1 MGWRIFLLSAGTAGVHCVQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGWSFIFLLSVTAGVHSEVLOQSGAELVRAGSSVVMKSCASGYTFTSNGINWVKORP 60

Qy 61 GQGLEWIGWIYPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCAR--- 117

Db 61 GQGLEWIGYINPGNGYINYNKFKGKTLTVDKSSSTAYMQLRSLTSEASAVYFCARSVY 120

Qy 118 -GGNPPSYAMDYWGQGTSTVSS 139

Db 121 YGG---SYFDYWGQGTSLTVSS 140

#### RESULT 13

PH1498

Ig heavy chain V region (clone X7-4G7H) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

A:Accession: PH1498

R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1498

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-140 <GIU>

A:Experimental source: hybridoma cell

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 542.5; DB 2; Length 140;

Best Local Similarity 75.5%; Pred. No. 3.4e-39;

Matches 108; Conservative 10; Mismatches 18; Indels 7; Gaps 2;

Qy 1 MGWRIFLLSAGTAGVHCVQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGWSFIFLLSVTAGVHSEVLOQSGAELVRAGSSVVMKSCASGYTFTSNGINWVKORP 60

Qy 61 GQGLEWIGWIYPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCAR--- 116

Db 61 GQGLEWIGYINPGNGYINYNKFKGKTLTADKSSSTAYMQLRSLTSEASAVYFCARSVY 120

Qy 117 RGNPPSYAMDYWGQGTSTVSS 139

Db 121 YGG---SYFDYWGQGTSLTVSS 140

#### RESULT 14

PH1492

Ig heavy chain V region (clone PH11-4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

C:Accession: PH1492

R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1492

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-135 <GIU>

A:Experimental source: hybridoma cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

F:79/Region: ochre stop codon

Query Match 71.4%; Score 539.5; DB 2; Length 135;

Best Local Similarity 76.8%; Pred. No. 6e-39;

Matches 106; Conservative 10; Mismatches 15; Indels 7; Gaps 2;

Qy 1 MGWRIFLLSAGTAGVHCVQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGWSFIFLLSVTAGVHSEVLOQSGAELVRAGSSVVMKSCASGYTFTSNGINWVKORP 60

Qy 61 GQGLEWIGWIYPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCAR--- 117

Db 61 GQGLEWIGYINPGNGYITKDEKFKGKTLTVDKSSSTAYMQLRSLTSEASAVYFCARSLY 120

Qy 118 -GGNPPSYAMDYWGQGTST 134

Db 121 YGG---SYFDYWGQGT 135

#### RESULT 15

PH1493

Ig heavy chain V region (clone PH14-3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

C:Accession: PH1493

R:Giusti, A.M.; Manser, T.

J. Exp. Med. 177, 797-809, 1993

A:Title: Hypermutation is observed only in antibody H chain V region transgenes that have d for somatic mutation.

A:Reference number: PH1482; MUID:93171820; PMID:8436910

A:Accession: PH1493

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-135 <GIU>

A:Experimental source: hybridoma cell

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.4%; Score 539.5; DB 2; Length 135;

Best Local Similarity 76.1%; Pred. No. 6e-39;

Matches 105; Conservative 11; Mismatches 15; Indels 7; Gaps 2;

Qy 1 MGWRIFLLSAGTAGVHCVQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGWSFIFLLSVTAGVHSEVLOQSGAELVRAGSSVVMKSCASGYTFTSNGINWVKORP 60

Qy 61 GQGLEWIGWIYPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCAR--- 117

Db 61 GQGLEWIGYINPGNGFTKYNEKFKGKTLTVDKSSSTAYMQLRSLTSEASAVYFCARSVY 120

Qy 118 -GGNPPSYAMDYWGQGTST 134

Db 121 YGG---SYFDYWGQGT 135

Search completed: May 25, 2005, 16:48:40

Job time : 20.654 secs



ID Q9DBL4; PRELIMINARY; PRT; 473 AA.  
AC Q9DBL4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched  
DE library, clone:181060009 product:immunoglobulin heavy chain 6 (heavy  
DE chain of IgM), full insert sequence.  
GN Name=Igh-1a;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning."  
RL Meth. Enzymol. 303:19-44(1999).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
[3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RA The FANTOM Consortium;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
[4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).  
[5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer."  
RL Genome Res. 10:1757-1771(2000).  
[6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Pancreas;  
RX STRAIN=C57BL/6J; TISSUE=Pancreas;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK007918; BAB25349.1; -.  
DR PIR; PH1165; PH1165.  
DR PIR; S19966; S19966.  
DR PIR; S26746; S26746.  
DR HSSP; P01864; 1BQG.  
DR MGI; MGI:96443; Igh-1a.  
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.  
DR GO; GO:0005771; C:multivesicular body; IDA.  
DR GO; GO:0003823; P:antigen binding; IDA.  
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.  
DR GO; GO:0030333; P:antigen processing; IDA.  
DR GO; GO:0006958; P:complement activation; IDA.  
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.  
DR GO; GO:0008333; P:endosome to lysosome transport; IDA.  
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.  
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.  
DR GO; GO:0050871; P:positive regulation of B-cell activation; IDA.  
DR GO; GO:0050778; P:positive regulation of immune response; IDA.  
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.  
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.  
DR GO; GO:0001798; P:positive regulation of type II hypersensitivity; IDA.  
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG\_C1.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_V.  
DR Pfam; PF07654; C1-set; 3.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS00835; IG-LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 1.  
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;  
Query Match 76.5%; Score 578.5; DB 2; Length 473;  
Best Local Similarity 81.0%; Pred. No. 4.5e-49;  
Matches 115; Conservative 4; Mismatches 16; Indels 7; Gaps 2;  
Qy 1 MGWRWIFLLSLGSGTAGVHCQVQLQSGPGLVPLKPKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 60  
Db 1 MEWSWVFLSLVSTAGVHCQVQLQSGAELVKPKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 60  
Qy 61 GQGLEWIGWYVGGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120  
Db 61 GQGLEWIGKIPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 119  
Qy 121 FPSYAMD---YWGQSTVTVSS 139  
Db 120 ---YDWFAYWGQGLTVTVSA 138  
RESULT 5  
Q6PF95 PRELIMINARY; PRT; 464 AA.  
AC Q6PF95;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C2EHC II; TISSUE=Mammary tumor;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II, TISSUE=Mammary tumor;  
RA Strausberg R.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC057672; AAH57672.1; -;  
DR HSSP; P01865; 1KB5.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-CL.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; Cl-set; 3.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 3.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00395; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 464 AA; 51096 MW; 5B837464D8A1888 CRC64;  
  
Query Match 74.7%; Score 564.5; DB 2; Length 464;  
Best Local Similarity 78.4%; Pred. No. 1.1e-47;  
Matches 109; Conservative 8; Mismatches 17; Indels 5; Gaps 1;  
  
QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
DB 1 MGWSVFLFLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRS 60  
  
QY 61 GQGLEWIGWIPYDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120  
DB 61 GQGLEWIGWIPYDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 118  
  
QY 121 FPSYANDYWGQTSVTSS 139  
DB 119 ---YDALYWGQTSVTSS 134  
  
RESULT 6  
HV02\_MOUSE STANDARD; PRT; 140 AA.  
AC P01746;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Ig heavy chain V region 93G7 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/J;  
RX MEDLINE=82152818; PubMed=6801765;  
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,  
RA Capra J.D.;  
RT "Somatic mutation in genes for the variable portion of the  
RT immunoglobulin heavy chain.";  
RL Science 216:309-311(1982).  
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC -----  
DR EMBL; J00493; AAA38128.1; -;  
DR PIR; A94264; HVMSG7.  
DR HSSP; P01747; 1JFQ.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00395; IG\_LIKE; 1.  
KW Hybridoma; Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 140 Ig heavy chain V region 93G7.  
FT DOMAIN 20 139 Ig-like.  
FT NON\_TER 140 140  
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;  
  
Query Match 74.4%; Score 562.5; DB 1; Length 140;  
Best Local Similarity 77.6%; Pred. No. 4.5e-48;  
Matches 111; Conservative 9; Mismatches 16; Indels 7; Gaps 2;  
  
QY 1 MGRWIFLLSGTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
DB 1 MGWSFIFLLSVTAGVHSEVQLQSGAELVRSVSKMSCKASGYTFTSYGINWVKQRP 60  
  
QY 61 GQGLEWIGWIPYDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCAR--- 117  
DB 61 GQGLEWIGWIPYDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARSHY 120  
  
QY 118 -GQNFPSYANDYWGQTSVTSS 139  
DB 121 YGG---SYDFDYWGQTSVTSS 140  
  
RESULT 7  
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ID Q7TWT6  
AC Q7TWT6;  
DT 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE MGC60843 protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;

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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 67.7544 Seconds  
(without alignments)  
1050.544 Million cell updates/sec

Title: US-10-006-773A-13  
Perfect score: 756  
Sequence: 1 MGWRWIFLFLSLGTVAGVHCQ.....NFPSYAMDYWGQTSVTVSS 139

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630.5	83.4	481	Q91WT1	Q91wt1 mus musculus
2	625.5	82.7	480	Q8K0Z4	Q8k0z4 mus musculus
3	622	82.3	117	HV52 MOUSE	P06327 mus musculus
4	578.5	76.5	473	Q9D8L4	Q9d8l4 mus musculus
5	564.5	74.7	464	Q6PF95	Q6pf95 mus musculus
6	562.5	74.4	140	HV02 MOUSE	P01746 mus musculus
7	555.5	73.5	614	Q7TMT6	Q7tmt6 mus musculus
8	555	73.4	465	Q6PJB2	Q6pjb2 mus musculus
9	549	72.6	463	Q99LC4	Q99lc4 mus musculus
10	542	71.7	488	Q91WR1	Q91wr1 mus musculus
11	541.5	71.6	472	Q6PJ7	Q6pja7 mus musculus
12	540	71.4	613	Q8VCX7	Q8vcx7 mus musculus
13	538	71.2	482	Q8K172	Q8k172 mus musculus
14	529.5	70.0	168	Q8VDC9	Q8vdc9 mus musculus
15	526	69.6	139	HV07 MOUSE	P01751 mus musculus
16	525.5	69.5	470	Q7TMK1	Q7tmk1 mus musculus
17	516.5	68.3	489	Q8VCX4	Q8vcx4 mus musculus
18	514	68.0	488	Q8K0F2	Q8k0f2 mus musculus
19	509	67.3	117	HV14 MOUSE	P01758 mus musculus
20	501	66.3	487	Q65ZL2	Q65zl2 mus sp. fv/
21	497.5	65.8	142	Q924Q1	Q924q1 mus musculus
22	496	65.6	137	HV11 MOUSE	P01755 mus musculus
23	494.5	65.4	138	HV48 MOUSE	P03980 mus musculus
24	494.5	65.4	474	Q8R3H6	Q8r3h6 mus musculus
25	492	65.1	145	Q924R1	Q924r1 mus musculus
26	492	65.1	145	Q924R4	Q924r4 mus musculus
27	490	64.8	145	Q924Q6	Q924q6 mus musculus
28	490	64.8	481	Q8VCV5	Q8vcv5 mus musculus
29	489.5	64.7	146	Q924Q3	Q924q3 mus musculus
30	489	64.7	145	Q924Q9	Q924q9 mus musculus
31	487	64.4	143	Q924R0	Q924r0 mus musculus

32	487	64.4	145	2	Q924P7	Q924p7 mus musculus
33	486.5	64.4	147	2	Q925S3	Q925s3 mus musculus
34	485.5	64.2	120	1	HV03 MOUSE	P01747 mus musculus
35	483	63.9	143	2	Q924Q0	Q924q0 mus musculus
36	480	63.5	117	1	HV04 MOUSE	P01748 mus musculus
37	478.5	63.3	140	2	Q924E2	Q924e2 mus musculus
38	475.5	62.9	117	2	Q9QXE9	Q9qxe9 mus musculus
39	475	62.8	117	1	HV06 MOUSE	P01750 mus musculus
40	474.5	62.8	134	2	Q65ZR6	Q65zr6 mus musculus
41	474	62.7	145	2	Q924Q7	Q924q7 mus musculus
42	472.5	62.5	140	2	Q924P8	Q924p8 mus musculus
43	469	62.0	117	1	HV05 MOUSE	P01749 mus musculus
44	468.5	62.0	146	2	Q924R8	Q924r8 mus musculus
45	465	61.5	111	2	Q9D9B8	Q9d9b8 mus musculus

ALIGNMENTS

RESULT 1

Q91WT1 PRELIMINARY; PRT; 481 AA.  
AC Q91WT1;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Igh-VJ558 protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RX MEDLINE=2338257; PubMed=1247732; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T.I., Wang J., Hsieh F.,  
Datchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,  
Diaple M., Soares M.B., Bonaldo A.F., Casavant T.L., Schetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Kryzwicki M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
SEQUENCE FROM N.A.  
STRAIN=FVB/N; TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC013490; AAH13490.1; -.  
DR HSSP; P01751; 1A6W.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS00835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
SQ SEQUENCE 481 AA; 52105 MW; 97DF68D159463F65 CRC64;

Query Match 83.4%; Score 630.5; DB 2; Length 481;

Best Local Similarity 85.6%; Pred. No. 3e-54; Mismatches 12; Indels 3; Gaps 1;

Matches 119; Conservative 5; Mismatches 5; Indels 3; Gaps 1;

Oy 1 MGWRWIFLFLSLGTVAGVHCQVQLQQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60

Db 1 MGRWIFLLSAGTGVQVQLQSGPELVKPGASVKISCKASGVTFTSYIHWKQRP 60  
QY 61 GQGLEWIGWIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFCARGN 120  
Db 61 GQGLVWIGWIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFCARGG- 119

QY 121 FPSYAMDYWGQGTSTVTVSS 139  
Db 120 --GAFDYWGQGTSTVTVSS 136

## RESULT 2

Q8K0Z4 PRELIMINARY; PRT; 480 AA.  
ID Q8K0Z4  
AC Q8K0Z4  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DE Hypothetical protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Hennessy C.F., Bhat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzaniak M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]

RP SEQUENCE FROM N.A.  
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;  
RA Strausberg R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
RE EMBL; BC029188; AAH29188.1; -

DR HSP; P01820; IG7J.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 480 AA; 51645 MW; 8690A63C6C9CDBED CRC64;

Query Match 82.7%; Score 625.5; DB 2; Length 480;  
Best Local Similarity 84.4%; Pred. No. 9.4e-54;  
Matches 119; Conservative 6; Mismatches 9; Indels 7; Gaps 2;

QY 1 MGRWIFLLSAGTGVQVQLQSGPELVKPGALVKISCKASGVTFTSYDINWVKQRP 60  
Db 1 MGRWIFLLSAGTGVQVQLQSGPELVKPGALVKISCKASGVTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFCARG-- 118  
Db 61 GQGPWIGWIPDGSSEYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFCARSKL 120  
QY 119 GNFPYSAMDYWGQGTSTVTVSS 139  
Db 121 GGFA-----YWGQGTSTVTVSA 136

## RESULT 3

HV52\_MOUSE  
ID HV52\_MOUSE STANDARD; PRT; 117 AA.  
AC P06327;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V region VH58 A1/A4 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=8509340; PubMed=2578321; DOI=10.1016/0092-8674(85)90141-2;  
RA Yancopoulos G.D.; Alt F.W.;  
RT "developmentally controlled and tissue-specific expression of  
unrearranged VH gene segments.";  
RL Cell 40:271-281(1985).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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the European Bioinformatics Institute. There are no restrictions on its  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC EMBL; M13787; AAA38499.1; -

DR FIR; A02029; HVMSAL.  
DR HSP; P01820; IG7J.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19  
FT CHAIN 20 117 Ig heavy chain V region VH58 A1/A4.  
FT DOMAIN 20 49 Framework-1.  
FT DOMAIN 50 54 Complementarity-determining-1.  
FT DOMAIN 55 68 Framework-2.  
FT DOMAIN 69 85 Complementarity-determining-2.  
FT DOMAIN 86 117 Framework-3.  
FT DISULFID 41 115 By similarity.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 82.3%; Score 622; DB 1; Length 117;  
Best Local Similarity 98.3%; Pred. No. 4.3e-54;  
Matches 115; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGRWIFLLSAGTGVQVQLQSGPELVKPGALVKISCKASGVTFTSYDINWVKQRP 60  
Db 1 MGRWIFLLSAGTGVQVQLQSGPELVKPGALVKISCKASGVTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFCAR 117  
Db 61 GQGLEWIGWIPDGSSTKYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFCAR 117

## RESULT 4

Q9D8L4

```
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAHS3409.1; -.
DR HSSP; P01820; IG7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;

Query Match 73.5%; Score 555.5; DB 2; Length 614;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
Matches 111; Conservative 6; Mismatches 21; Indels 1; Gaps 1;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPGLVKPGALVKISKASGYTFTSYDINWVKQRP 60
DB 1 MEWPCIFLLSIVTEGVHSQVLOQSGPGLVKPGASVKISKASGYAFSSMMWVKQRP 60

QY 61 GQGLEWIGWYVPGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GNGLEWIGRVPGDGTNYNGFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARDY 120

QY 121 FPSYANDYWGQGTSTVTVSS 139
DB 121 -SSRYFAWYWGQGLTVVSA 138

RESULT 8
Q6PJB2 PRELIMINARY; PRT; 465 AA.
AC Q6PJB2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

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RP SEQUENCE FROM N.A.
RC STRAIN=Czech II; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018280; AAH18280.1; -.
DR HSSP; P01865; 1KB5.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 3.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51329 MW; 394F43C4E8DB3E21 CRC64;

Query Match 73.4%; Score 555; DB 2; Length 465;
Best Local Similarity 76.3%; Pred. No. 9.7e-47;
Matches 106; Conservative 12; Mismatches 17; Indels 4; Gaps 1;

QY 1 MGWRWIFLLSGTAGVHCQVLOQSGPGLVKPGALVKISKASGYTFTSYDINWVKQRP 60
DB 1 MGCVWFLLSIVTEGVHSQVLOQSGPGLVKPGASVKISKASGYTFTSYDINWVKQRP 60

QY 61 GQGLEWIGWYVPGDGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120
DB 61 GQGLEWIGYFSPYNDTKCKEKFATLTADKSSSTAYMQLSSLTSENSAVYFCARGN 120

QY 121 FPSYANDYWGQGTSTVTVSS 139
DB 119 -YVFDYWGQGTITVSS 135

RESULT 9
Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-4 protein.
GN Name=Igh-4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

```

RT and mouse cDNA sequences." ;
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR FJF; B45837; B45837.
DR HSP; P01869; ICL7.
DR MGD; MGI:96446; Igh-4.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0019733; P:antibacterial humoral response (sensu Verte. .; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type I hypersensit. .; IDA.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003597; Igh cl.
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003596; Igh-V.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 463 AA; 51007 MW; EA674C6BBC30783 CRC64;

Query Match 72.6%; Score 549; DB 2; Length 463;
Best Local Similarity 74.1%; Pred. No. 3.8e-46;
Matches 103; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGRWIFLLSLGTAGVHCOVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKORP 60
DB 1 MEWIFLLSLGTAGVHCOVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKORP 60

QY 61 GQGLEWIGWIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
DB 61 GQGLEWIGWIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120

QY 121 FPSYANDYWGQSTVTSS 139
DB 121 YSYDLFAYWGQSTVTSSA 139

RESULT 10
Q91WR1 ID Q91WR1 PRELIMINARY; PRT; 488 AA.
AC Q91WR1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Hale S., Garcia A.M., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

and mouse cDNA sequences." ;
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) .
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR FJF; B45837; B45837.
DR HSP; P01869; ICL7.
DR MGD; MGI:96446; Igh-4.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0019733; P:antibacterial humoral response (sensu Verte. .; IDA.
DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
DR GO; GO:0042830; P:defense response to pathogenic bacteria; IDA.
DR GO; GO:0006911; P:phagocytosis, engulfment; IDA.
DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
DR GO; GO:0050778; P:positive regulation of immune response; IDA.
DR GO; GO:0050766; P:positive regulation of phagocytosis; IDA.
DR GO; GO:0001812; P:positive regulation of type I hypersensitivity; IDA.
DR GO; GO:0001798; P:positive regulation of type I hypersensit. .; IDA.
DR InterPro; IPR007110; Igh-like.
DR InterPro; IPR003597; Igh cl.
DR InterPro; IPR003006; Igh_MHC.
DR InterPro; IPR003596; Igh-V.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 463 AA; 51007 MW; EA674C6BBC30783 CRC64;

Query Match 72.6%; Score 549; DB 2; Length 463;
Best Local Similarity 74.1%; Pred. No. 3.8e-46;
Matches 103; Conservative 11; Mismatches 25; Indels 0; Gaps 0;

QY 1 MGRWIFLLSLGTAGVHCOVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKORP 60
DB 1 MEWIFLLSLGTAGVHCOVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKORP 60

QY 61 GQGLEWIGWIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120
DB 61 GQGLEWIGWIPDGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSSENSAVYFCARGGN 120

QY 121 FPSYANDYWGQSTVTSS 139
DB 121 YSYDLFAYWGQSTVTSSA 139

RESULT 10
Q91WR1 ID Q91WR1 PRELIMINARY; PRT; 488 AA.
AC Q91WR1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Hale S., Garcia A.M., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
DR EMBL; BC018535; AAH18535.1; -
DR HSSP; P01865; IKBS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_Y.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 52299 MW; 165169C23D5D4B CRC64;

Query Match 71.6%; Score 541.5; DB 2; Length 472;
Best Local Similarity 73.2%; Pred. No. 2.2e-45;
Matches 104; Conservative 16; Mismatches 19; Indels 3; Gaps 2;

QY 1 MGWRIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60
D 1 MGWSIFLLSGTAGVLSVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKQSH 60
QY 61 GQGLEWIGWIYPGDGTYNEKFKGKATLTADKSSSTAYMQLSSITSENSAVYFCARGG- 119
D 61 GKSLEWIGWIYPNGGNGYQKFKGKATLTVDKSSSTAYMELRLSITSDSAVYVCARGY 120
QY 120 NPPSY--AMDYWGQGTSTVTVSS 139
D 121 SYISYDHYFDYWGQGTITTVSS 142

RESULT 12
Q8VCX7 PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
DR EMBL; BC018315; AAH18315.1; -
DR PIR; C30562; C30562.
DR HSSP; P01751; 1A6W.
DR MGD; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B-cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0050871; P:positive regulation of B-cell activation; IDA.
DR GO; GO:0030890; P:positive regulation of B-cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 71.4%; Score 540; DB 2; Length 613;
Best Local Similarity 75.5%; Pred. No. 4.1e-45;
Matches 105; Conservative 9; Mismatches 23; Indels 2; Gaps 1;

QY 1 MGWRIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60
D 1 MEWTWVFLLSVTAGVHSQVLOQSGALNKPASVKISKATGYTFTSSWIEWVKORP 60
QY 61 GQGLEWIGWIYPGDGTYNEKFKGKATLTADKSSSTAYMQLSSITSENSAVYFCARGN 120
D 61 GHGLEWIGEILPGSGSTNYNEKFKGKATFTADTSSNTAYMQLSSITSDSAVYVCAR--R 118
QY 121 FPSYAMDYWGQGTSTVTVSS 139
D 119 LGRWYFDYWGAGTTTVTVSS 137

RESULT 13
Q8K172 PRELIMINARY; PRT; 482 AA.
AC Q8K172;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein.
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

```

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC028249; AH28249.1; -;  
 DR PIR; F33932; F33932.  
 DR PIR; PH1105; PH1105.  
 DR PIR; PH1108; PH1108.  
 DR PIR; PH1114; PH1114.  
 DR PIR; PH1118; PH1118.  
 DR PIR; PH1119; PH1119.  
 DR PIR; PH1125; PH1125.  
 DR PIR; PH1126; PH1126.  
 DR PIR; PH1128; PH1128.  
 DR PIR; PH1131; PH1131.  
 DR PIR; PH1134; PH1134.  
 DR PIR; PH1139; PH1139.  
 DR PIR; PH1142; PH1142.  
 DR PIR; PH1149; PH1149.  
 DR PIR; PH1150; PH1150.  
 DR PIR; PH1151; PH1151.  
 DR PIR; PH1152; PH1152.  
 DR PIR; PH1153; PH1153.  
 DR HSSP; P01751; 1A6W.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig cl.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; Cl-set; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
 SQ SEQUENCE 482 AA; 52121 MW; A06FF083E771D084 CRC64;  
 Query Match 71.2%; Score 538; DB 2; Length 482;  
 Best Local Similarity 75.5%; Pred. No. 5e-45;  
 Matches 105; Conservative 9; Mismatches 23; Indels 2; Gaps 1;  
 QY 1 MGRWIFLLSCTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
 DB 1 MGRSCIMFLFAATATGVSQVQLQSGPELVKPGASVKLSCKASGYTFTSYDINWVKQRP 60  
 QY 61 GQGLEWIGWYFGDGGTNNYNEKFKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120  
 DB 61 GRGLEWIGRIDPNSGGTKYNEKFKATLTVDPSSTAYMQLSSLTSEDSAVYCYTRGD 120  
 QY 121 FPSYAMDYWGQGTSTVTVSS 139  
 DB 121 YD-AMDYWGQGTSTVTVSS 137  
 RESULT 14  
 Q8VDC9 PRELIMINARY; PRT; 168 AA.  
 AC Q8VDC9;  
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
 DE Anti-MOG Z12 variable gamma 2a (Fragment).  
 GN Name-IgG2a;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]\_TaxID=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Semb P.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Chernaiovsky Y.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ416332; CAC94867.1; -;  
 DR HSSP; P01863; 1E4W.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON TER 168 168  
 SQ SEQUENCE 168 AA; 18293 MW; 1E3719FCC0E72723 CRC64;  
 Query Match 70.0%; Score 529.5; DB 2; Length 168;  
 Best Local Similarity 74.1%; Pred. No. 1.1e-44;  
 Matches 103; Conservative 11; Mismatches 24; Indels 1; Gaps 1;  
 QY 1 MGRWIFLLSCTAGVHCQVQLQSGPELVKPGALVKISCKASGYTFTSYDINWVKQRP 60  
 DB 1 MEWTVFLLSVLTAGVHSQVQLQSGPELVKPGASVKISCKATGTFSSYDINWVKQRP 60  
 QY 61 GQGLEWIGWYFGDGGTNNYNEKFKATLTADKSSSTAYMQLSSLTSENSAVYFCARGGN 120  
 DB 61 GHGLEWIGELIPSGRTNNEKFKGKTTFTADTSSNTAYIQFSSLTSEDSAVYCYCNGS 120  
 QY 121 FPSYAMDYWGQGTSTVTVSS 139  
 DB 121 SRWY-FDVMGAGTTVTVSS 138  
 RESULT 15  
 HV07\_MOUSE STANDARD; PRT; 139 AA.  
 AC P01751; P01752;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Ig heavy chain V region B1-8/186-2 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;  
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPb family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 CC Cell 24:623-637(1981).  
 CC -!- MISCELLANEOUS: The B1-8 mu chain mRNA was cloned from a hybridoma  
 CC making antibodies to the haptens (4-hydroxy-3-nitrophenyl)acetyl  
 CC (NPb antibodies).  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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or send an email to license@isb-sib.ch).

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CC -----
DR EMBL; J00529; AAA38170.1; -.
DR PIR; A90809; MHMS18.
DR PDB; 1A6U; X-ray; H=20-139.
DR PDB; 1A6V; X-ray; H/I/J=20-139.
DR PDB; 1A6W; X-ray; H=20-139.
DR PDB; 1NQB; X-ray; A/C=20-139.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW 3D-structure; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 124
FT DOMAIN 125 139
FT DISULFID 41 115
FT STRAND 22 24
FT STRAND 28 31
FT TURN 33 34
FT STRAND 37 44
FT HELIX 48 50
FT STRAND 52 58
FT TURN 60 61
FT STRAND 64 70
FT TURN 72 74
FT STRAND 77 79
FT HELIX 81 83
FT TURN 84 86
FT STRAND 87 92
FT TURN 93 96
FT STRAND 97 102
FT HELIX 107 109
FT STRAND 111 118
FT TURN 120 123
FT STRAND 129 129
FT STRAND 133 137
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match 69.6%; Score 526; DB 1; Length 139;
Best Local Similarity 73.4%; Pred. No. 1.9e-44;
Matches 102; Conservative 10; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MGWRWIFLLSGTAGVHCQVLOQSGPELVKPGALVKISKASGYTFTSYDINWVKORP 60
Db ||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 MGWSCIMLFLLATATGVHSQVLOQPGAEVLKPGASVKLSKASGYTFTSYMHWVKORP 60

Qy 61 GQGLEWIGWYPGDGTNNYNEKFKGKATLTADKSSSTAYMOLSSLTSSENSAVYFCARGN 120
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 GRGLEWIGRIDPNSGGTYNEKFKSKATLTVDKPSSTAYMQLSSLTSSEDSAVYVCARYDY 120

Qy 121 FPSYAMDYWGQGTSTVTS 139
Db : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 YGSSYFDYWGQGTTLTVSS 139
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Search completed: May 25, 2005, 15:56:06  
Job time : 68.7544 secs



GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 62.1321 Seconds  
(without alignments)  
821.675 Million cell updates/sec

Title: US-10-006-773A-15

Perfect score: 686

Sequence: 1 MKLPVRLVLVFWIPASNSD.....FQSHVPYAFGGTGKLEIKR 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	686	100.0	132	6	ABG74246 Mouse ant
2	646	94.2	131	2	AAR52772 Murine KC
3	646	94.2	131	2	AAR52790 Murine KC
4	646	94.2	131	2	AAR70457 VL sequen
5	645	94.0	238	2	AAY17416 Mouse imm
6	644	93.9	131	6	ABP72116 Mouse FGF
7	644	93.9	131	7	ADD28184 Mouse lec
8	644	93.9	131	7	ADE36480 Mouse lec
9	644	93.9	131	7	ADL35318 Murine an
10	639	93.1	149	2	AAR03199 Anti-idi
11	639	93.1	149	2	AAY21545 Monoclon
12	638	93.0	132	8	ADH17810 Murine an
13	637	92.9	131	2	AAR31587 BR55-2 li
14	637	92.9	131	2	AAR32241 Chimeric
15	637	92.9	131	7	AAY42958 Mouse 12B
16	637	92.9	131	7	AAY42968 Chimeric
17	637	92.9	139	7	ABR82782 Hybridoma
18	637	92.9	139	7	ABR82892 Hybridoma
19	635	92.6	149	2	AAY49209 MAB 1A7 1
20	635	92.6	149	2	AAY28468 Light cha
21	635	92.6	149	6	ADA14768 Mouse ant
22	635	92.6	149	7	ADC35310 Monoclon
23	633	92.3	149	8	ADL27486 Amino aci
24	631	92.0	131	2	AAR32245 BR55-2 mu
25	631	92.0	238	2	AAW14937 Murine an

## ALIGNMENTS

### RESULT 1

ABG74246

ID ABG74246 standard; protein; 132 AA.

XX AC ABG74246;

DT 22-APR-2003 (first entry)

DE Mouse antibody 4D4 light chain variable region.

XX T-cell receptor; cytostatic; dermatological; neuroprotective;

KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;

KW 3E11; prostate-specific membrane antigen; zeta signalling chain;

KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;

XX small cell lung cancer; light chain variable region; mouse.

OS Mus sp.

XX US2002132983-A1.

PN 19-SEP-2002.

PD 10-DEC-2001; 2001US-00006773.

XX 30-NOV-2000; 2000US-0250087P.

XX 30-NOV-2000; 2000US-0250089P.

XX (JUNG/) JUNGHANS R P.

XX Junghans RP;

XX WPI; 2003-208946/20.

XX N-PSDB; ABX16572.

XX New chimeric molecule useful in treating patients with disorders, such as melanoma, neuroendocrine disorders, prostate and small cell lung cancer comprises GD3 and/or PSMA binding domains of antibody.

XX Disclosure; Page 15-16; 35pp; English.

XX The invention relates to a chimaeric molecule comprising the GD3 (ganglioside antigen) binding domain of antibody MB3.6, with any of 3

XX variable gene sequences, or the PSMA (prostate-specific membrane antigen) binding domain of antibody 3D8, 4D4 and 3E11, with variable gene

XX sequences, the zeta signalling chain of the T cell receptor and an intervening CD8alpha hinge in which cysteine residues have been mutated.

XX The chimaeric molecules expressed in T cells or NK cells or other effector cells are useful in treating patients with cancers expressing

26	631	92.0	238	2	AAW14942	Aaw14942 3F4 Human
27	630	91.8	132	2	AAW60867	Aaw60867 Variable
28	630	91.8	132	3	AAAY80294	Aay80294 IgM chime
29	630	91.8	144	8	ADM33981	Adm33981 Anti-Nogo
30	630	91.8	238	2	AAW31752	Aaw31752 L chain s
31	630	91.8	238	2	AAW71889	Aaw71889 Anti-huma
32	630	91.8	238	3	AAAB12909	Aab12909 Anti-huma
33	627	91.4	144	8	ADM33982	Adm33982 Anti-Nogo
34	625	91.1	132	4	AAAG67666	Aag67666 Amino aci
35	625	91.1	132	6	ABR40285	AbR40285 Murine am
36	625	91.1	238	6	ABP58288	Abp58288 Humanised
37	624	91.0	131	2	AAR52822	Aar52822 Humanised
38	624	91.0	131	2	AAR70470	Aar70470 Humanised
39	624	91.0	131	5	ABG76933	Abg76933 Mouse 10D
40	624	91.0	131	8	ADR88418	Adr88418 Murine 10
41	623	90.8	140	2	AAW68492	Aaw68492 Variable
42	620	90.4	131	7	ADE36531	Ade36531 Anti-FGF-
43	617	89.9	131	3	AAAB23812	Aab23812 Plasmid p
44	617	89.9	131	4	AAAG67488	Aag67488 Amino aci
45	617	89.9	131	5	AAW47626	Aaw47626 Murine MA

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),  
CC and/or together with each other or with heterologous constructs to engage  
CC additional stimulatory and functional properties of the effector cells to  
CC enhance the antitumour therapeutic efficacy (claimed). They are  
CC particularly useful in disorders including melanoma, neuroendocrine  
CC tumours and prostate and small cell lung cancer. The present sequence  
CC represents the mouse antibody 4D4 light chain variable region  
XX  
SQ Sequence 132 AA;

RESULT 2	
AARS2772	
ID	AARS2772 standard; protein; 131 AA.
XX	
XX	AARS2772;
XX	
DT	25-MAR-2003 (revised)
DT	24-JAN-1995 (first entry)
XX	
DE	Murine KC-4 immunoglobulin light chain variable region (deduced).
XX	
KW	Immunoglobulin variable domain; primer; polymerase chain reaction
KW	chimeric antibody; human milk fat globule; human breast carcinoma
KW	murine anti-human carcinoma monoclonal antibody KC-4

```

-XX (CANC-) CANCER RES FUND CONTRA COSTA.
XX
XX WPI; 1994-183509/22.
XX N-PSDB; AAQ62763.
XX
XX Chimeric human-murine polypeptide(s) specific for human mammary fat
PT globule antigen - for imaging, diagnosing and treating neoplasia, with
PT less undesirable immunogenic response.
XX
XX Example 27; Page 41; 54pp; English.
XX
XX An initial isolation of cDNAs coding for murine anti-human breast
CC carcinoma MAb KC-4 was performed using PCR with commercially available
CC primers (see AAQ62751-062758, available from NOVAGEN). Subsequent cloning
CC using PCR primers JO20, JO21, JO22 and JO24 (see AAQ62759-062762)
CC resulted in the isolation of the mouse Ig variable domains. The amplified
CC cDNAs were sequenced (AAQ62763 and AAQ62764) and amino acid sequences
CC were deduced from them. Chimeric mouse-human antibodies were constructed
CC using human constant regions so as to produce less immunogenic
CC polypeptides which retained the anti-human carcinoma binding specificity
CC of KC-4. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 131 AA;
XX
XX Query Match 94.2%; Score 646; DB 2; Length 131;
XX Best Local Similarity 93.9%; Pred. No. 4.9e-49;
XX Matches 123; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
XX
QY 1 MKLPLVLLVLMFWIPASNSDVLMTQSPSLPVSIGDQASISCRSSQSIHVSNGTYLEWY 60
DB 1 MKLPLVLLVLMFWIPASSDVLMTQTPLSLPVSIGDQASISCRSSQSIHVSNGTYLEWY 60
QY 61 LQKPGQPKLLIYKVSFRFGSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPVY 120
DB 61 LQKPGQPKLLIYKVSIRFGSGVDPDRFSGSGGTDTFTLKISRVEAEDLGIYFCQGSHPVY 120
QY 121 AFGGQTKLEIK 131
DB 121 TFGGQTKLEIK 131
XX
RESULT 3
AARS52790
ID AARS52790 standard; protein; 131 AA.
XX
XX AARS52790;
XX
XX 25-MAR-2003 (revised)
XX 24-JAN-1995 (first entry)
XX
XX Murine KC-4 immunoglobulin light chain variable region (deduced).
XX
XX Immunoglobulin variable domain; primer; polymerase chain reaction;
KW chimeric antibody; human milk fat globule; human breast carcinoma;
KW murine anti-human carcinoma monoclonal antibody KC-4.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Protein 20..131
XX Region /label= KC-4_mature_VL-chain
XX Region /label= FR1
XX Region 43..58
XX Region /label= CDR1
XX Region 59..73
XX Region /label= FR2
XX Region 74..80
XX Region /label= CDR2
XX Region 81..112
XX Region /label= FR3
XX Modified-site 98..100

```

```

FT Region /note= "putative glycosylation site"
FT 113. .121
FT /label= CDR3
FT 122. .131
FT /label= FR4
XX
XX WO9411509-A2.
XX
XX 26-MAY-1994.
XX
XX 16-NOV-1993; 93WO-US011445.
XX
XX 16-NOV-1992; 92US-00977696.
XX
XX 30-SEP-1993; 93US-00129930.
XX
XX 08-OCT-1993; 93US-00134346.
XX
XX (CANC-) CANCER RES FUND CONTRA COSTA.
XX
XX Do Couto FJR, Ceriani RL, Peterson JA, Padlan EA;
XX
XX WPI; 1994-183510/22.
XX
XX New analogue peptide(s) comprising antibody variable regions - used to
XX develop prods. for use in the detection, diagnosis, therapy and
XX prevention of neoplasms.
XX
XX Example 26; Page 61; 109pp; English.
XX
XX An initial isolation of cDNAs coding for murine anti-human breast
XX carcinoma MAB KC-4 was performed using PCR with commercially available
XX primers (see AAQ62776-Q62783, available from NOVAGEN). Subsequent cloning
XX using PCR primers JO20, JO21, JO22 and JO24 (see AAQ62784-Q62787)
XX resulted in the isolation of the mouse Ig variable domains. The amplified
XX cDNAs were sequenced (AAQ62788 and AAQ62789) and amino acid sequences
XX were deduced from them. Chimeric mouse-human antibodies were constructed
XX using human constant regions so as to produce less immunogenic
XX polypeptides which retained the anti-human carcinoma binding specificity
XX of KC-4. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 131 AA;

Query Match 94.2%; Score 646; DB 2; Length 131;
Best Local Similarity 93.9%; Pred. No. 4.9e-49;
Matches 123; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MKLPVRLVLVLMFWIPASNSDVLMTQSLPLSVLGDQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLVLMFWIPASSSDVLTQTPLSLPVLGDQASISCRSSQSIHNSGDTYLEWY 60
Oy 61 LQKPGQSPKLLIYKVSIRFSGVDPDRFSGSGSGTDFTLTIISRVEAEDLGVYFCFGSHVPY 120
Db 61 LQKPGQSPKLLIYKVSIRFSGVDPDRFSGSGSGTDFTLTIISRVEAEDLGVYFCFGSHVPY 120
Oy 121 AFGGGTKLEIK 131
Db 121 TFGGGTKLEIK 131

RESULT 4
AAR70457
ID AAR70457 standard; peptide; 131 AA.
XX
XX AAR70457;
XX
XX 25-MAR-2003 (revised)
XX
XX 27-OCT-1995 (first entry)
XX
XX VL sequence of anti-KC-4 monoclonal antibody (KII-Jk2).
XX
XX Anti-KC-4 antibody; monoclonal antibody; cancer; VL chain.
XX
XX Synthetic.
XX

/label= immunoglobulin_E_light_chain

PN WO9510776-A1.
XX
XX 20-APR-1995.
XX
XX 16-NOV-1993; 93WO-US011444.
XX
XX 08-OCT-1993; 93US-00134346.
XX
XX (CANC-) CANCER RES FUND CONTRA COSTA.
XX
XX Do Couto JJR, Ceriani RL, Peterson JA;
XX
XX WPI; 1995-161912/21.
XX
XX N-PSDB; AAQ87531.
XX
XX New humanised anti-KC-4 monoclonal antibody - used for detection of
XX cancer cells, in vivo imaging, ex-vivo purging and treatment of cancers.
XX
XX Example; Table 14, Page 31; 61pp; English.
XX
XX The cDNAs that encode the anti-KC-4 murine immunoglobulin VH and VL were
XX prepared by PCR from polyadenylated RNA isolated from 100 million KC-4
XX hybridoma cells. All clones were obtd. from independent PCRs. The
XX sequences of the primers are given in AAQ87519-Q87526. The PCR products
XX were cloned, without prior purificn., into pCR1000 (Invitrogen) and
XX sequenced in both directions. The VL DNA sequence and its derived protein
XX sequences are shown in AAQ87531 and AAR70449-R70457. The mature VL chain
XX begins at AA D of framework 1 (FR1). VL is a group II kappa chain. Part
XX of the CDR3 and all of the FR4 are encoded by Jk2. There is an
XX asparagine glycosylation site in the light chain in FR3. The site reads
XX NIS. AAR70457 is a composite sequence of AAR70449-R70456. (Updated on 25-
XX MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA
XX field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 131 AA;

Query Match 94.2%; Score 646; DB 2; Length 131;
Best Local Similarity 93.9%; Pred. No. 4.9e-49;
Matches 123; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MKLPVRLVLVLMFWIPASNSDVLMTQSLPLSVLGDQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLVLMFWIPASSSDVLTQTPLSLPVLGDQASISCRSSQSIHNSGDTYLEWY 60
Oy 61 LQKPGQSPKLLIYKVSIRFSGVDPDRFSGSGSGTDFTLTIISRVEAEDLGVYFCFGSHVPY 120
Db 61 LQKPGQSPKLLIYKVSIRFSGVDPDRFSGSGSGTDFTLTIISRVEAEDLGVYFCFGSHVPY 120
Oy 121 AFGGGTKLEIK 131
Db 121 TFGGGTKLEIK 131

RESULT 5
AAY17416
ID AAY17416 standard; protein; 238 AA.
XX
XX AAY17416;
XX
XX 26-JUL-1999 (first entry)
XX
XX Mouse immunoglobulin E light chain.
XX
XX Mouse; immunoglobulin E; IgE; allergy; transgenic animal.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX FH Peptide 1. .19
XX FT Peptide /label= signal
XX FT Protein 20. .238
XX /label= immunoglobulin_E_light_chain
XX

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PN EF921189-A1.  
 XX 09-JUN-1999.  
 XX 13-NOV-1998; 98EP-00309340.  
 XX 14-NOV-1997; 97JP-00313989.  
 XX (SANY ) SANKYO CO LTD.  
 PA (TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI.  
 XX Karasuyama H, Yonemawa H, Taya C, Matsuoka K;  
 PI WPI; 1999-315404/27.  
 DR N-PSDB; AAX61085.  
 XX Transgenic non-human animal allergy models.  
 PT Claim 28; Page 30-32; 42pp; English.  
 XX The present invention describes a transgenic, non-human animal with its  
 CC genome altered to constitutively express a molecule having a constant  
 CC region which can bind an IGE receptor on mast cells in the animals, the  
 CC molecule having an immunoglobulin structure and being further capable of  
 CC specifically binding a predetermined antigen. The transgenic animal is  
 CC useful as a model for evaluating the activity and the ability of  
 CC substances i.e. with anti-allergic activity, to affect any allergic  
 CC reaction caused in the animal by the administration of the antigen to the  
 CC animal, and applying the substance to be evaluated. The present sequence  
 CC is the mouse immunoglobulin E (IgE) light chain, given in the present  
 CC invention  
 XX  
 SQ Sequence 238 AA;  
 Query Match 94.0%; Score 645; DB 2; Length 238;  
 Best Local Similarity 93.2%; Pred. No. 1.1e-48;  
 Matches 123; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSICRSSQSIHVSNGDTYLEWY 60  
 DB 1 MKLPVRLVLMFWIPASSDVLMTQSLPVSLSGDAQSICRSSQSIHVSNGNTYLEWY 60  
 QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGYVFCFQGSHPVY 120  
 DB 61 LQKPGQSPKLLIYKVSNRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGYVFCFQGSHPV 120  
 QY 121 AFGGGTKLEIKR 132  
 DB 121 TFGAGTKLEIKR 132  
 RESULT 6  
 ABP72116  
 ID ABP72116 standard; protein; 131 AA.  
 XX  
 AC ABP72116;  
 XX  
 DT 03-JUN-2003 (first entry)  
 XX  
 XX Mouse FGF-8 related protein SEQ ID 4.  
 DE  
 XX Mouse; humanised; antibody; fibroblast growth factor 8; FGF8; cytostatic;  
 KW cancer; prostate; breast; ovarian; testicular.  
 KW  
 XX Mus musculus.  
 OS  
 XX WO2003002608-A1.  
 PN  
 XX 09-JAN-2003.  
 PD  
 XX 28-JUN-2002; 2002WO-JP006591.  
 PF  
 XX 28-JUN-2001; 2001JP-00196176.  
 PR

XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA Shitara K, Nakamura K, Hirota M, Shimada N;  
 PI WPI; 2003-239169/23.  
 XX N-PSDB; AB299466.  
 DR  
 XX Humanised antibodies and antibody fragments reacting with fibroblast  
 PT growth factor 8 useful for the treatment and diagnosis of cancer.  
 PT  
 XX Example 1; Page 67-68; 86pp; Japanese.  
 PS  
 XX The invention relates to novel humanised antibodies and antibody  
 CC fragments which react with fibroblast growth factor 8 (FGF8) and inhibit  
 CC its biological functions. The polypeptides of the invention have  
 CC cytosstatic activity. The antibody is useful for the treatment of cancer,  
 CC including prostate, breast, ovarian and testicular cancer. The present  
 CC sequence is used in the exemplification of the invention  
 XX  
 SQ Sequence 131 AA;  
 Query Match 93.9%; Score 644; DB 6; Length 131;  
 Best Local Similarity 93.9%; Pred. No. 7.4e-49;  
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSICRSSQSIHVSNGDTYLEWY 60  
 DB 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSICRSSQSLVHSGRTYLEWY 60  
 QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGYVFCFQGSHPVY 120  
 DB 61 LQKPGQSPKLLIYKVSNRISGVDPDRFSGSGGTDTFTLKISRVEAEDLGYVFCFQGSHPVY 120  
 QY 121 AFGGGTKLEIK 131  
 DB 121 TFGGGTKLEIK 131  
 RESULT 7  
 ADD28184  
 ID ADD28184 standard; protein; 131 AA.  
 XX  
 AC ADD28184;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 XX Mouse lectin tolerance related protein SEQ ID NO:17.  
 DE  
 XX mouse; antibody; lectin; sugar; N-acetylglucosamine;  
 KW Fc gamma receptor IIIfa; cytostatic; anti-allergic; immunomodulator;  
 KW cardiant; virucide; antibacterial; tumour; allergy; inflammation;  
 KW autoimmune disease; circulatory system; viral infection;  
 KW bacterial infection.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003084570-A1.  
 XX  
 PD 16-OCT-2003.  
 XX  
 XX 09-APR-2003; 2003WO-JP004505.  
 PF  
 XX 09-APR-2002; 2002JP-00106951.  
 PR  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Nakamura K, Shitara K, Hatanaka S, Niwa R, Okazaki A;  
 PI WPI; 2003-812677/76.  
 DR N-PSDB; ADD28183.  
 XX  
 XX Drugs containing antibody compositions produced by cells tolerant to



PT lectin recognizing specific sugar-chain structure, appropriate for  
 PT patients suffering from FcγRIIIa polymorphism e.g. in treating  
 XX tumors.  
 PS Example 3; SEQ ID NO 17; 214pp; Japanese.  
 XX  
 CC The invention relates to a novel drug containing as the active ingredient  
 CC an antibody composition produced by cells tolerant to a lectin  
 CC recognising a sugar-chain structure in which an alpha-bond is formed  
 CC between the 6-position of N-acetylglucosamine at the reducing end of an N  
 CC -glycoside bond-type complex sugar chain and the 1-position of fucose,  
 CC which has affinity to human Fc gamma receptor IIIa. A drug of the  
 CC invention has cytostatic, antiallergic, immunomodulator, cardiant,  
 CC virucide, and antibacterial activity. The drugs are useful in screening  
 CC and treating patients not suitable for drugs not derived from these  
 CC cells, particularly as diagnostics, preventives or remedies for diseases  
 CC accompanying tumour, allergy or inflammation, autoimmune diseases,  
 CC diseases of the circulatory system, and viral or bacterial infections.  
 CC The present sequence is used in the exemplification of the invention.  
 XX  
 SQ Sequence 131 AA;  
 Query Match 93.9%; Score 644; DB 7; Length 131;  
 Best Local Similarity 93.9%; Pred. No. 7.4e-49;  
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSIGDQASISCRSSQSIHNSGTYLEWY 60  
 DB 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSIGDQASISCRSSQSIHNSGTYLEWY 60  
 QY 61 LQKPGQSPKLLIYKVSDFRFGSGSGTDFTLKISRVEAEDLGVYFCFGSHVPY 120  
 DB 61 LQKPGQSPKLLIYKVSDFRFGSGSGTDFTLKISRVEAEDLGVYFCFGSHVPY 120  
 QY 121 AFGGGTKLEIK 131  
 DB 121 TFGGGTKLEIK 131  
 RESULT 8  
 ADE36480  
 ID ADE36480 standard; protein; 131 AA.  
 XX  
 AC ADE36480;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Mouse anti-FGF-8 antibody-related protein #2.  
 XX  
 KW arthritis; anti-FGF-8; sic fibroblast growth factor;  
 KW cartilage protection agent; joint destruction inhibitor;  
 KW synovial proliferation inhibitor; mouse; murine.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003057251-A1.  
 XX  
 PD 17-JUL-2003.  
 XX  
 PF 26-DEC-2002; 2002WO-JP013650.  
 XX  
 PR 28-DEC-2001; 2001JP-00400677.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Tamura T, Uchii M, Suda T, Miki I, Tanaka A;  
 XX  
 DR WPI; 2003-587078/55.  
 DR N-PSDB; ADE36479.  
 XX  
 XX Treatment and prevention of arthritis comprising the use of anti-FGF-8  
 PT (sic fibroblast growth factor) antibody.  
 XX

PS Example; SEQ ID NO 4; 193pp; Japanese.  
 XX  
 CC The invention comprises a method for treating and preventing arthritis,  
 CC the method involves the use of anti-FGF-8 (sic fibroblast growth factor)  
 CC antibody. The antibody and method of the invention is useful for: the  
 CC detection, treatment and prevention of arthritis; as a cartilage  
 CC protection agent; as a joint destruction inhibitor; and as a synovial  
 CC proliferation inhibitor. The present amino acid sequence represents a  
 CC mouse protein that was used in an example of the invention.  
 XX  
 SQ Sequence 131 AA;  
 Query Match 93.9%; Score 644; DB 7; Length 131;  
 Best Local Similarity 93.9%; Pred. No. 7.4e-49;  
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSIGDQASISCRSSQSIHNSGTYLEWY 60  
 DB 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSIGDQASISCRSSQSIHNSGTYLEWY 60  
 QY 61 LQKPGQSPKLLIYKVSDFRFGSGSGTDFTLKISRVEAEDLGVYFCFGSHVPY 120  
 DB 61 LQKPGQSPKLLIYKVSDFRFGSGSGTDFTLKISRVEAEDLGVYFCFGSHVPY 120  
 QY 121 AFGGGTKLEIK 131  
 DB 121 TFGGGTKLEIK 131  
 RESULT 9  
 ADL35318  
 ID ADL35318 standard; protein; 131 AA.  
 XX  
 AC ADL35318;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Murine anti-Fcγ receptor IIIa antibody-related protein - SEQ 75.  
 XX  
 KW antibody binding; Fcγ receptor IIIa; Fc region sugar chain;  
 KW cytostatic; antiallergic; antiinflammatory; immunosuppressive;  
 KW vasotropic; virucide; cancer; allergy; inflammatory; autoimmune;  
 KW circulatory; viral infection; murine; mouse.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003085119-A1.  
 XX  
 PD 16-OCT-2003.  
 XX  
 PF 09-APR-2003; 2003WO-JP004504.  
 XX  
 PR 09-APR-2002; 2002JP-00106950.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX  
 PI Nakamura K, Shitara K;  
 XX  
 DR WPI; 2003-812729/76.  
 DR P-PSDB; ADL35317.  
 XX  
 PT Method of enhancing the binding activity of antibody to Fc-gamma receptor  
 PT IIIa for production of antibodies with high cytotoxicity as cancer,  
 PT allergic, viral and other disease therapeutic agents.  
 XX  
 PS Example 14; SEQ ID NO 75; 296pp; Japanese.  
 XX  
 CC The invention relates to a novel method for enhancing the binding  
 CC activity of an antibody to the Fcγ receptor IIIa by increasing the  
 CC proportion of N-glycoside bond type complex sugar chains attached to the  
 CC Fc region of the antibody which do not have the 1-position of fucose  
 CC bound to the 6-position of N-acetylglucosamine at the reducing end of the  
 CC sugar chain. The method of the invention has cytostatic, antiallergic,

CC antiinflammatory, immunosuppressive, vasotropic and virucide applications  
 CC and may be useful for generating antibodies to be used in the treatment,  
 CC prevention and diagnosis of diseases including cancer, allergies,  
 CC inflammatory disorders, autoimmune diseases, circulatory disorders and  
 CC viral infections. The current sequence is that of an anti-Fcγ<sub>3</sub>α  
 CC receptor IIIa antibody-related protein of the invention.  
 XX  
 SQ Sequence 131 AA;

Query Match 93.9%; Score 644; DB 7; Length 131;  
 Best Local Similarity 93.9%; Pred. No. 7.4e-49;  
 Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSICRSSQSIHVSNGDTYLEWY 60  
 DB 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSICRSSQSIHVSNGDTYLEWY 60  
 QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYFCFGSHVPY 120  
 DB 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYFCFGSHVPY 120  
 QY 121 AFGGGTKLEIK 131  
 DB 121 TFGGGTKLEIK 131

RESULT 10  
 AAW03199  
 ID AAW03199 standard; protein; 149 AA.  
 XX  
 AC AAW03199;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-FEB-1997 (first entry)  
 XX  
 DE Anti-idiotypic monoclonal antibody 1A7 variable light chain.

XX Murine; mouse; anti-idiotypic; monoclonal antibody; MAb; 1A7;  
 KW variable light chain; ganglioside 2; GD2; 14G2a; neuroblastoma;  
 KW glycosphingolipid; human; neuroectodermal; tumour; glioma; lung;  
 KW malignant melanoma; soft tissue sarcoma; small cell carcinoma; vaccine;  
 KW treatment; palliate; detection; diagnosis; recombinant production;  
 KW purification; probe; primer; assay; amplification; gene therapy.  
 XX  
 OS Mus musculus.

Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= sig\_peptide  
 FT Region 20..42  
 FT /note= "framework region 1"  
 FT Region 43..58  
 FT /note= "complementarity determining region 1"  
 FT Region 59..73  
 FT /note= "framework region 2"  
 FT Region 74..80  
 FT /note= "complementarity determining region 2"  
 FT Region 81..112  
 FT /note= "framework region 3"  
 FT Region 113..121  
 FT /note= "complementarity determining region 3"  
 FT Region 122..131  
 FT /note= "framework region 4"

XX WO9622373-A2.  
 XX  
 XX 25-JUL-1996.  
 XX  
 XX 17-JAN-1996; 96WO-US000882.  
 XX  
 XX 17-JAN-1995; 95US-00372676.  
 PR 16-JAN-1996; 96US-00591196.  
 XX

PA (KENT ) UNIV KENTUCKY.  
 XX Chatterjee M, Chatterjee SK, Foon KA;  
 XX WPI; 1996-354530/35.  
 DR N-PSDB; AAT31332.  
 XX  
 PT Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s)  
 PT - useful to treat or palliate a GD2-associated disease, e.g. melanoma and  
 PT glioma.  
 XX  
 PS Claim 8; Fig 1; 141pp; English.

XX The present sequence is that of the murine anti-idiotypic monoclonal  
 CC antibody (MAb) 1A7 variable light chain. MAb 1A7 was raised against the  
 CC anti-ganglioside 2 (GD2) MAb 14G2a, which binds an unique epitope of GD2.  
 CC As the glycosphingolipid GD2 is expressed at high density by human  
 CC neuroectodermal tumours, e.g. malignant melanoma, neuroblastoma, glioma,  
 CC soft tissue sarcoma and small cell carcinoma of the lung, MAb 1A7, or its  
 CC cDNA can be used in a vaccine to treat or palliate such diseases. They  
 CC can also be used to reduce the risk of recurrence of a clinically  
 CC detectable tumour, and detect an anti-GD2 Ab bound to a tumour cell. MAb  
 CC 1A7 overcomes immune tolerance and induces an immune response against  
 CC GD2, which comprises anti-GD2 Ab (humoral response) and GD2-specific  
 CC cells (cellular response). It can be used to purify anti-1A7 (Ab3), anti-  
 CC GD2 (Ab1) or 14G2a (Ab1), detect anti-1A7 or anti-GD2 in a sample or  
 CC measure the level of cellular anti-1A7 or anti-GD2 activity. The cDNA can  
 CC be used in expression systems for 1A7 prodn., and in the prepn. of probes  
 CC and primers to respectively assay for 1A7 cDNA, and amplify desired  
 CC polynucleotides for use in gene therapy. (Updated on 25-MAR-2003 to  
 CC correct PR field.)  
 XX

SQ Sequence 149 AA;

Query Match 93.1%; Score 639; DB 2; Length 149;  
 Best Local Similarity 92.4%; Pred. No. 2.3e-48;  
 Matches 122; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSICRSSQSIHVSNGDTYLEWY 60  
 DB 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSLSGDAQSICRSSQSIHVSNGDTYLEWY 60  
 QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYFCFGSHVPY 120  
 DB 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYFCFGSHVPY 120  
 QY 121 AFGGGTKLEIKR 132  
 DB 121 TFGGGTKLEIKR 132

RESULT 11  
 AAY21545  
 ID AAY21545 standard; protein; 149 AA.

XX AAY21545;  
 XX  
 DT 03-AUG-1999 (first entry)  
 XX  
 DE Monoclonal antibody 1A7 light chain variable region.  
 XX  
 KW Psoriasis; immunological response; anti-idiotypic antibody; glutamate;  
 KW chronic plaque; pustular; plaque-type psoriasis; psoriatic arthritis;  
 KW monoclonal antibody; 1A7.

XX Unidentified.  
 XX  
 XX WO9325380-A2.  
 XX  
 XX 27-MAY-1999.  
 XX  
 XX 17-NOV-1998; 98WO-US024607.  
 XX

```

PR 17-NOV-1997; 97US-0065774P.
XX 16-NOV-1998; 98US-00192838.
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX Chatterjee M, Foon KA;
PI 1999-347407/29.
XX WPI; 1999-347407/29.
XX N-PSDB; AAX60629.
XX
XX Treatment of psoriasis comprises administration of antigen which
XX simulates the generation of anti-idiotypic antibodies.
XX
XX Disclosure; Fig 2; 48pp; English.
XX
XX The invention provides a method of treating of psoriasis by administering
XX an antigen which has similar immunogenic properties to an antigen
XX expressed on cells of psoriatic tissue so that an immunological response
XX is elicited in the individual. The antigen stimulates the generation of
XX anti-idiotypic antibodies that neutralize the aberrant immune response
XX causing the psoriasis. The method is used to treat psoriasis, especially
XX chronic plaque, psoriasis, plaque-type psoriasis or psoriatic
XX arthritis. The compositions allow the individual's own immune system to
XX act against psoriatic tissue. The present sequence represents the light
XX chain variable region of monoclonal antibody 1A7
XX
XX Sequence 149 AA;
SQ
    Query Match      93.1%; Score 639; DB 2; Length 149;
    Best Local Similarity 92.4%; Pred. No. 2.3e-48;
    Matches 122; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGDQASISCRSSQSIHNSGNTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVLTMTQTLPLSLPVLGDQASISCRSSQSIHNSGNTYLEWY 60
QY 61 LQKPGQSPKLLIYKVSDFRFGSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
DB 61 LQKPGQSPNLLIYFYVSNRFGSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPW 120
QY 121 AFGGGTKLEIKR 132
DB 121 TFGGGTKLEIKR 132
XX
RESULT 12
ADH17810
ID ADH17810 standard; protein; 132 AA.
XX
XX ADH17810;
XX
XX 11-MAR-2004 (first entry)
XX
XX Murine antibody EM164 light chain leader and variable region protein.
XX
XX antibody EM164; insulin-like growth factor-I receptor; IGF-IR antagonist;
XX breast cancer; colon; ovarian carcinoma; osteosarcoma; cervical;
XX prostate; lung; synovial carcinoma; pancreatic; murine; mouse;
XX light chain leader; variable region.
XX
XX Mus sp.
XX
XX WO2003106621-A2.
XX
XX 24-DEC-2003.
XX
XX 12-JUN-2003; 2003WO-US016211.
XX
XX 14-JUN-2002; 2002US-00170390.
XX
XX (IMMU-) IMMUNOGEN INC.
XX
XX Singh R, Tavares DJ, Dagdigian NE;

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XX WPI; 2004-082172/08.
XX N-PSDB; ADH17809.
XX
XX Novel murine antibody EM164 or antibody fragment that specifically binds
XX to insulin-like growth factor-I-receptor useful for treating breast
XX cancer, colon cancer, lung cancer, prostate cancer.
XX
XX Example 1; SEQ ID NO 50; 155pp; English.
XX
XX The invention relates to a novel murine antibody EM164 or antibody
XX fragment that specifically binds to insulin-like growth factor-I receptor
XX (IGF-IR) where the antibody is an antagonist of the receptor, is
XX substantially devoid of agonist activity toward the receptor and is
XX capable of inhibiting the growth of a cancer cell by greater than 80% in
XX the presence of a growth stimulant chosen from serum, IGF-I and IGF-II.
XX The antibody of the invention may be useful for diagnosing or treating a
XX patient having a cancer selected from breast cancer, colon cancer,
XX ovarian carcinoma, osteosarcoma, cervical cancer, prostate cancer, lung
XX cancer, synovial carcinoma and pancreatic cancer. The current sequence is
XX that of the murine anti-IGF-IR antibody EM164-related protein of the
XX invention.
XX
XX Sequence 132 AA;
SQ
    Query Match      93.0%; Score 638; DB 8; Length 132;
    Best Local Similarity 92.4%; Pred. No. 2.5e-48;
    Matches 122; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLPSLGDQASISCRSSQSIHNSGNTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSDDVLTMTQTLPLSLPVLGDQASISCRSSQSIHNSGNTYLEWY 60
QY 61 LQKPGQSPKLLIYKVSDFRFGSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
DB 61 LQKPGQSPKLLIYKVSDFRFGSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPP 120
QY 121 AFGGGTKLEIKR 132
DB 121 TFGGGTKLEIKR 132
XX
RESULT 13
AAR31587
ID AAR31587 standard; protein; 131 AA.
XX
XX AAR31587;
XX
XX 25-MAR-2003 (revised)
XX 09-JUN-1993 (first entry)
XX
XX BR55-2 light chain variable domain.
XX
XX Monoclonal; antibody; MAb; light; heavy; chain; variable; region;
XX human/mouse; chimeric; difucosyl; Lewis; blood group; murine; BR55-2;
XX expression vector; IgG3; IgG3; pVg3; pVg3; gamma; kappa; constant;
XX pVg1c; pVg3c; PCR; plasmid; host cell; sp2/O-Ag 14; electroporation;
XX antigen; Y-6; B-7-2; binding specificity; erythrocyte; diagnosis; cancer;
XX epithelial; breast; colorectal; ovarian; prostate; pancreatic; gastric;
XX small cell lung; immunotherapy; HIV.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX Peptide 20..131
XX /note= "Mature peptide"
XX
XX EP528767-A1.
XX
XX 24-FEB-1993.
XX
XX 18-AUG-1992; 92EP-00810633.
XX
XX

```

PR 21-AUG-1991; 91GB-00018013.  
 XX 02-MAR-1992; 92GB-00004514.  
 XX (SANO ) SANDOZ LTD.  
 PA (SANO ) SANDOZ PATENT GMBH.  
 PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
 XX  
 XX Co MS, Loibner H;  
 XX  
 DR WPI; 1993-060580/08.  
 DR N-PSDB; AAQ36536.  
 XX  
 PT Human-mouse chimeric monoclonal antibodies - recognise difucosyl Lewis  
 PT blood group antigens Y-6 and B-7-2, useful for treating cancer and HIV  
 PT infection.  
 XX  
 PS Disclosure; Fig 8; 65pp; English.  
 XX  
 CC The sequences given in AAR31587-88 represent the light and heavy chain  
 CC variable regions respectively from the murine monoclonal (MAB) BR55-2.  
 CC BR55-2 was used as a basis for the construction of a chimeric MAB which  
 CC recognises the difucosyl Lewis blood group. Separate expression vectors  
 CC were used to express the chimeric human BR55-2 IgG1 and IgG3 antibody  
 CC light and heavy chains: pVg for the light chain, pVg for the gamma 1  
 CC heavy chain and pVg3 for the gamma 3 heavy chain. The actual expressed  
 CC chimeric BR55-2 light chain gene and the heavy chain gene consist of two  
 CC adjacent parts. The kappa/gamma constant regions were built into the  
 CC vectors pVg and pVg3c (or pVg3c) respectively and the variable regions  
 CC were constructed by PCR. The resulting plasmids were used to transfect  
 CC the host cell line sp2/O-Ag 14 by electroporation. The resulting MABs  
 CC recognise the difucosyl Lewis blood group antigens Y-6 and B-7-2 but do  
 CC not induce human anti-mouse antibody response. The MABs show a restricted  
 CC binding specificity which is associated with a lack of cross-reactivity to  
 CC related antigens expressed on blood cells eg. erythrocytes. This allows  
 CC the MABs to be particularly useful for therapeutic use in humans. The  
 CC MABs are useful in the diagnosis and treatment of cancer of epithelial  
 CC origin, eg. breast, colorectal, ovarian, prostate, pancreatic or gastric  
 CC cancer and small cell lung cancer. The MABs are also useful for  
 CC immunotherapy of HIV infections since the Lewis Y antigen is also  
 CC selectively expressed on HIV infected cells. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 XX  
 SQ Sequence 131 AA;  
 Query Match 92.9%; Score 637; DB 2; Length 131;  
 Best Local Similarity 93.1%; Pred. No. 3.1e-48;  
 Matches 122; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MKLPVRLVLLMFIPASNSDVLMTQSPVSLGPDQASISCRSSQSIHNSGNTYLEWY 60  
 DB 1 MKLPVRLVLLMFIPASSDVLMTQTPVSLGPDQASISCRSSQSIHNSGNTYLEWY 60  
 QY 61 LQPGQSPKLLIYKVSDFSGVDPDRFSGSGGTFTLKISRVEAEDLGVYFCFGSHVPY 120  
 DB 61 LQPGQSPKLLISKVNSRFGVDPDRFSGSGGTFTLKISRVEAEDLGVYFCFGSHVPF 120  
 QY 121 AFGGGTKLEIK 131  
 DB 121 TFGSGTKLEIK 131  
 RESULT 14  
 AAR32241  
 ID AAR32241 standard; protein; 131 AA.  
 XX  
 AC AAR32241;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 09-JUN-1993 (first entry)  
 XX  
 XX Chimeric MAB light chain variable region.  
 DE Monoclonal; antibody; MAB; light; heavy; chain; variable; region;  
 XX  
 KW human/mouse; chimeric; difucosyl; Lewis; blood group; murine; BR55-2;  
 KW expression vector; IgG1; IgG3; pVg; pVg3; gamma; kappa; constant;  
 KW pVg1c; pVg3c; PCR; plasmid; host cell; sp2/O-Ag 14; electroporation;  
 KW antigen; Y-6; B-7-2; binding specificity; erythrocyte; diagnosis; cancer;  
 KW epithelial; breast; colorectal; ovarian; prostate; pancreatic; gastric;  
 KW small cell lung; immunotherapy; HIV.  
 XX  
 OS Mus musculus.  
 XX  
 XX Key Location/Qualifiers  
 PH Region 43..58  
 FT /label= CDR1  
 FT /note= "Claim 4"  
 FT Region 74..80  
 FT /label= CDR2  
 FT /note= "Claim 4"  
 FT Region 113..121  
 FT /label= CDR3  
 FT /note= "Claim 4"  
 XX  
 XX EP528767-A1.  
 XX  
 XX 24-FEB-1993.  
 XX  
 XX 18-AUG-1992; 92EP-00810633.  
 XX  
 XX 21-AUG-1991; 91GB-00018013.  
 XX 02-MAR-1992; 92GB-00004514.  
 XX  
 XX (SANO ) SANDOZ LTD.  
 XX (SANO ) SANDOZ PATENT GMBH.  
 XX (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
 XX  
 XX Co MS, Loibner H;  
 XX  
 XX WPI; 1993-060580/08.  
 XX N-PSDB; AAQ36529.  
 XX  
 XX Human-mouse chimeric monoclonal antibodies - recognise difucosyl Lewis  
 XX blood group antigens Y-6 and B-7-2, useful for treating cancer and HIV  
 XX infection.  
 XX  
 XX Claim 3; Page 18; 65pp; English.  
 XX  
 CC The sequences given in AAR32241-42 are the light and heavy chain variable  
 CC regions respectively from a human/mouse chimeric monoclonal antibody  
 CC (MAB) which recognises the difucosyl Lewis blood group. The murine MAB  
 CC BR55-2 was used as a basis for the construction of this chimeric MAB.  
 CC Separate expression vectors were used to express the chimeric human BR55-  
 CC 2 IgG1 and IgG3 antibody light and heavy chains: pVg for the light chain,  
 CC pVg for the gamma 1 heavy chain and pVg3 for the gamma 3 heavy chain. The  
 CC actual expressed chimeric BR55-2 light chain gene and the heavy chain  
 CC gene consist of two adjacent parts. The kappa/gamma constant regions were  
 CC built into the vectors pVg and pVg3c (or pVg3c) respectively and the  
 CC variable regions were constructed by PCR (see also AAQ36531-33). The  
 CC resulting plasmids were used to transfect the host cell line sp2/O-Ag 14  
 CC by electroporation. The resulting MABs recognise the difucosyl Lewis  
 CC blood group antigens Y-6 and B-7-2 but do not induce human anti-mouse  
 CC antibody response. The MABs show a restricted binding specificity which is  
 CC associated with a lack of cross-reactivity to related antigens expressed  
 CC on blood cells eg. erythrocytes. This allows the MABs to be particularly  
 CC useful for therapeutic use in humans. The MABs are useful in the  
 CC diagnosis and treatment of cancer of epithelial origin, eg. breast,  
 CC colorectal, ovarian, prostate, pancreatic or gastric cancer and small  
 CC cell lung cancer. The MABs are also useful for immunotherapy of HIV  
 CC infections since the Lewis Y antigen is also selectively expressed on HIV  
 CC infected cells. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 131 AA;  
 Query Match 92.9%; Score 637; DB 2; Length 131;  
 Best Local Similarity 93.1%; Pred. No. 3.1e-48;  
 Matches 122; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLPVSIGDQASISCRSSQSIHSHNGDTYLEWY 60
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Db 1 MKLPVRLVLMFWIPASSSDVLTQTPLSLPVSIGDQASISCRSSQSIHSHNGDTYLEWY 60
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LQKPGQSPKLLIYKVSDFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVYPY 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LQKPGQSPKLLIYKVSDFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVYPY 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 AFGGGTKLEIK 131
  |||||
Db 121 TFGAGTKLELK 131
  |||||

RESULT 15
AA42958
ID AA42958 standard; protein; 131 AA.
XX
AC AA42958;
XX
DT 12-FEB-2004 (first entry)
XX
DE Mouse 12B4 antibody VL sequence.
XX
KW Immunoglobulin; Ig; neuroprotective; nootropic; gene therapy; vaccine;
  amyloidogenic disease; antibody.
XX
OS Mus sp.
XX
FH Key
FT Peptide
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  /note= "leader peptide"
FT Protein
  20..131
  /note= "mature protein"
FT Region
  43..58
  /note= "CDR 1"
FT Region
  74..79
  /note= "CDR 2"
FT Region
  114..121
  /note= "CDR 3"
XX
PN WO2003077858-A2.
XX
XX
XX 25-SEP-2003.
XX
XX 12-MAR-2003; 2003WO-US007715.
XX
XX 12-MAR-2002; 2002US-0363751P.
XX
XX (NEUR-) NEURALAB LTD.
XX
XX (AMHP ) WYETH.
XX
XX Basi G, Saldanha J;
XX
XX WPI; 2003-779077/73.
XX
XX N-PSDB; ACF58517.
XX
XX New humanized immunoglobulin light or heavy chains comprising variable
  region complementary determining regions and variable framework regions,
  useful for preventing or treating e.g., Alzheimer's disease.
XX
XX Claim 1; Page 64; 122pp; English.
XX
XX The invention relates to humanized immunoglobulin (Ig) light or heavy
  chains comprising variable region complementary determining regions
  (CDRs) from the 12B4 Ig variable region sequence and variable framework
  regions from a human acceptor Ig light chain or heavy chain sequence. The
  humanized Ig light or heavy chain or its nucleic acid molecule is useful
  for preventing or treating an amyloidogenic disease in humans, associated
  with amyloid deposits of Abeta in the brain, e.g., Alzheimer's disease,
  Down's syndrome or mild cognitive impairment, all characterized by
  cognitive impairment. The variable region sequence is useful in producing
  a three-dimensional image of a 12B4 Ig, 12B4 Ig chain or its domain. A
```

```
CC humanized antibody is useful for reducing plaque or neuritic burden in a
  subject. The present sequence represents a mouse 12B4 antibody variable
  light chain sequence
XX
SQ Sequence 131 AA;
  Query Match 92.9%; Score 637; DB 7; Length 131;
  Best Local Similarity 92.4%; Pred. No. 3.1e-48;
  Matches 121; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
  QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLPVSIGDQASISCRSSQSIHSHNGDTYLEWY 60
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  Db 1 MKLPVRLVLMFWIPASSSDVLTQTPLSLPVSIGDQASISCRSSQSIHSHNGDTYLEWY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  QY 61 LQKPGQSPKLLIYKVSDFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVYPY 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  Db 61 LQKPGQSPKLLIYKVSDFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVPL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
  QY 121 AFGGGTKLEIK 131
    |||||
  Db 121 TFGAGTKLELK 131
    |||||
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Search completed: May 25, 2005, 15:47:21  
Job time : 63.1321 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 16.454 Seconds  
(without alignments)  
598.864 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	645	94.0	238	3	US-09-192-545-4
2	639	93.1	149	3	US-09-192-838B-2
3	639	93.1	149	3	US-09-324-191-2
4	637	92.9	131	1	US-08-053-171-5
5	637	92.9	131	1	US-08-053-171-9
6	635	92.6	149	2	US-08-752-844-2
7	635	92.6	149	2	US-08-591-196-2
8	635	92.6	149	4	US-09-293-533-2
9	624	91.0	131	1	US-08-129-930B-55
10	624	91.0	131	3	US-08-134-346A-50
11	624	91.0	131	3	US-08-976-288A-95
12	612	89.2	131	3	US-08-589-939-7
13	610	88.9	173	5	PCT-US91-02942-3
14	610	88.9	173	5	PCT-US91-02946-3
15	595	86.7	131	1	US-07-977-696C-11
16	595	86.7	131	1	US-08-129-930B-11
17	595	86.7	131	3	US-08-976-288A-11
18	580.5	84.6	127	1	US-08-482-882-45
19	580.5	84.6	127	2	US-08-483-389-45
20	580.5	84.6	127	2	US-08-487-113D-45
21	580.5	84.6	127	2	US-08-473-503-45
22	580.5	84.6	127	2	US-08-483-932-45
23	580.5	84.6	127	2	US-08-720-420A-45
24	580.5	84.6	127	3	US-08-714-017-45
25	580.5	84.6	127	3	US-08-475-680-45
26	562	81.9	249	4	US-09-726-219A-190
27	556	81.0	125	1	US-08-331-398A-67

28	556	81.0	125	2	US-08-331-397B-67	Sequence 67, Appl
29	556	81.0	125	2	US-08-759-804A-66	Sequence 66, Appl
30	555	80.9	247	3	US-09-227-693-34	Sequence 34, Appl
31	555	80.9	248	1	US-08-331-398A-34	Sequence 34, Appl
32	555	80.9	248	2	US-08-331-397B-34	Sequence 34, Appl
33	555	80.9	248	2	US-08-759-804A-34	Sequence 34, Appl
34	551	80.3	112	1	US-08-331-398A-48	Sequence 48, Appl
35	551	80.3	112	1	US-08-077-252B-3	Sequence 3, Appl
36	551	80.3	112	2	US-08-888-366-16	Sequence 16, Appl
37	551	80.3	112	2	US-08-331-397B-48	Sequence 48, Appl
38	551	80.3	112	2	US-08-759-804A-48	Sequence 48, Appl
39	551	80.3	112	3	US-09-002-753A-3	Sequence 3, Appl
40	551	80.3	112	3	US-09-227-693-48	Sequence 48, Appl
41	551	80.3	112	4	US-09-657-274-3	Sequence 3, Appl
42	551	80.3	112	5	PCT-US94-06687-3	Sequence 66, Appl
43	550	80.2	263	2	US-08-752-844-66	Sequence 66, Appl
44	550	80.2	263	4	US-09-293-533-66	Sequence 19, Appl
45	549	80.0	112	2	US-08-859-649-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-192-545-4  
; Sequence 4, Application US/09192545  
; Patent No. 6118044  
; GENERAL INFORMATION:  
; APPLICANT: Karasuyama, Hajime  
; APPLICANT: Yonekawa, Hiromichi  
; APPLICANT: Taya, Choji  
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use  
; FILE REFERENCE: 799P79570  
; CURRENT APPLICATION NUMBER: US/09/192,545  
; CURRENT FILING DATE: 1998-11-13  
; EARLIER APPLICATION NUMBER: JP HEI 9-313989  
; EARLIER FILING DATE: 1997-11-14  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Description of Artificial Sequence: Designed heavy

Query Match	94.0%	Score 645;	DB 3;	Length 238;
Best Local Similarity	93.2%;	Pred. No. 4e-56;		
Matches 123;	Conservative 6;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	MKLPVRLVLMFWIPASNSDVLMTQSPVLSGLDQASISCRSSQSIHNSGDTYLEWY	60	
Db	1	MKLPVRLVLMFWIPASNSDVLMTQSPVLSGLDQASISCRSSQSIHNSGDTYLEWY	60	
Qy	61	LQKQSQPKLIYKVNSDRFSGVDPFRFSGSGGTFTLKISRVEADLGVYFCQGSHPVY	120	
Db	61	LQKQSQPKLIYKVNSDRFSGVDPFRFSGSGGTFTLKISRVEADLGVYFCQGSHPVY	120	
Qy	121	AFGGTKLEIKR	132	
Db	121	TFGAGTKLEIKR	132	

RESULT 2

US-09-192-838B-2  
; Sequence 2, Application US/09192838B  
; Patent No. 6355244  
; GENERAL INFORMATION:  
; APPLICANT: POON, Kenneth A.  
; APPLICANT: CHATTERJEE, Malaya  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS  
; FILE REFERENCE: 304142000500

```
; CURRENT APPLICATION NUMBER: US/09/192,838B
; CURRENT FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PR1
; ORGANISM: Mus Musculus
; ORGANISM: Mus Musculus
US-09-192-838B-2

Query Match          93.1%; Score 639; DB 3; Length 149;
Best Local Similarity 92.4%; Pred. No. 8.9e-56;
Matches 122; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSIGDQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDDVLTQTPLSLPVSIGDQASISCRSSQSIHVSNGNTYLEWY 60

QY 61 LQPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVFCFGSHVPY 120
Db 61 LQPGQSPNLLIYFVSNRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVYCFQGSHPV 120

QY 121 AFGGGTKLEIKR 132
Db 121 TFGGGTKLEIKR 132

RESULT 3
US-09-324-191-2
; Sequence 2, Application US/09324191
; Patent No. 6562798
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
; APPLICANT: CHATTERJEE, Malaya
; APPLICANT: FOON, Kenneth A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 304142000540
; CURRENT APPLICATION NUMBER: US/09/324,191
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: 60/065,774
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PR1
; ORGANISM: Mus Musculus
US-09-324-191-2

Query Match          93.1%; Score 639; DB 4; Length 149;
Best Local Similarity 92.4%; Pred. No. 8.9e-56;
Matches 122; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSIGDQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDDVLTQTPLSLPVSIGDQASISCRSSQSIHVSNGNTYLEWY 60

QY 61 LQPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVFCFGSHVPY 120
Db 61 LQPGQSPNLLIYFVSNRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVYCFQGSHPV 120

QY 121 AFGGGTKLEIKR 132
Db 121 TFGGGTKLEIKR 132

RESULT 4
US-08-053-171-5
; Sequence 5, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew.
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
```

```
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-053-171-5

Query Match          92.9%; Score 637; DB 1; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.2e-55;
Matches 122; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVSIGDQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDDVLTQTPLSLPVSIGDQASISCRSSQSIHVSNGNTYLEWY 60

QY 61 LQPGQSPKLLIYKVSDFRSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVFCFGSHVPY 120
Db 61 LQPGQSPKLLISKVSNRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVVYCFQGSHPV 120

QY 121 AFGGGTKLEIK 131
Db 121 TFGGGTKLEIK 131

RESULT 5
US-08-053-171-9
; Sequence 9, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew.
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
```



```

; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-053-171-9

Query Match          92.9%; Score 637; DB 1; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.2e-55;
Matches 122; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDVLMTQTPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120
Db 61 LQKPGQSPKLLIYKVSDFRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120

Qy 121 AFGGSKLEIK 131
Db 121 TFGSGTKLEIK 131

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RESULT 6
US-08-752-844-2
; Sequence 2, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Roon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-844-2

Query Match          92.6%; Score 635; DB 2; Length 149;
Best Local Similarity 91.7%; Pred. No. 2.2e-55;
Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDVLMTQTPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120
Db 61 LQKPGQSPKLLIYKVSDFRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120

Qy 121 AFGGSKLEIK 132
Db 121 TFGGSKLEIK 132

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RESULT 7
US-08-591-196-2
; Sequence 2, Application US/08591196
; Patent No. 5977316
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Roon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591,196
; FILING DATE: 16-JAN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 149 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-591-196-2

Query Match          92.6%; Score 635; DB 2; Length 149;
Best Local Similarity 91.7%; Pred. No. 2.2e-55;
Matches 121; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDVLMTQTPVSLPVLGDAQASISCRSSQSIHNSGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPY 120

```



```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,346A
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608
; TELEPHONE: 212-826-6565
; TELEFAX: 212-826-5909
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-134-346A-50
;
; Query Match 91.0%; Score 624; DB 3; Length 131;
; Best Local Similarity 90.1%; Pred. No. 2.3e-54;
; Matches 118; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
;
; QY 1 MKPLVRLVLMFWIPASNSDVLMTQSPVSLPVLGDAQASISCRSSQSIHNSNGDTYLEWY 60
; DB 1 MKPLVRLVLMFWIPASSSDVLMQTPLSLPTVTPGEPASISCRSSQSIHNSNGTYLEWY 60
;
; QY 61 LQKPGSQPKLLIYKVSDFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQGSHPY 120
; DB 61 LQKPGSQPKLLIYKVSIRFSGVDPDRFSGSGGTDTFLKISRVEADVGIIYFCQGSHPY 120
;
; QY 121 AFGGGTKLEIK 131
; DB 121 TFGGGTKLEIK 131
;
; RESULT 11
; US-08-976-288A-95
; Sequence 95, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: Go Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,346A
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608
; TELEPHONE: 212-826-6565
; TELEFAX: 212-826-5909
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-134-346A-50
;
; Query Match 91.0%; Score 624; DB 3; Length 131;
; Best Local Similarity 90.1%; Pred. No. 2.3e-54;
; Matches 118; Conservative 9; Mismatches 4; Indels 0; Gaps 0;
;
; QY 1 MKPLVRLVLMFWIPASNSDVLMTQSPVSLPVLGDAQASISCRSSQSIHNSNGDTYLEWY 60
; DB 1 MKPLVRLVLMFWIPASSSDVLMQTPLSLPTVTPGEPASISCRSSQSIHNSNGTYLEWY 60
;
; QY 61 LQKPGSQPKLLIYKVSDFSGVDPDRFSGSGGTDTFLKISRVEADLGVYFCQGSHPY 120
; DB 61 LQKPGSQPKLLIYKVSIRFSGVDPDRFSGSGGTDTFLKISRVEADVGIIYFCQGSHPY 120
;
; QY 121 AFGGGTKLEIK 131
; DB 121 TFGGGTKLEIK 131
;
; RESULT 12
; US-08-589-939-7
; Sequence 7, Application US/08589939
; Patent No. 6015662
; GENERAL INFORMATION:
; APPLICANT: Hackett, Jr., John R.
; APPLICANT: Hoff, Jane A.
; APPLICANT: Ostrow, David H.
; APPLICANT: Golgen, Alan M.
; TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND
; TITLE OF INVENTION: CONTROLS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: US
; ZIP: 60064-3500
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,939
; FILING DATE:
; CLASSIFICATION: 424
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5865. US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-589-939-7

Query Match      89.2%; Score 612; DB 3; Length 131;
Best Local Similarity 89.3%; Pred. No. 3.6e-53;
Matches 117; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDDVMTQSLPVLVSLGDAQASISCRSSQSLVHSYNGTYLHWY 60
QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPW 120
QY 121 AFGGGTKLEIK 131
Db 121 TFGGGTKLEIK 131

RESULT 13
PCT-US91-02942-3
; Sequence 3, Application PC/TUS9102942
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ADHAWAL, DILJEET S
; TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 102
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02942
; FILING DATE: 19910429
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0586600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 466-0800
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 173 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-02946-3

Query Match      88.9%; Score 610; DB 5; Length 173;
Best Local Similarity 88.6%; Pred. No. 7.9e-53;
Matches 117; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPDSSDDVMTQSLPVLVSLGDAQASISCRSSQSLVHSNGNYLHWY 60
QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPL 120

; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5865. US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-589-939-7

Query Match      89.2%; Score 612; DB 3; Length 131;
Best Local Similarity 89.3%; Pred. No. 3.6e-53;
Matches 117; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSDDVMTQSLPVLVSLGDAQASISCRSSQSLVHSYNGTYLHWY 60
QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPW 120
QY 121 AFGGGTKLEIK 131
Db 121 TFGGGTKLEIK 131

RESULT 14
PCT-US91-02946-3
; Sequence 3, Application PC/TUS9102946
; GENERAL INFORMATION:
; APPLICANT: ROTHLEIN, ROBERT
; APPLICANT: ADAIR, JOHN R
; APPLICANT: ROBINSON, MARTYN K
; APPLICANT: BRIGHT, SUSAN M
; TITLE OF INVENTION: HUMANIZED CHIMERIC ICAM-1 ANTIBODY
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Ave. NW Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02946
; FILING DATE: 19910429
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, SAM L
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 1011.0576600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 173 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US91-02946-3

Query Match      88.9%; Score 610; DB 5; Length 173;
Best Local Similarity 88.6%; Pred. No. 7.9e-53;
Matches 117; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSLPVLVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPDSSDDVMTQSLPVLVSLGDAQASISCRSSQSLVHSNGNYLHWY 60
QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPL 120
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Qy 121 AFGGKLEIKR 132  
Db 121 TFGGKLEIKR 132

RESULT 15  
US-07-977-696C-11  
; Sequence 11, Application US/07977696C  
; Patent No. 5792852  
; GENERAL INFORMATION:  
; APPLICANT: do Couto, Fernando J.R.  
; APPLICANT: Ceriani Dr., Roberto L.  
; APPLICANT: Peterson Dr., Jerry A.  
; APPLICANT: Fadlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides with Specificity  
; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination  
; TITLE OF INVENTION: and Therapeutic Methods.  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/977,696C  
; FILING DATE: 11-16-92  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Anzel Ph.D., Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: P66 38227  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (510) 748-6868  
; TELEFAX: (510) 748-6688  
; TELEX: n.a.  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-07-977-696C-11

Query Match 86.7%; Score 595; DB 1; Length 131;  
Best Local Similarity 86.3%; Pred No. 1.7e-51;  
Matches 113; Conservative 11; Mismatches 7; Indels 0; Gaps 0;  
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Db 1 MKLPVRLVLMFWIPASISDVMTQTPSLPVLGDAQASISCRSSQNLVHNGNTLYWY 60  
Qy 61 LQKQGQSKLLIYKVSDRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120  
Db 61 LQKQGQSKLLIYRASIRFSGGSGTDFTLKISRVEADLGVYFCQGTHVPW 120  
Qy 121 AFGGKLEIK 131  
Db 121 TFGGKLEIK 131

Search completed: May 25, 2005, 15:58:26  
Job time : 17.454 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 60.9042 Seconds  
(without alignments)  
724.991 Million cell updates/sec

Title: US-10-006-773A-15  
Perfect score: 686  
Sequence: 1 MKLPVRLVLMFWIPASNSD.....FGSHVYAFGGGKLEIKR 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
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19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686	100.0	132	13	US-10-006-773-15
2	644	93.9	131	15	US-10-434-469-6
3	644	93.9	131	17	US-10-409-608A-17
4	639	93.1	149	9	US-09-990-205-2
5	637	92.9	131	15	US-10-388-214A-2
6	637	92.9	139	15	US-10-372-481-29
7	637	92.9	139	15	US-10-371-797-29
8	635	92.6	149	14	US-10-153-401-2
9	633	92.3	149	15	US-10-226-795-27
10	625	91.1	132	9	US-09-796-744-16
11	625	91.1	132	14	US-10-231-452-64
12	624	91.0	131	10	US-09-947-839-95
13	624	91.0	131	14	US-10-010-942B-14

14	624	91.0	131	15	US-10-388-389-14	Sequence 14, Appl
15	624	91.0	131	16	US-10-703-713-14	Sequence 14, Appl
16	624	91.0	131	16	US-10-704-070-14	Sequence 14, Appl
17	624	91.0	131	17	US-10-232-030-14	Sequence 14, Appl
18	619	90.2	140	9	US-09-341-894-4	Sequence 4, Appl
19	617	89.9	131	14	US-10-138-505-6	Sequence 6, Appl
20	617	89.9	131	15	US-10-227-864A-85	Sequence 85, Appl
21	617	89.9	131	15	US-10-221-131-90	Sequence 90, Appl
22	617	89.9	131	15	US-10-399-518-114	Sequence 114, Appl
23	615	89.7	256	15	US-10-257-864A-98	Sequence 98, Appl
24	615	89.7	256	15	US-10-221-131-103	Sequence 103, Appl
25	615	89.7	256	15	US-10-399-518-127	Sequence 127, Appl
26	614	89.5	131	14	US-10-138-505-10	Sequence 10, Appl
27	614	89.5	131	15	US-10-257-864A-87	Sequence 87, Appl
28	614	89.5	131	15	US-10-221-131-92	Sequence 92, Appl
29	614	89.5	131	15	US-10-399-518-116	Sequence 116, Appl
30	608	88.6	131	17	US-10-687-035-27	Sequence 27, Appl
31	595	86.7	131	10	US-09-947-839-11	Sequence 11, Appl
32	594	86.6	131	17	US-10-735-316A-63	Sequence 63, Appl
33	593	86.4	131	17	US-10-735-316A-67	Sequence 67, Appl
34	586	85.4	131	17	US-10-687-035-29	Sequence 29, Appl
35	584	85.1	122	17	US-10-735-316A-49	Sequence 49, Appl
36	580.5	84.6	127	9	US-09-753-436-45	Sequence 45, Appl
37	580.5	84.6	127	14	US-10-163-942-45	Sequence 45, Appl
38	562.5	82.0	132	15	US-10-388-214A-6	Sequence 6, Appl
39	562	81.9	249	16	US-10-803-622-190	Sequence 190, Appl
40	562	81.9	249	16	US-10-803-653-190	Sequence 190, Appl
41	559	81.5	112	10	US-09-995-529-10	Sequence 10, Appl
42	559	81.5	112	11	US-09-995-529-10	Sequence 10, Appl
43	559	81.5	112	17	US-10-735-316A-56	Sequence 56, Appl
44	556	81.0	112	17	US-10-735-316A-57	Sequence 57, Appl
45	553	80.6	112	15	US-10-434-469-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1  
US-10-006-773-15  
; Sequence 15, Application US/10006773  
; Publication No. US20020132983A1  
; GENERAL INFORMATION:  
; APPLICANT: Junghans, Richard P.  
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Ant  
; FILE REFERENCE: 003  
; CURRENT APPLICATION NUMBER: US/10/006,773  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/250,089  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-006-773-15

Query Match 100.0%; Score 686; DB 13; Length 132;  
Best Local Similarity 100.0%; Pred. No. 9.5e-57;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPPLSLPVSLGDAQISCRSSQSIHVSNGDTYLEWY 60  
DB 1 MKLPVRLVLMFWIPASNSDVLMTQSPPLSLPVSLGDAQISCRSSQSIHVSNGDTYLEWY 60  
QY 61 LQKPEQSPKLLIYKVYSDRFSGVDPDRFSGSGGTFTLKISRVEADLGVYFCQGSHPY 120  
DB 61 LQKPEQSPKLLIYKVYSDRFSGVDPDRFSGSGGTFTLKISRVEADLGVYFCQGSHPY 120  
QY 121 AFGGKTKLEIKR 132  
DB 121 AFGGKTKLEIKR 132

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RESULT 2
US-10-434-469-6
; Publication 6, Application US/10434469
; Publication No. US20040091480A1
; GENERAL INFORMATION:
; APPLICANT: Nobuo HANAI
; APPLICANT: Motoo YAMASAKI
; APPLICANT: Akiko FURUYA
; APPLICANT: Akira TANAKA
; APPLICANT: Kenya SHITARA
; APPLICANT: Naoki SHIMADA
; TITLE OF INVENTION: Anti-fibroblast growth factor-8 monoclonal antibody
; FILE REFERENCE: 249-310
; CURRENT APPLICATION NUMBER: US/10/434,469
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: JP 08-081754
; PRIOR FILING DATE: 1996-04-03
; PRIOR APPLICATION NUMBER: US 08/832,236
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: US 09/326,590
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: US 09/876,040
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-434-469-6

Query Match          93.9%; Score 644; DB 15; Length 131;
Best Local Similarity 93.9%; Pred. No. 8.4e-53;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVRLLLVLMFWIPASNSDVLMTQSLPVLPSLGLDQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLLLVLMFWIPASNSDVLMTQSLPVLPSLGLDQASISCRSSQSIHVSNGRTYLEWY 60

QY 61 LQKPGQSPKLLIYKVSVDPSGSGSGTDFTLKISRVEADLGYVFCQGSHPVY 120
Db 61 LQKPGQSPKLLIYKVSNRISGVDPDRFSGSGGTDFTLKISRVEADLGYVFCQGSHPVY 120

QY 121 AFGGGTKLEIK 131
Db 121 TFGGGTKLEIK 131

RESULT 3
US-10-409-608A-17
; Sequence 17, Application US/10409608A
; Publication No. US20050031613A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
; TITLE OF INVENTION: Therapeutic agent for patients having human FcγRIIIa
; FILE REFERENCE: 249-304
; CURRENT APPLICATION NUMBER: US/10/409,608A
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: 2002-106951
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-409-608A-17

Query Match          93.9%; Score 644; DB 17; Length 131;
Best Local Similarity 93.9%; Pred. No. 8.4e-53;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MKLPVRLLLVLMFWIPASNSDVLMTQSLPVLPSLGLDQASISCRSSQSIHVSNGRTYLEWY 60

QY 61 LQKPGQSPKLLIYKVSVDPSGSGSGTDFTLKISRVEADLGYVFCQGSHPVY 120
Db 61 LQKPGQSPKLLIYKVSNRISGVDPDRFSGSGGTDFTLKISRVEADLGYVFCQGSHPVY 120

QY 121 AFGGGTKLEIK 131
Db 121 TFGGGTKLEIK 131

RESULT 5
US-10-388-214A-2
; Sequence 2, Application US/10388214A
; Publication No. US20040082762A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE BETA
; TITLE OF INVENTION: AMYLOID PEPTIDE
; FILE REFERENCE: ELN-004
; CURRENT APPLICATION NUMBER: US/10/388,214A
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/363,751
; PRIOR FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-388-214A-2

Query Match          93.1%; Score 639; DB 9; Length 149;
Best Local Similarity 92.4%; Pred. No. 2.9e-52;
Matches 122; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MKLPVRLLLVLMFWIPASNSDVLMTQSLPVLPSLGLDQASISCRSSQSIHVSNGRTYLEWY 60

QY 61 LQKPGQSPKLLIYKVSVDPSGSGSGTDFTLKISRVEADLGYVFCQGSHPVY 120
Db 61 LQKPGQSPKLLIYFVSNRFGVDPDRFSGSGGTDFTLKISRVEADLGYVFCQGSHPVW 120

QY 121 AFGGGTKLEIKR 132
Db 121 TFGGGTKLEIKR 132

RESULT 6
US-09-990-205-2
; Sequence 2, Application US/09990205
; Patent No. US20020150572A1
; GENERAL INFORMATION:
; APPLICANT: FOON, Kenneth A.
; APPLICANT: CHATTERJEE, Malaya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
; FILE REFERENCE: 30414200501
; CURRENT APPLICATION NUMBER: US/09/990,205
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: U.S. 09/192,838
; PRIOR FILING DATE: 1998-11-16
; PRIOR APPLICATION NUMBER: U.S. 60/065,774
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-990-205-2

Query Match          93.1%; Score 639; DB 9; Length 149;
Best Local Similarity 92.4%; Pred. No. 2.9e-52;
Matches 122; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MKLPVRLLLVLMFWIPASNSDVLMTQSLPVLPSLGLDQASISCRSSQSIHVSNGRTYLEWY 60

QY 61 LQKPGQSPKLLIYKVSVDPSGSGSGTDFTLKISRVEADLGYVFCQGSHPVY 120
Db 61 LQKPGQSPKLLIYFVSNRFGVDPDRFSGSGGTDFTLKISRVEADLGYVFCQGSHPVW 120

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; FEATURE:
; NAME/KEY: SIGNAL
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US-10-388-214A-2

Query Match          92.9%; Score 637; DB 15; Length 131;
Best Local Similarity 92.4%; Pred. No. 3.8e-52;
Matches 121; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60
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Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQSHVPY 120

Qy 121 AFGGGTKLEIK 131
Db 121 TFGAGTKLEIK 131

RESULT 6
US-10-372-481-29
; Sequence 29, Application US/10372481
; Publication No. US20030202975A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405.306
; CURRENT APPLICATION NUMBER: US/10/372,481
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-481-29

Query Match          92.9%; Score 637; DB 15; Length 139;
Best Local Similarity 91.7%; Pred. No. 4.1e-52;
Matches 121; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MKLPVRLVLMFWIPASSSDVMTQTPVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQSHVPY 120

Qy 121 AFGGGTKLEIK 131
Db 121 TFGAGTKLEIK 131

RESULT 7
US-10-371-797-29
; Sequence 29, Application US/10371797
; Publication No. US20040001828A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; TITLE OF INVENTION: ANTIBODIES
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; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 139
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-371-797-29

Query Match          92.9%; Score 637; DB 15; Length 139;
Best Local Similarity 91.7%; Pred. No. 4.1e-52;
Matches 121; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60
Db 1 MKLPVRLVLMFWIPASSSDVMTQTPVSLGDAQASISCRSSQSIHVSNGDTYLEWY 60

Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQSHVPY 120
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQSHVPY 120

Qy 121 AFGGGTKLEIK 132
Db 121 TFGGGTKLEIK 132

RESULT 8
US-10-153-401-2
; Sequence 2, Application US/10153401
; Publication No. US20030114398A1
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malay A.
; Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/153,401
; FILING DATE: 27-Aug-2002
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/293,533
; FILING DATE: 1999-04-15
; APPLICATION NUMBER: US 08/372,676
; FILING DATE: 1995-01-17
; APPLICATION NUMBER: US 08/591,196
; FILING DATE: 1996-01-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine M. Polizzi
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 304142000202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
```



QY 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQGSHPY 120  
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQGSHPY 120

QY 121 AFGGGTKLEIKR 132  
Db 121 TFGGGRLEIR 132

## RESULT 12

US-09-947-839-95  
; Sequence 95, Application US/09947839  
; Publication No. US20030138428A1  
; GENERAL INFORMATION:  
; APPLICANT: do Couto Dr., Fernando J.R.  
; Ceriani Dr., Roberto L.  
; Peterson Dr., Jerry A.  
; Padlan Dr., Eduardo A.  
; TITLE OF INVENTION: Analogue Peptides With Broad  
; Carcinoma Specificity, and Kit and  
; Diagnostic Vaccination and  
; Therapeutic Methods  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pretty, Schroeder & Poplawski  
; STREET: 444 South Floor St., 19th Floor  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: USA  
; ZIP: 90071

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/09/947,839  
; FILING DATE: 06-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/976,288  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 07/977,696  
; FILING DATE: NO. US20030138428A1ember 16, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Viviana Amzel Ph.D.  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: P6639938  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 622-7700  
; TELEFAX: (213) 489-4210  
; TELEX: n.a.

INFORMATION FOR SEQ ID NO: 95:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 131 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:  
US-09-947-839-95

Query Match 91.0%; Score 624; DB 10; Length 131;  
Best Local Similarity 90.1%; Pred. No. 6.3e-51;  
Matches 118; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGNTYLEWY 60  
Db 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGNTYLEWY 60  
QY 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQGSHPY 120  
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQGSHPY 120

QY 121 AFGGGTKLEIK 131  
Db 121 TFGGGTKLEIK 131

## RESULT 13

US-10-010-942B-14  
; Sequence 14, Application US/10010942B  
; Publication No. US20030165496A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; FILE REFERENCE: ELN-002  
; CURRENT APPLICATION NUMBER: US/10/010,942B  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1).....(19)  
US-10-010-942B-14

Query Match 91.0%; Score 624; DB 14; Length 131;  
Best Local Similarity 88.5%; Pred. No. 6.3e-51;  
Matches 116; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGNTYLEWY 60  
Db 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHNSGNTYLEWY 60  
QY 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQGSHPY 120  
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSDTFTLKISRVEADLGVYFCQGSHPY 120  
QY 121 AFGGGTKLEIK 131  
Db 121 TFGAGTKLELE 131

## RESULT 14

US-10-388-389-14  
; Sequence 14, Application US/10388389  
; Publication No. US2004008777A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; FILE REFERENCE: ELN-002CP  
; CURRENT APPLICATION NUMBER: US/10/388,389  
; CURRENT FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL

; LOCATION: (1)...(19)  
US-10-388-389-14  
Query Match 91.0%; Score 624; DB 15; Length 131;  
Best Local Similarity 88.5%; Pred. No. 6.3e-51;  
Matches 116; Conservative 11; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MKLPVLLVLMFWIPASNSDVLMTQSLPVSLSGDAQISCRSSQSIHVSNGDTYLEWY 60  
Db 1 MKLPVLLVLMFWIPASSDVLMTQSLPVSLSGDAQISCRSSQSIHVSNGDTYLEWY 60  
QY 61 LQKPGQSPKLLIYKVDVRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCFQGSHPVY 120  
Db 61 LQKPGQSPKLLIYKVDVRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCFQGSHPVY 120  
QY 121 AFGGTTKLEIK 131  
Db 121 TFGAGTKLELE 131

RESULT 15  
US-10-703-713-14  
; Sequence 14, Application US/10703713  
; Publication No. US20040171815A1  
; GENERAL INFORMATION:  
; APPLICANT: Basi, Guriq  
; APPLICANT: Saidanha, Jose  
; APPLICANT: Yednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA-AMYLROID PEPTIDE  
; FILE REFERENCE: ELN-002CP  
; CURRENT APPLICATION NUMBER: US/10/703,713  
; CURRENT FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(19)  
US-10-703-713-14

Query Match 91.0%; Score 624; DB 16; Length 131;  
Best Local Similarity 88.5%; Pred. No. 6.3e-51;  
Matches 116; Conservative 11; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MKLPVLLVLMFWIPASNSDVLMTQSLPVSLSGDAQISCRSSQSIHVSNGDTYLEWY 60  
Db 1 MKLPVLLVLMFWIPASSDVLMTQSLPVSLSGDAQISCRSSQSIHVSNGDTYLEWY 60  
QY 61 LQKPGQSPKLLIYKVDVRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCFQGSHPVY 120  
Db 61 LQKPGQSPKLLIYKVDVRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGVYFCFQGSHPVY 120  
QY 121 AFGGTTKLEIK 131  
Db 121 TFGAGTKLELE 131

Search completed: May 25, 2005, 16:06:53  
Job time : 62.0292 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 18.6642 Seconds  
(without alignments)  
680.480 Million cell updates/sec

Title: US-10-006-773A-15  
Perfect score: 686  
Sequence: 1 MKLPVRLVLMFWIPASNSD.....FQGSHPVYAFGGTKLEIKR 132

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	646	94.2	131	2 B39276	Ig light chain pre
2	627	91.4	131	2 B34904	Ig kappa chain pre
3	623	90.8	131	2 B32513	Ig kappa chain pre
4	623	90.8	131	2 C34904	Ig kappa chain pre
5	620	90.4	131	2 B30577	Ig kappa chain pre
6	619	90.2	131	2 D34904	Ig kappa chain pre
7	618	90.1	131	2 S09259	Ig kappa chain pre
8	616	89.8	132	2 PH0106	anti-digoxin trans
9	611	89.1	131	2 G34903	Ig kappa chain pre
10	601	87.6	131	2 S2449	Ig kappa chain v r
11	599.5	87.4	131	2 D29380	Ig kappa chain pre
12	594	86.6	131	2 PT0178	Ig kappa chain pre
13	593	86.4	119	2 A49032	Ig kappa chain v r
14	591.5	86.2	130	2 C29380	Ig kappa chain pre
15	590	86.0	118	2 S24503	Ig kappa chain v r
16	585	85.3	118	2 S24500	Ig kappa chain v r
17	584	85.1	118	2 S24529	Ig kappa chain v r
18	583	85.0	118	2 S24536	Ig kappa chain v r
19	581	84.7	118	2 S24535	Ig kappa chain v r
20	578	84.3	118	2 S24533	Ig kappa chain v r
21	571	83.2	118	2 S24532	Ig kappa chain v r
22	568	82.8	118	2 S24530	Ig kappa chain v r
23	567	82.7	118	2 S24538	Ig kappa chain v r
24	558	81.3	118	2 S24506	Ig kappa chain v r
25	558	81.3	118	2 S24509	Ig kappa chain v r
26	557	81.2	219	2 PC4203	Ig kappa chain (mo
27	556	81.0	112	2 A31807	Ig kappa chain v r
28	555	80.9	110	2 S26335	Ig kappa chain v r
29	554	80.8	219	2 S52028	Ig kappa chain - m

Query Match 94.2%; Score 646; DB 2; Length 131;  
Best Local Similarity 93.9%; Pred. No. 1.3e-50;  
Matches 123; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVLSLGDQASISCRSSQSIHNSGNTYLEWY 60  
Db 1 MKLPVRLVLMFWIPVSSDVLMTQTPVLSLGDQASISCRSSQSIHNSGNTYLEWY 60

Qy 61 LQKFGQSPKLIYKVSDRFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPVY 120  
Db 61 LQKFGQSPKLIYKVSNRFSVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPVY 120

Qy 121 AFGGGTKLEIK 131  
Db 121 TFGSGTKLEIK 131

RESULT 2  
B34904  
Ig kappa chain precursor V region (12-40 and 5-14) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 21-Jul-2000  
C:Accession: B34904; H34903  
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A:Title: Active site structure and antigen binding properties of idiotypically cross-reacting antibodies  
A:Reference number: A34903; MUID:90094387; PMID:2104617  
A:Accession: B34904  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-131 <BED>  
A:Cross-references: GB:M32384; GB:J05237; GB:J05238; NID:G639656; PIDN:AAA61589.1; PID:G

RESULT 1  
B39276  
Ig light chain precursor V-D-J region (6-19) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 21-Jan-2000  
C:Accession: B39276  
R:Reininger, L.; Berner, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.  
Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990  
A:Title: Cryoglobulinemia induced by a murine ICG3 rheumatoid factor: skin vasculitis as a model for human disease  
A:Reference number: A39276; MUID:91088540; PMID:2263605  
A:Accession: B39276  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-131 <REI>  
A:Cross-references: GB:M55313; NID:G198095; PIDN:AAA63385.1; PID:G198096  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:35-114/Domain: immunoglobulin homology <IMM>

ALIGNMENTS

C;Keywords: heterotetramer; immunoglobulin  
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 91.4%; Score 627; DB 2; Length 131;  
Best Local Similarity 90.8%; Pred. No. 6.6e-49;  
Matches 119; Conservative 8; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIYVHSGDITYLEWY 60  
DB 1 MKLPVRLVLMFWIPASSDDVMTQTPLSPLVSLGDAQASISCRSSQSLVHSGNTYLVHWY 60  
  
QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSGHVPY 120  
DB 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSGHVPY 120  
  
QY 121 AFGGGTKLEIK 131  
DB 121 TFGGGTKLEIK 131

RESULT 3  
B32513  
Ig kappa chain precursor V region (MRL4) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 21-May-1990 #sequence\_revision 31-Dec-1990 #text\_change 21-Jan-2000  
C;Accession: B32513  
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;  
J. Clin. Invest. 82, 852-860, 1988  
A;Title: Immunoglobulin kappa light chain variable region gene complex organization and  
A;Reference number: A94689; MUID:88331394; PMID:3138286  
A;Accession: B32513  
A;Molecule type: DNA  
A;Residues: 1-131 <KOF>  
A;Cross-references: GB:M20828; NID:gl96937; PIDN:AAA38843.1; PID:gl96938  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.8%; Score 623; DB 2; Length 131;  
Best Local Similarity 90.8%; Pred. No. 1.5e-48;  
Matches 119; Conservative 6; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIYVHSGDITYLEWY 60  
DB 1 MKLPVRLVLMFWIPASSDDVMTQTPLSPLVSLGDAQASISCRSSQSLVHSGNTYLVHWY 60  
  
QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSGHVPY 120  
DB 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSGHVPY 120  
  
QY 121 AFGGGTKLEIK 131  
DB 121 TFGGGTKLEIK 131

RESULT 4  
C34904  
Ig kappa chain precursor V region (3-24) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 09-Jul-2004  
C;Accession: C34904; I31485  
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A;Title: Active site structure and antigen binding properties of idiotypically cross-re  
A;Reference number: A34903; MUID:90094387; PMID:2104617  
A;Accession: C34904  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-131 <BED>  
R;Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.  
J. Biol. Chem. 264, 1565-1569, 1989  
A;Title: Comparison of variable region primary structures within an anti-fluorescein idi

A;Reference number: A31485; MUID:89109167; PMID:2492278  
A;Accession: I31485  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 20-52 <BE2>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.8%; Score 623; DB 2; Length 131;  
Best Local Similarity 90.1%; Pred. No. 1.5e-48;  
Matches 118; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIYVHSGDITYLEWY 60  
DB 1 MKLPVRLVLMFWIPASSDDVMTQTPLSPLVSLGDAQASISCRSSQSLVHSGNTYLVHWY 60  
  
QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSGHVPY 120  
DB 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSGHVPY 120  
  
QY 121 AFGGGTKLEIK 131  
DB 121 TFGGGTKLEIK 131

RESULT 5  
B30577  
Ig kappa chain precursor V region (MRL10) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 04-May-1989 #sequence\_revision 04-May-1989 #text\_change 09-Jul-2004  
C;Accession: B30577  
R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theo  
J. Exp. Med. 161, 805-815, 1985  
A;Title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely rel  
A;Reference number: A30577; MUID:85159423; PMID:3920343  
A;Accession: B30577  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-131 <KOF>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.4%; Score 620; DB 2; Length 131;  
Best Local Similarity 90.1%; Pred. No. 2.7e-48;  
Matches 118; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIYVHSGDITYLEWY 60  
DB 1 MKLPVRLVLMFWIPASSDDVMTQTPLSPLVSLGDAQASISCRSSQSLVHSGNTYLVHWY 60  
  
QY 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSGHVPY 120  
DB 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSGHVPY 120  
  
QY 121 AFGGGTKLEIK 131  
DB 121 TFGGGTKLEIK 131

RESULT 6  
D34904  
Ig kappa chain precursor V region (3-13) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 21-Jan-2000  
C;Accession: D34904  
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A;Title: Active site structure and antigen binding properties of idiotypically cross-re  
A;Reference number: A34903; MUID:90094387; PMID:2104617  
A;Accession: D34904

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-131 <BED>

A;Cross-references: GB:L39105; NID:G639658; PIDN:AAA61590.1; PID:G639659

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.2%; Score 619; DB 2; Length 131;  
Best Local Similarity 89.3%; Pred. No. 3.4e-48;  
Matches 117; Conservative 9; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60  
Db 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60  
  
Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120  
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120  
  
Qy 121 AFGGGTKLEIK 131  
Db 121 TFGGGTKLEIK 131

#### RESULT 7

S09259

Ig kappa chain precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 21-Jan-2000

C;Accession: S09259

R;Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRX

A;Reference number: S09258; MUID:90245594; PMID:2110659

A;Accession: S09259

A;Molecule type: mRNA

A;Residues: 1-131 <HAN>

A;Cross-references: EMBL:X51720; NID:G53213; PIDN:CAA36013.1; PID:G53214

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 90.1%; Score 618; DB 2; Length 131;  
Best Local Similarity 90.1%; Pred. No. 4.1e-48;  
Matches 118; Conservative 7; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60  
Db 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60  
  
Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120  
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120  
  
Qy 121 AFGGGTKLEIK 131  
Db 121 TFGGGTKLEIK 131

#### RESULT 8

PH0106

anti-digoxin transfectoma antibody heavy chain V region precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C;Accession: PH0106

R;Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.

Mol. Immunol. 27, 901-909, 1990

A;Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain

A;Reference number: PH0105; MUID:91015092; PMID:2120577

A;Accession: PH0106

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-132 <NEA>

A;Cross-references: UNIPROT:Q8VCI6

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 89.8%; Score 616; DB 2; Length 132;  
Best Local Similarity 89.4%; Pred. No. 6.3e-48;  
Matches 118; Conservative 8; Mismatches 6; Indels 0; Gaps 0;  
  
Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60  
Db 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60  
  
Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120  
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120  
  
Qy 121 AFGGGTKLEIK 132  
Db 121 TFGGGTKLEIK 132

#### RESULT 9

G34903

Ig kappa chain precursor V region (10-25) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 21-Jan-2000

C;Accession: G34903

R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

J. Biol. Chem. 265, 133-138, 1990

A;Title: Active site structure and antigen binding properties of idiotypically cross-reac

A;Reference number: A34903; MUID:90094387; PMID:2104617

A;Accession: G34903

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-131 <BED>

A;Cross-references: GB:M32381; GB:J05237; GB:J05238; NID:G639654; PIDN:AAA61588.1; PID:G

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 89.1%; Score 611; DB 2; Length 131;  
Best Local Similarity 87.8%; Pred. No. 1.7e-47;  
Matches 115; Conservative 9; Mismatches 7; Indels 0; Gaps 0;  
  
Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60  
Db 1 MKLPVRLVLMFWIPASNSDVLMTQSPVSLVSLGDAQASISCRSSQSIHNSGDTYLEWY 60  
  
Qy 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120  
Db 61 LQKPGQSPKLLIYKVSDFRFGSGGSGTDFTLKISRVEADLGVYFCQGSHPY 120  
  
Qy 121 AFGGGTKLEIK 131  
Db 121 TFGGGTKLEIK 131

#### RESULT 10

S52449

Ig kappa chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000

C;Accession: S52449

R;Berdos, J.; Kraehenbuhl, J.P.

submitted to the EMBL Data Library, November 1994

A;Description: Specific amplification by the polymerase chain reaction of rearranged gen

A;Reference number: S52445

A;Accession: S52449

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-131 <BER>

A;Cross-references: EMBL:X82691; NID:G673446; PIDN:CAAS8012.1; PID:G673447

C;Genetics: 16/1  
 A;Introns: 16/1  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 87.6%; Score 601; DB 2; Length 131;  
 Best Local Similarity 85.5%; Pred. No. 1.3e-46;  
 Matches 112; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPSLPVLGDAQASISCRSSQSI VHSNGDTYLEWY 60  
 DB 1 MKLPVRLVLMFWIPVSSSDVVMVTQTPSLPVLGDAQASISCRSSQSLVHNGDTYLYHWY 60

QY 61 LQKPGQSPKLLIYKVSDRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120  
 DB 61 LQKPGSPKLLIYKVSDRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSTHVPW 120

QY 121 AFGGGTKLEIK 131  
 DB 121 TFGGGTKLEIK 131

RESULT 11  
 D29380  
 IG kappa chain precursor V region (B003 46/2D7) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
 C;Accession: D29380  
 R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.  
 J. Biol. Chem. 262, 13579-13583, 1987  
 A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable  
 A;Reference number: A92612; MUID:88007582; PMID:3115981  
 A;Accession: D29380  
 A;Molecule type: mRNA  
 A;Residues: 1-131 <CHE>  
 A;Cross-references: UNIPROT:Q8VC16  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;34-113/Domain: immunoglobulin homology <IMM>

Query Match 87.4%; Score 599.5; DB 2; Length 131;  
 Best Local Similarity 87.9%; Pred. No. 1.8e-46;  
 Matches 116; Conservative 9; Mismatches 6; Indels 1; Gaps 1;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPSLPVLGDAQASISCRSSQSI VHSNGDTYLEWY 60  
 DB 1 MKLPVRLVLMFWIPASSSDVVMVTQTPSLPVLGDAQASISCRSSQSLVHNGDTYLOWY 59

QY 61 LQKPGQSPKLLIYKVSDRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120  
 DB 60 LQKPGQSPKLLIYKVSDRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSTHLP 119

QY 121 AFGGGTKLEIK 132  
 DB 120 TFGGGTKLEIK 131

RESULT 12  
 PT0178  
 IG kappa chain precursor V region (IGB5.7) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C;Accession: PT0178  
 R;Perfetti, V.; Borden, P.; Tao, M.H.; Morrison, S.L.; Kabat, E.A.  
 Mol. Immunol. 28, 505-515, 1991  
 A;Title: Specificity and variable region cDNA sequence of an isogeneic monoclonal antiid  
 A;Reference number: PT0174; MUID:91287738; PMID:1712074  
 A;Accession: PT0178  
 A;Molecule type: mRNA  
 A;Residues: 1-131 <PER>  
 A;Cross-references: UNIPROT:Q8VC16  
 A;Experimental source: strain BALB/c

C;Comment: Idb5.7 is an antibody to anti-alpha (1-6) dextran.  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 86.6%; Score 594; DB 2; Length 131;  
 Best Local Similarity 85.5%; Pred. No. 5.7e-46;  
 Matches 112; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPSLPVLGDAQASISCRSSQSI VHSNGDTYLEWY 60  
 DB 1 MKLPVRLVLMFWIPASSSDVVMVTQTPSLPVLGDAQASISCRSSQSLVHNGDTYLYHWY 60

QY 61 LQKPGQSPKLLIYKVSDRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPY 120  
 DB 61 LQKPGQSPKLLIYKVSDRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSTHVP 120

QY 121 AFGGGTKLEIK 131  
 DB 121 TFGGGTKLEIK 131

RESULT 13  
 A49032  
 IG kappa chain V region (anti-phenylloxazalone) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 19-Dec-1993 #sequence\_revision 19-Apr-1996 #text\_change 21-Jan-2000  
 C;Accession: A49032; S24528; S24512  
 R;Kaartinen, M.; Solin, M.L.; Makela, O.  
 Eur. J. Immunol. 21, 2863-2869, 1991  
 A;Title: V genes of oxazolone antibodies in 10 strains of mice.  
 A;Reference number: A49032; MUID:92037836; PMID:1936125  
 A;Accession: A49032  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-119 <KAA>  
 A;Cross-references: NID:G238586; PIDN:AAB20266.1; PID:G238587  
 A;Experimental source: C57BL/10  
 A;Note: sequence extracted from NCBI backbone (NCBIN:64186, NCBI:64193)  
 R;Kaartinen, M.  
 submitted to the EMBL Data Library, October 1991  
 A;Reference number: S24490  
 A;Accession: S24528  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-118 <KAA>  
 A;Cross-references: EMBL:X66624; EMBL:X66631  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotetramer; immunoglobulin  
 F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 86.4%; Score 593; DB 2; Length 119;  
 Best Local Similarity 95.0%; Pred. No. 6.3e-46;  
 Matches 113; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLPVRLVLMFWIPASNSDVLMTQSPSLPVLGDAQASISCRSSQSI VHSNGDTYLEWY 60  
 DB 1 MKLPVRLVLMFWIPASSSDVVMVTQTPSLPVLGDAQASISCRSSQSI VHSNGDTYLEWY 60

QY 61 LQKPGQSPKLLIYKVSDRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVP 119  
 DB 61 LQKPGQSPKLLIYKVSDRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSHVP 119

RESULT 14  
 C29380  
 IG kappa chain precursor V region (BC-1004) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 21-Jul-2000  
 C;Accession: C29380  
 R;Chen, H.T.; Kabat, E.A.; Lundblad, A.; Ratcliffe, R.M.  
 J. Biol. Chem. 262, 13579-13583, 1987  
 A;Title: Nucleotide and translated amino acid sequences of cDNA coding for the variable



A:Reference number: A92612; MUID:88007582; PMID:3115981  
A:Accession: C29380  
A:Molecule type: mRNA  
A:Residues: 1-130 <CHE>  
A:Cross-references: GB:M17162; GB:J02815; NID:g196899; PIDN:AAA38826.1; PID:g196900  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-113/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 591.5; DB 2; Length 130;  
Best Local Similarity 87.8%; Pred. No. 9.4e-46;  
Matches 115; Conservative 9; Mismatches 6; Indels 1; Gaps 1;  
Qy 2 KLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHSHNGDTYLEWYL 61  
Db 1 KLPVRLVLMFWIPASSDVLMTQSPLSPLVSLGDAQASISCRSSQSLVHSHNGNTYLQWYL 60  
Qy 62 QKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPYA 121  
Db 61 QKPGQSPKLLIYTVSNRFGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHTL-RT 119  
Qy 122 FGGGTKLEIKR 132  
Db 120 FGGGTKLEIKR 130

RESULT 15  
S24503  
Ig kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S24503; S24499  
R:Kaartinen, M.  
submitted to the EMBL Data Library, October 1991  
A:Reference number: S24490  
A:Accession: S24503  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-118 <KAA>  
A:Cross-references: UNIPROT:Q99M37; EMBL:X66640; EMBL:X66636  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 86.0%; Score 590; DB 2; Length 118;  
Best Local Similarity 95.8%; Pred. No. 1.1e-45;  
Matches 113; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKLPVRLVLMFWIPASNSDVLMTQSPLSPLVSLGDAQASISCRSSQSIHSHNGDTYLEWY 60  
Db 1 MKLPVRLVLMFWIPASSDVLMTQSPLSPLVSLGDAQASISCRSSQSLVHSHNGNTYLEWY 60  
Qy 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 118  
Db 61 LQKPGQSPKLLIYKVSDFSGVDPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQGSHPV 118

Search completed: May 25, 2005, 16:48:40  
Job time : 18.6642 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	555	80.9	248	2	K65207	Q652q7 mus sp. b3 (
2	524	76.4	113	1	KV2G_MOUSE	P01631 mus musculu
3	518.5	75.6	239	2	Q8TCD0	Q8tcd0 homo sapien
4	514.5	75.0	133	1	KV2F_HUMAN	P06310 homo sapien
5	505	73.6	219	2	Q652C0	P06320 mus musculu
6	497.5	72.5	239	2	Q6P491	Q6p491 homo sapien
7	494.5	72.1	239	2	Q8NEK0	Q8nek0 homo sapien
8	480	70.0	240	2	Q6PIH6	Q6pih6 homo sapien
9	456	66.5	117	1	KV2E_HUMAN	P06309 homo sapien
10	448	65.3	113	1	KV2D_HUMAN	P01617 homo sapien
11	447.5	65.2	114	2	Q9UL80	Q9ul80 homo sapien
12	445	64.9	113	1	KV2B_HUMAN	P01615 homo sapien
13	434	63.3	113	1	KV2E_MOUSE	P03976 mus musculu
14	431.5	62.9	115	1	KV2A_HUMAN	P01614 homo sapien
15	420.5	61.3	112	1	KV2C_HUMAN	P01616 homo sapien
16	415	60.5	112	1	KV2D_MOUSE	P01629 mus musculu
17	413	60.2	113	1	KV2F_MOUSE	P01630 mus musculu
18	401	58.5	134	1	KV4C_HUMAN	P06314 homo sapien
19	400.5	58.4	133	1	KV4B_HUMAN	P06313 homo sapien
20	396	57.7	112	2	Q6LEM8	Q6lem8 mus musculu
21	390.5	56.9	114	1	KV4A_HUMAN	P01625 homo sapien
22	388.5	56.6	132	1	KV3F_MOUSE	P01658 mus musculu
23	386.5	56.3	131	1	KV3I_MOUSE	P01661 mus musculu
24	383.5	55.9	235	2	Q6GMV9	Q6gmV9 homo sapien
25	382.5	55.8	129	1	KV3L_HUMAN	P18135 homo sapien
26	381.5	55.6	129	1	KV3M_HUMAN	P18136 homo sapien
27	380.5	55.5	238	2	Q66J57	Q66j57 mus musculu
28	380	55.4	236	2	Q6PIL8	Q6pil8 homo sapien
29	379.5	55.3	108	1	KV1_CANFA	P01618 canis famli
30	378	55.1	113	1	KV2C_MOUSE	P01628 mus musculu
31	373	54.4	128	1	KV3K_HUMAN	P06311 homo sapien

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=A/J;  
RX MEDLINE=83178921; PubMed=6404298;  
RA Novotny J., Margolies M.N.;  
RT "Amino acid sequence of the light chain variable region from a mouse  
anti-digoxin hybridoma antibody";  
RL Biochemistry 22:1153-1158(1983).  
CC -I- MISCELLANEOUS: This chain was isolated from an IgG2a hybridoma  
protein that binds digoxin.  
DR PIR; A01914; KVM526.  
DR HSSP; Q99M37; 1191.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region;  
KW Monoclonal antibody.  
FT DOMAIN 1 23 Framework-1.  
FT DOMAIN 24 39 Complementarity-determining-1.  
FT DOMAIN 40 54 Framework-2.  
FT DOMAIN 55 61 Complementarity-determining-2.  
FT DOMAIN 62 93 Framework-3.  
FT DOMAIN 94 102 Complementarity-determining-3.  
FT DOMAIN 103 112 Framework-4.  
FT DISULFID 23 93 By similarity.  
FT NON TER 113 113  
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;  
  
Query Match 76.4%; Score 524; DB 1; Length 113;  
Best Local Similarity 88.5%; Pred. No. 9.6e-46;  
Matches 100; Conservative 7; Mismatches 6; Indels 0; Gaps 0;  
  
QY 20 DVLMTQPSLPSVLGDAQISCRSSQSIIVHSGNDTYLWYLOKQPSKLLIYKVSDFR 79  
DB 1 DVMTQPSLPSVLGDAQISCRSSQSIIVHSGNDTYLWYLOKQPSKLLIYKVSDFR 60  
  
QY 80 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPYAFGGGTGLEIKR 132  
DB 61 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVPYAFGGGTGLEIKR 113  
  
RESULT 3  
Q8TCD0 PRELIMINARY; PRT; 239 AA.  
AC Q8TCD0  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Uudin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzyszewski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; BC022362; AAH2362.1; -.  
DR PIR; S22658; S22658.  
DR PIR; S34095; S34095.  
DR PIR; S40324; S40324.  
DR PIR; S40374; S40374.  
DR PIR; S42267; S42267.  
DR PIR; S42268; S42268.  
DR HSSP; P01834; 1172.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig-cl.  
DR InterPro; IPR003006; Ig MHC.  
DR InterPro; IPR003596; Ig V.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;  
  
Query Match 75.6%; Score 518.5; DB 2; Length 239;  
Best Local Similarity 73.7%; Pred. No. 8.6e-45;  
Matches 98; Conservative 19; Mismatches 15; Indels 1; Gaps 1;  
  
QY 1 MKLPVRLRL-VLMFWIPASNSDVLMTQPSLPSVLGDAQISCRSSQSIIVHSGNDTYLW 59  
DB 1 MKLPVRLRL-VLMFWIPASNSDVLMTQPSLPSVLGDAQISCRSSQSIIVHSGNDTYLW 60  
  
QY 60 YLQKPGQSKLLIYKVSDFRFGVPRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVP 119  
DB 61 FQQRPGQSKLLIYKVSDFRFGVPRFSGSGGTDTFTLKISRVEAEDLGVYFCFGSHVP 120  
  
QY 120 YAFGGGTGLEIKR 132  
DB 121 STFGGTGLEIKR 133  
  
RESULT 4  
KV2P\_HUMAN STANDARD; PRT; 133 AA.  
ID KV2P\_HUMAN  
AC P06310;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region RPMI 6410 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=86041852; PubMed=2997711;  
RX Klobbeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;  
RT "Human immunoglobulin kappa light chain genes of subgroups II and  
III";  
RL Nucleic Acids Res. 13:6499-6513(1985).  
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between the Swiss Institute of Bioinformatics and the EMBL outstation  
at the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way



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DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00230; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match 72.5%; Score 497.5; DB 2; Length 239;
Best Local Similarity 69.2%; Pred. No. 1.2e-42;
Matches 92; Conservative 22; Mismatches 18; Indels 1; Gaps 1;

QY 1 MKLPVRL-LVLMFWIPASNSDVLMTQSPSLPVSIGDQASISCRSSQSVHNSGDTYLEW 59
Db 1 MRLLAQLGLLMLWPGSGDIVMTQTPLSSPTLGPASISCRSSSELHNSGNTYLSW 60
QY 60 YLQKPGSQKLLIYKVSRFSGVDPDRFSGSGGTFTLKISRVEADLGVYCFQGSHPV 119
Db 61 LHQRPGQPPRLIYKISNRFSGVDPDRFSGSGAGTFTLKISRVEADVGYYCMQVSHFP 120
QY 120 YAFGGGTKEIKR 132
Db 121 RTFGQGTKEIKR 133

RESULT 7
Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk U., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AAH30814.1; -.
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSP; P01834; I172.
DR InterPro; IPR007110; IG-like.
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DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 72.1%; Score 494.5; DB 2; Length 239;
Best Local Similarity 69.9%; Pred. No. 2.5e-42;
Matches 93; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

QY 1 MKLPVRL-LVLMFWIPASNSDVLMTQSPSLPVSIGDQASISCRSSQSVHNSGDTYLEW 59
Db 1 MRLPAQLGLLMLWPGSGDIVMTQSPSLPVTGEPASISCRSSQSLHSDGNYLDM 60
QY 60 YLQKPGSQKLLIYKVSRFSGVDPDRFSGSGGTFTLKISRVEADLGVYCFQGSHPV 119
Db 61 YLQKPGSQKLLIYKSNRSGVDPDRFSGSGGTFTLKISRVEADVGYYCMQGLQTP 120
QY 120 YAFGGGTKEIKR 132
Db 121 QTFGQGTKEIKR 133

RESULT 8
Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk U., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034142; AAH34142.1; -.
DR HSP; P01837; IKB5.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8B8B781EC4 CRC64;

Query Match 70.0%; Score 480; DB 2; Length 240;
Best Local Similarity 70.1%; Pred. No. 7.6e-41;
Matches 94; Conservative 16; Mismatches 22; Indels 2; Gaps 2;

Qy 1 MKLPVRLIL-VLMFWIPASNDVLTQSPSLSPVSLGDAQSICRSSOSIVHSNGDTYLEW 59
Db 1 MRLPAQLGLMLVSGSGDIVMAQSPSLSVTFGEPASISCRSSQSLHSNGVYFDW 60

Qy 60 YLQKPGQPKLLIYKVSDFSGVDFRFGSGSGTDFTLKISRVEADLGVYFCFGSHV- 118
Db 61 YLQKPGQPKLLIYKVSDFSGVDFRFGSGSGTDFTLKISRVEADLGVYFCFGSHV- 118

Qy 119 PYAFGGGTTKLEIKR 132
Db 121 PYTFGGGTTKLEIKR 134

RESULT 9
KV2D_HUMAN
ID KV2D_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RL Nature 309:73-76 (1984).
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DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 4
FT CHAIN 5 117 Ig kappa chain V-II region GM607.
FT DOMAIN 5 27 Framework-1.
FT DOMAIN 28 43 Complementarity-determining-1.

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FT DOMAIN 44 58 Framework-2.
FT DOMAIN 59 65 Complementarity-determining-2.
FT DOMAIN 66 97 Framework-3.
FT DOMAIN 98 106 Complementarity-determining-3.
FT DOMAIN 107 116 Framework-4.
FT DISULFID 27 97 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 65.5%; Score 456; DB 1; Length 117;
Best Local Similarity 75.0%; Pred. No. 9.2e-39;
Matches 87; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 17 SNSDLVMTQSPSLSPVSLGDAQSICRSSOSIVHSNGDTYLEWYLOKPGQPKLLIYKVS 76
Db 2 SSGDIVMTQSPSLSPVTFGEPASISCRSSQSLHSNGVYLDWYLOKPGQPKLLIYLG 61

Qy 77 DRFSGVDFRFGSGSGTDFTLKISRVEADLGVYFCFGSHVPAFAGGTTKLEIKR 132
Db 62 NRASGVDFRFGSGSGTDFTLKISRVEADLGVYFCFGSHVPAFAGGTTKLEIKR 117

RESULT 10
KV2D_HUMAN
ID KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RT Primary amyloidosis.";
RL Biochemistry 12:3763-3780 (1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Ooserman E.F.;
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281 (1973).
CC -1- MISCELLANEOUS: The major amyloid protein appears to be identical
CC with the Bence Jones protein isolated from the same patient.
CC -1- MISCELLANEOUS: This protein was isolated from the urine of a
CC patient with plasma cell dyscrasia and amyloidosis.
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
DR PIR; A90370; K2HUTW.
DR HSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Amyloid; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.

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FT DOMAIN      103   112   Framework-4.
FT DISULFID    23    93   By similarity.
FT NON_TER     113   113
SQ SEQUENCE    113 AA; 12316 MW; 0C3C8F81F1843CA CRC64;

Query Match      65.3%; Score 448; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 5.8e-38;
Matches 84; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 20 DVLMTQSPSLPVSIGDQASISCRSSQSIHVHNGDTYLEWYIQKPGQSPKLIYKVSDRF 79
Db 1 DIVMTQSPSLPVTGPAPASISCRSSQSLHSDGFDYLNWYIQKPGQSPZLLIYALSNDRA 60

QY 80 SGVPRDFSGSGSGTDFTLKISRVEADLGIVYCFQGSHPVYAFGGTGLEIKR 132
Db 61 SGVPRDFSGSGSGTDFTLKISRVEADGVYVCMZALQAPITFGQGTGLEIKR 113

RESULT 11
Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment)...
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]_TaxID=9606;
RN SEQUENCE FROM N.A.
RP MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -.
DR PIR; B49002; B49002.
DR PIR; S23638; S23638.
DR PIR; S34094; S34094.
DR PIR; S34095; S34095.
DR HSSP; P01625; ILVE.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match      65.2%; Score 447.5; DB 2; Length 114;
Best Local Similarity 76.3%; Pred. No. 6.6e-38;
Matches 87; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

QY 20 DVLMTQSPSLPVSIGDQASISCRSSQSIHVHNGDTYLEWYIQKPGQSPKLIYKVSDRF 79
Db 1 DIVMTQSPSLPVTLPQAPASISCRSSQSPVSDGNTYLNWYIQKPGQSPRLIYKVSNRD 60

QY 80 SGVPRDFSGSGSGTDFTLKISRVEADLGIVYCFQGSHPVYAFGGTGLEIKR 132
Db 61 SGVPRDFSGSGSGTDFTLKISRVEADGVYVCMZALQAPITFGQGTGLEIKR 114

RESULT 12
KV2B_HUMAN STANDARD; PRT; 113 AA.
AC F01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)

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DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]_TaxID=9606;
RN SEQUENCE.
RP MEDLINE=76253627; PubMed=821524;
RX Riesen W.F., Jaton J.-C.;
RA "variable region sequence of the light chain from a Waldenstroms IgM
RT with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -I- MISCELLANEOUS; This chain was isolated from a Waldenstrom's
CC macroglobulin that binds phosphorylcholine.
DR PIR; A01886; K2HUPR.
DR HSSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 39 Complementarity-determining-1.
FT DOMAIN 40 54 Framework-2.
FT DOMAIN 55 61 Complementarity-determining-2.
FT DOMAIN 62 93 Framework-3.
FT DOMAIN 94 102 Complementarity-determining-3.
FT DOMAIN 103 112 Framework-4.
FT DISULFID 23 93 By similarity.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match      64.9%; Score 445; DB 1; Length 113;
Best Local Similarity 73.5%; Pred. No. 1.2e-37;
Matches 83; Conservative 15; Mismatches 15; Indels 0; Gaps 0;

QY 20 DVLMTQSPSLPVSIGDQASISCRSSQSIHVHNGDTYLEWYIQKPGQSPKLIYKVSDRF 79
Db 1 DIVMTQSPSLPVTLPQAPASISCRSSQSLVYRBGTYLWYIQKPGQSPZLLIYLVSSYRD 60

QY 80 SGVPRDFSGSGSGTDFTLKISRVEADLGIVYCFQGSHPVYAFGGTGLEIKR 132
Db 61 SGVPRDFSGSGSGTDFTLKISRVEADGVYVCMZALQAPITFGQGTGLEIKR 113

RESULT 13
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]_TaxID=10090;
RN SEQUENCE.
RP TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Aebersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 2S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -I- FUNCTION: Anti-streptococcal group A carbohydrate antibody.
DR PIR; A01912; KVM517.
DR HSSP; Q99M37; 1191.

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DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Hybridoma; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 63.3%; Score 434; DB 1; Length 113;
Best Local Similarity 71.7%; Pred. No. 1.6e-36;
Matches 81; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 20 DVLMTQSPSLSPVSLGDOASISCRSSQSIHVSNGDTYLEWYLOKPGQSPKLLIYKVSDFR 79
Db 1 DIVMTQAVFSPNVTIGTSASISCRSKSLHNSGITYLYWYLOKPGQSPQLLYQMSNLA 60

QY 80 SGVPRDFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVYPVAFGGTKLEIKR 132
Db 61 SGVPRDFSGSGSGTDFTLKISRVEAEDVGVYCAHNLELPYTFGGTKLEIKR 113

RESULT 14
KV2A HUMAN
ID KV2A HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01887; K2HUML.
DR HSSP; Q99M37; 119I.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 61.3%; Score 420.5; DB 1; Length 112;
Best Local Similarity 66.4%; Pred. No. 3.8e-35;
Matches 75; Conservative 23; Mismatches 14; Indels 1; Gaps 1;

QY 20 DVLMTQSPSLSPVSLGDOASISCRSSQSIHVSNGDTYLEWYLOKPGQSPKLLIYKVSDFR 79
Db 1 DIVLTQSPSLSPVTPGEPASISCRSSQNLQZSBGB-YLDWYLZKPGZSPZLLIYGSNRA 59

QY 80 SGVPRDFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVYPVAFGGTKLEIKR 132
Db 60 SGVPRDFSGSGSGTDFTLKISRVAZABGVYVYCAQLQTLTFFGGTINVEIKR 112

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Job time : 64.3423 secs
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Run on: May 25, 2005, 15:35:17 ; Search time 65.427 Seconds  
(without alignments)  
821.675 Million cell updates/sec

Title: US-10-006-773A-17  
Perfect score: 726  
Sequence: 1 MNFGLSLFLVLKVGQCE.....HSVGCWFATWGGTLVTVSA 139

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	726	100.0	139	6	ABG74247
2	590	81.3	133	6	ABG74243
3	581	80.0	137	2	AAW57592
4	581	80.0	137	2	AAW89625
5	581	80.0	137	3	AAW7513
6	581	80.0	137	4	AAW67102
7	581	80.0	137	4	AAW64775
8	581	80.0	137	4	AAW63393
9	581	80.0	137	5	ABW95208
10	581	80.0	137	6	ABJ36667
11	581	80.0	137	8	ADQ33883
12	578.5	79.7	138	2	AAW20064
13	578.5	79.7	138	8	ADR88408
14	577.5	79.5	138	5	ABG76924
15	562.5	77.5	144	5	ABW79720
16	555	76.4	141	8	ADQ43551
17	554	76.3	139	2	AAW52773
18	554	76.3	139	2	AAW52791
19	553.5	76.2	140	6	ABG74241
20	553.5	76.2	142	2	AAW30982
21	552	76.0	141	8	ADQ43555
22	550.5	75.8	136	2	AAW06251
23	546	75.2	139	2	AAW21656
24	543	74.8	140	2	AAW21654
25	542.5	74.7	138	2	AAW32246

26	542.5	74.7	138	2	AAW32242
27	542.5	74.7	139	2	AAW31588
28	542.5	74.7	462	6	AAO29869
29	542.5	74.7	462	7	ADJ79787
30	542.5	74.7	464	5	AAU72801
31	541.5	74.6	138	8	ADR47397
32	541	74.5	471	8	ADM72029
33	538.5	74.2	144	8	ADR47417
34	534.5	73.6	138	5	ABG76928
35	534.5	73.6	138	8	ADR88412
36	534.5	73.6	477	2	AAW47450
37	534.5	73.6	477	2	AAW47453
38	534	73.6	139	2	AAW52823
39	534	73.6	139	2	AAW70471
40	533.5	73.5	138	4	AAW67665
41	533.5	73.5	138	6	ABR40284
42	533.5	73.5	468	6	ABP58275
43	532.5	73.3	138	5	ABG76932
44	532.5	73.3	138	8	ADR88416
45	531.5	73.2	136	2	AAW56962

## ALIGNMENTS

RESULT 1  
ABG74247

ID ABG74247 standard; protein; 139 AA.

AC ABG74247;

DT 22-APR-2003 (first entry)

DE Mouse antibody 3E11 heavy chain variable region.

XX T-cell receptor; cytostatic; dermatological; neuroprotective;  
immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;  
3E11; prostate-specific membrane antigen; zeta signalling chain;  
CDalpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;  
small cell lung cancer; heavy chain variable region; mouse.

OS Mus sp.

PN US2002132983-A1.

XX 19-SEP-2002.

PD 10-DEC-2001; 2001US-00006773.

XX 30-NOV-2000; 2000US-0250087P.

XX 30-NOV-2000; 2000US-0250089P.

PA (JUNG/) JUNGHANS R P.

PI Junghans RP;

XX WPI; 2003-208946/20.

DR N-PSDB; ABX16573.

XX New chimeric molecule useful in treating patients with disorders, such as

PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer

XX comprises GD3 and/or PSMA binding domains of antibody.

PS Disclosure; Page 17; 35pp; English.

XX The invention relates to a chimaeric molecule comprising the GD3  
(ganglioside antigen) binding domain of antibody MB3.6, with any of 3  
variable gene sequences, or the PSMA (prostate-specific membrane antigen)  
binding domain of antibody 3D8, 4D4 and 3E11, with variable gene  
sequences, the zeta signalling chain of the T cell receptor and an  
intervening CD8alpha hinge in which cysteine residues have been mutated.  
The chimaeric molecules expressed in T cells or NK cells or other  
effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),  
 CC and/or together with each other or with heterologous constructs to engage  
 CC additional stimulatory and functional properties of the effector cells to  
 CC enhance the antitumour therapeutic efficacy (claimed). They are  
 CC particularly useful in disorders including melanoma, neuroendocrine  
 CC tumours and prostate and small cell lung cancer. The present sequence  
 CC represents the mouse antibody 3E11 heavy chain variable region  
 XX  
 SQ Sequence 139 AA;

Query Match 100.0%; Score 726; DB 6; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-59;  
 Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNYGMSWVRQTS 60  
 DB 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNYGMSWVRQTS 60  
 QY 61 DKRLWVASISTGGANTFYPDNVKGRTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120  
 DB 61 DKRLWVASISTGGANTFYPDNVKGRTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120  
 QY 121 SVGCWFATWGQGLTVTVSA 139  
 DB 121 SVGCWFATWGQGLTVTVSA 139

RESULT 2  
 ABG74243  
 ID ABG74243 standard; protein; 133 AA.

XX AC ABG74243;

XX DT 22-APR-2003 (first entry)

XX DE Mouse antibody 3D8 heavy chain variable region.

XX KW T-cell receptor; cytostatic; dermatological; neuroprotective;  
 KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;  
 KW 3E11; prostate-specific membrane antigen; zeta signalling chain;  
 KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;  
 KW small cell lung cancer; heavy chain variable region; mouse.

XX OS Mus sp.

XX PN US2002132983-A1.

XX PP 19-SEP-2002.

XX PF 10-DEC-2001; 2001US-00006773.

XX PR 30-NOV-2000; 2000US-0250087P.

XX PR 30-NOV-2000; 2000US-0250089P.

XX PA (JUNG/) JUNGHANS R P.

XX PI Junghans RP;

XX PI WPI; 2003-208946/20.

XX DR N-PSDB; ABX16569.

XX PT New chimeric molecule useful in treating patients with disorders, such as  
 PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer  
 PT comprises GD3 and/or PSMA binding domains of antibody.

XX PS Disclosure; Page 12; 35pp; English.

XX CC The invention relates to a chimeric molecule comprising the GD3  
 CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3  
 CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)  
 CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene  
 CC sequences, the zeta signalling chain of the T cell receptor and an  
 CC intervening CD8alpha hinge in which cysteine residues have been mutated.

CC The chimaeric molecules expressed in T cells or NK cells or other  
 CC effector cells are useful in treating patients with cancers expressing  
 CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),  
 CC and/or together with each other or with heterologous constructs to engage  
 CC additional stimulatory and functional properties of the effector cells to  
 CC enhance the antitumour therapeutic efficacy (claimed). They are  
 CC particularly useful in disorders including melanoma, neuroendocrine  
 CC tumours and prostate and small cell lung cancer. The present sequence  
 CC represents the mouse antibody 3D8 heavy chain variable region  
 XX  
 SQ Sequence 133 AA;

Query Match 81.3%; Score 590; DB 6; Length 133;  
 Best Local Similarity 83.5%; Pred. No. 6.6e-47;  
 Matches 116; Conservative 8; Mismatches 9; Indels 6; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNYGMSWVRQTS 60  
 DB 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFTFSNYGMSWVRQTS 60  
 QY 61 DKRLWVASISTGGANTFYPDNVKGRTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120  
 DB 61 DKRLWVASISSGGSTFYADNVKGRFTISRANAKNTLYLQMSLSKSEDTALYFCARDH 119  
 QY 121 SVGCWFATWGQGLTVTVSA 139  
 DB 120 ----LFWNGQGLTVTVSS 133

RESULT 3  
 AAW57592

ID AAW57592 standard; protein; 137 AA.

XX AC AAW57592;

XX DT 03-SEP-1998 (first entry)

XX DE Chimeric antibody against hPTRP H chain V region SEQ ID NO:57.

XX KW Chimeric; antibody; human parathormone related peptide; hPTRP; mouse;  
 KW L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR;  
 KW hypophosphataemia; pathogen; vitamin D resistance; V region; C region;  
 KW humanised.

XX OS Synthetic.

XX OS Mus sp.

XX OS Homo sapiens.

XX OS Chimeric.

XX PN WO9813388-A1.

XX PD 02-APR-1998.

XX PF 24-SEP-1997; 97WO-JP003382.

XX PR 26-SEP-1996; 96JP-00255196.

XX PR 24-JUL-1997; 97JP-00214169.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Sato K, Wakahara Y, Yabuta N;

XX DR WPI; 1998-230640/20.

XX DR N-PSDB; AAV24232.

XX PT New chimeric antibodies against human parathormone related peptide(s) -  
 PT useful for, e.g. treatment of hypercalcaemia and other disorders caused  
 PT by malignant neoplasm(s).

XX PS Claim 52; Page 120-121; 182pp; Japanese.

XX CC New antibodies have been developed which are specific for human  
 CC parathormone related peptides (hPTRP). The antibodies comprise chimeric L

CC and/or H chains, where the C region is of human and L region of mouse,  
 CC origin. The present sequence represents a specifically claimed region of  
 CC an antibody of the invention. Host cells, transformed with vectors  
 CC containing DNA encoding antibodies of the invention, can be used to  
 CC produce the antibodies. The antibodies may be used to treat  
 CC hypercalcaemia, especially that due to a malignancy, e.g. cancers of  
 CC pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,  
 CC breast, kidney, bladder, womb or prostate or malignant lymphoma. They may  
 CC also be used for treatment of hypophosphataemia such as that due to  
 CC pathogens or to vitamin D resistance

XX SQ Sequence 137 AA;

Query Match 80.0%; Score 581; DB 2; Length 137;  
 Best Local Similarity 79.1%; Pred. No. 4.7e-46;  
 Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;  
 Qy 1 MNFGLSLIFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSFNSYGMWVROTS 60  
 Db 1 MNFGLSLIFLALILKGVQCEVQLVSGGDLVKGPGSLKLSCAASGFTFSSYGMWIRQTP 60  
 Qy 61 DKRLWVASISTGGANTFYPDNVKGRTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120  
 Db 61 DKRLWVASISTGGSYTYPPDSVKGRTISRDNKNTLYLQMSLSKSDTAMFYCARQTT 120  
 Qy 121 SVGCWFATWGQGLTVTVSA 139  
 Db 121 MT--YFAYWGQGLTVTVSA 137

RESULT 4

AAW89625  
 ID AAW89625 standard; protein; 137 AA.

AC AAW89625;

DT 14-APR-1999 (first entry)

DE Mouse humanised antibody #23-57-137-1 heavy chain protein.

KW Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;  
 KW inhibitor; humanised.

OS Mus sp.

OS Synthetic.

PH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= signal  
 FT Protein 20..137

XX WO9851329-A1.

XX PD 19-NOV-1998.

XX PF 13-MAY-1998; 98WO-JP002116.

XX PR 15-MAY-1997; 97JP-00125505.

XX PR 18-JUL-1997; 97JP-00194445.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Sato K, Tunenari T, Ishii K;

XX DR WPI; 1999-070101/06.

XX DR N-ESDB; AAX00092.

XX PT Inhibitors of binding of parathyroid hormone related peptide to its  
 PT receptor - useful for, e.g. treatment of cachexia arising from cancer or  
 PT other diseases.

XX Example 2; Page 82; 125pp; Japanese.

XX

CC The present invention describes compositions for the treatment of  
 CC cachexia containing a substance which inhibits the binding of a  
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an active  
 CC component. This substance may be an antagonist to the receptor, or an  
 CC antibody (preferably monoclonal) or antibody fragment, recognising PTHrP.  
 CC The antibody is preferably humanised or chimeric. The present invention  
 CC also describes a humanised antibody prepared by hybridoma 23-57-137-1  
 CC (FERM BP-5631). The composition is used for the treatment of cachexia  
 CC arising in connection with diseases such as cancer, thereby improving the  
 CC quality of life of the patient. The present sequence represents mouse  
 CC humanised antibody heavy chain from #23-57-137-1 from the present  
 CC invention

XX SQ Sequence 137 AA;

Query Match 80.0%; Score 581; DB 2; Length 137;  
 Best Local Similarity 79.1%; Pred. No. 4.7e-46;  
 Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;  
 Qy 1 MNFGLSLIFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSFNSYGMWVROTS 60  
 Db 1 MNFGLSLIFLALILKGVQCEVQLVSGGDLVKGPGSLKLSCAASGFTFSSYGMWIRQTP 60  
 Qy 61 DKRLWVASISTGGANTFYPDNVKGRTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120  
 Db 61 DKRLWVASISTGGSYTYPPDSVKGRTISRDNKNTLYLQMSLSKSDTAMFYCARQTT 120  
 Qy 121 SVGCWFATWGQGLTVTVSA 139  
 Db 121 MT--YFAYWGQGLTVTVSA 137

RESULT 5

AAW77513  
 ID AAW77513 standard; protein; 137 AA.

AC AAW77513;

DT 26-APR-2000 (first entry)

DE Mouse antibody H chain V region.

KW Hypercalcaemic crisis; parathyroid hormone related peptide; PTHrP; tumour.

OS Mus musculus.

XX WO200000219-A1.

XX PD 06-JAN-2000.

XX PF 25-JUN-1999; 99WO-JP003433.

XX PR 26-JUN-1998; 98JP-00180143.

XX PA (CHUS ) CHUGAI SEIYAKU KK.

XX PI Sato K, Tsunenari T;

XX DR WPI; 2000-117115/10.

XX DR N-ESDB; AAZ58913.

XX PT Treatment of hypercalcaemic crisis with a substance inhibiting binding of  
 PT parathyroid hormone related peptide to its receptor.

XX Example 2; Page 96-97; 120pp; Japanese.

XX The invention relates to a method of treatment of hypercalcaemic crisis. A  
 CC composition for the treatment of hypercalcaemic crisis contains as active  
 CC component a substance which inhibits the binding of parathyroid hormone  
 CC related peptide (PTHrP) to its receptor. The inhibitor is used for the  
 CC treatment of hypercalcaemic crisis, such as that associated with a  
 CC malignant tumour

XX

4

CC analgesic. The present sequence represents the heavy chain variable  
CC region (VH) precursor of anti-human PTHrP murine monoclonal antibody 23-  
CC 57-137-1

XX Sequence 137 AA;

Query Match 80.0%; Score 581; DB 4; Length 137;  
Best Local Similarity 79.1%; Pred. No. 4.7e-46;  
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVRQTS 60  
DB 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVRQTP 60  
QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120  
DB 61 DKRLWVATISSGGSYTYPPDSVKGRFTISRDNKNTLYLQMSLSKSDTAMFYCARQTT 120

QY 121 SVGCWFATWGQGLTVTVSA 139  
DB 121 MT--YFAYWGQGLTVTVSA 137

RESULT 8  
AAG63393  
ID AAG63393 standard; protein; 137 AA.

AC AAG63393;

DT 15-OCT-2001 (first entry)

DE Amino acid sequence of a murine polypeptide.

KW Parathyroid hormone-associated peptide; PTHrP; dental disease.

OS Mus musculus.

XX Key Location/Qualifiers  
FH Peptide 20..137  
FT /note= "mature protein"

XX WO200154725-A1.

XX 02-AUG-2001.

XX 14-DEC-2000; 2000WO-JP008875.

XX 25-JAN-2000; 2000JP-00083034.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Kato A, Suzuki M, Sugimoto T;

XX WPI; 2001-465459/50.

XX N-PSDB; AAH74284.

XX Parathyroid hormone-associated peptide binding inhibitors useful for  
XX treating dental disease.

XX Disclosure; Page 111-112; 140pp; Japanese.

XX The specification describes a treatment for dental diseases. The  
XX treatment comprises a substance that inhibits binding between parathyroid  
XX hormone-associated peptide and its receptor. The present sequence  
XX represents a murine protein, which is used in the course of the invention

XX Sequence 137 AA;

Query Match 80.0%; Score 581; DB 4; Length 137;  
Best Local Similarity 79.1%; Pred. No. 4.7e-46;  
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVRQTS 60

DB 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVRQTP 60  
QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120  
DB 61 DKRLWVATISSGGSYTYPPDSVKGRFTISRDNKNTLYLQMSLSKSDTAMFYCARQTT 120  
QY 121 SVGCWFATWGQGLTVTVSA 139  
DB 121 MT--YFAYWGQGLTVTVSA 137

RESULT 9  
ABB95208

ID ABB95208 standard; protein; 137 AA.

AC ABB95208;

XX 17-JUN-2002 (first entry)

DT Mouse joint disease realted protein SEQ ID NO 57.

KW Joint disease; PTH; PTHrP; parathyroid hormone-related peptide;  
KW parathyroid hormone; osteopathic; rheumatoid arthritis; arthritis.

XX Mus musculus.

XX WO200213865-A1.

XX 21-FEB-2002.

XX 15-AUG-2001; 2001WO-JP007044.

XX 16-AUG-2000; 2000JP-00247013.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Yoshikawa H;

XX WPI; 2002-257551/30.

XX N-PSDB; ABL94765.

XX Agents for ameliorating symptoms caused by joint diseases relating to PTH  
XX or PTHrP e.g. chronic rheumatoid arthritis, containing inhibitors on  
XX receptor binding of parathyroid hormone-related peptide.

XX Disclosure; Page 88-89; 112pp; Japanese.

XX The invention relates to agents for ameliorating symptoms causing joint  
XX diseases, containing a substance inhibiting the binding of a parathyroid  
XX hormone-related peptide to its receptor as active ingredient. The agents  
XX have osteopathic activity are useful for ameliorating symptoms caused by  
XX joint diseases relating to PTH or PTHrP e.g. chronic rheumatoid arthritis  
XX and arthritis deformans. The agents particularly improve the lowering of  
XX bone amount or suppression of bone reduction. The present sequence is  
XX that of a joint disease related protein, useful to the invention

XX Sequence 137 AA;

Query Match 80.0%; Score 581; DB 5; Length 137;  
Best Local Similarity 79.1%; Pred. No. 4.7e-46;  
Matches 110; Conservative 17; Mismatches 10; Indels 2; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVRQTS 60

DB 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSPSYGMSWVRQTP 60

QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120

DB 61 DKRLWVATISSGGSYTYPPDSVKGRFTISRDNKNTLYLQMSLSKSDTAMFYCARQTT 120

QY 121 SVGCWFATWGQGLTVTVSA 139

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XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 27-MAR-1992 (first entry)
XX MRK16-H chain.
XX Monoclonal antibody; light; heavy; chain; cancer; drug resistance.
XX Homo; sapiens.
OS Mus musculus.
OS Chimeric.
XX JP03254691-A.
XX 13-NOV-1991.
XX 02-MAR-1990; 90JP-00051563.
XX 02-MAR-1990; 90JP-00051563.
XX (GANK-) ZH GAN KENYUKAI.
PA (FUJI-) FUJITA GAKUEN GH.
PA (NICA-) JAPAN FOUND CANCER RES.
XX WPI; 1992-002461/01.
DR N-PSDB; AAQ20070.
XX Chimeric antibody against drug resistant cancer - comprises variable
PT region homologous to region in mouse monoclonal antibody and constant
PT region homologous to region in human immunoglobulin.
XX Disclosure; Fig 4; 20pp; Japanese.
XX A chimeric antibody against drug-resistant cancer consists of (1) a
CC variable region having an amino acid sequence homologous to a variable
CC region in the mouse monoclonal antibody against drug- resistance and (2)
CC a constant region having an amino acid sequence homologous to the
CC constant region in human immunoglobulin. The chimeric antibody
CC selectively inhibits the growth of cancer cells showing drug resistance
CC or enhances the sensitivity to the drug. The antibody is very low in
CC immunogenicity. The MRK16-L chain is shown in AAQ20071. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX Sequence 138 AA;
Query Match 79.7%; Score 578.5; DB 2; Length 138;
Best Local Similarity 79.9%; Pred. No. 8e-46;
Matches 111; Conservative 14; Mismatches 13; Indels 1; Gaps 1;
Qy 1 MNFGLSLIFLVILKGVQCEVLVESGGDLMPGASLKLSCAASGFSPSYNGMSWVROT 60
Db 1 MNFGLSLIFLVILKGVQCEVLVESGGDLMPGASLKLSCAASGFSPSYNGMSWVROT 60
Qy 61 DKRLWVASISTGGANTFYDPNVKGRFTISRENKNTLYLQWSSLSKSDTALYFCARDSH 120
Db 61 EKRLWVASISSGGNTYDPNVKGRFTISRDNAKNLYLQWSSLSKSDTALYFCAR-YY 119
Qy 121 SVGCWFATWGQGLTVTUSA 139
Db 120 RYEAWFASWGQGLTVTUSA 138
RESULT 13
ADR88408
ID ADR88408 standard; protein; 138 AA.
XX AC ADR88408;
XX 16-DEC-2004 (first entry)
DT Murine 3D6 immunoglobulin heavy chain variable region SEQ ID NO:4.
DE

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XX 3D6; heavy chain variable region; immunoglobulin;
KW complementarity determining region; CDR; 10D5; variable framework region;
KW neuroprotective; neurotropic; gene therapy; amyloidogenic disease;
KW Alzheimer's disease.
XX Mus musculus.
XX Key Location/Qualifiers
FH 1.19
FT /label= signal peptide
FT Protein 20.138
FT /label= mature protein
XX WO2004080419-A2.
XX 23-SEP-2004.
XX 12-MAR-2004; 2004WO-US007503.
XX 12-MAR-2003; 2003US-00388389.
XX (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX Basi G, Saldanha JW, Yednock T;
XX WPI; 2004-668880/65.
DR N-PSDB; ADR88407.
XX New humanized antibodies that recognize beta amyloid peptides, useful for
PT preventing or treating amyloidogenic diseases, such as Alzheimer's
PT disease.
XX Claim 2; SEQ ID NO 4; 176pp; English.
XX The invention relates to a novel humanised immunoglobulin light or heavy
CC chain. The humanised immunoglobulin light or heavy chain comprises:
CC variable region complementarity determining regions (CDR's) from the 3D6
CC immunoglobulin light chain variable region sequence of 132 amino acids
CC fully defined in the specification (ADR88406), or heavy chain variable
CC region sequence of 138 amino acids fully defined in the specification
CC (ADR88408); or from the 10D5 immunoglobulin light chain variable region
CC sequence of 131 amino acids given in the specification (ADR88418) or
CC heavy chain variable region sequence of 142 amino acids fully defined in
CC the specification (ADR88420); and a variable framework region from a
CC human acceptor immunoglobulin light or heavy chain sequence, provided
CC that at least one framework residue is substituted with the corresponding
CC amino acid residue from the mouse 3D6 or 10D5 light or heavy chain
CC variable region sequence, where the framework residue is a residue that
CC non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR
CC -interacting residue or a residue participating in the VL-VH interface.
CC An antibody of the invention has neuroprotective and neurotropic activity,
CC and may have a use in gene therapy. The composition and methods are
CC useful for preventing or treating an amyloidogenic disease, such as
CC Alzheimer's disease. The variable region sequence is useful in producing
CC a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin
CC chain, or its domain. The present sequence represents the murine 3D6
CC immunoglobulin heavy chain variable region.
XX Sequence 138 AA;
Query Match 79.7%; Score 578.5; DB 8; Length 138;
Best Local Similarity 82.7%; Pred. No. 8e-46;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;
Qy 1 MNFGLSLIFLVILKGVQCEVLVESGGDLMPGASLKLSCAASGFSPSYNGMSWVROT 60
Db 1 MNFGLSLIFLVILKGVQCEVLVESGGDLMPGASLKLSCAASGFSPSYNGMSWVROT 60
Qy 61 DKRLWVASISTGGANTFYDPNVKGRFTISRENKNTLYLQWSSLSKSDTALYFCARDSH 120
Db 61 DKRLWVASIRSGGRTYSDNVKGRFTISRENKNTLYLQWSSLSKSDTALYFCARDSH 120

```

```

QY 121 SVGCWFATWGGTFLVTVA 139
DB 121 YSGS-SDYWGQGTITVSS 138

RESULT 14
ABG76924
ID ABG76924 standard; protein; 138 AA.
XX
AC ABG76924;
XX
DT 05-NOV-2002 (first entry)
XX
DE Mouse 3D6 VH protein.
XX
KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW neutropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta.
XX
OS Mus musculus.
XX
PN WO200246237-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046587.
XX
PR 06-DEC-2000; 2000US-0251892P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP ) WYETH.
XX
PI Basi G, Saldanha J, Yednock T;
XX
WPI; 2002-519658/55.
DR N-PSDB; ABS59427.
XX
PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
PS Claim 68; Fig 2; 171pp; English.
XX
CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
CC variable heavy (VH) chain protein of the invention
XX
SQ Sequence 138 AA;

Query Match 79.5%; Score 577.5; DB 5; Length 138;
Best Local Similarity 82.0%; Pred. No. 1e-45;
Matches 114; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPFGASLKLSCAASGFSFNGYMSWVRQTS 60
DB 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPFGASLKLSCAASGFTFSNGYMSWVRQNS 60
QY 61 DKRLWVASISTGGANTFPDVKGRFTISRANKNTLYLQMSLSKSDTALYFCARDSH 120
DB 61 DKRLWVASIRSGGRTYSDNVKGRFTISRANKNTLYLQMSLSKSDTALYFCVRYDH 120
QY 121 SVGCWFATWGGTFLVTVA 139

RESULT 15
ABE79730
ID ABE79730 standard; protein; 144 AA.
XX
AC ABE79730;
XX
DT 29-OCT-2002 (first entry)
XX
DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VH.
XX
KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;
KW antibody; anticaries; transgenic plant; transgenic animal; caries;
KW immunotherapy; therapy.
XX
OS Mus musculus.
XX
PN US2002068066-A1.
XX
PD 06-JUN-2002.
XX
PF 15-JUN-2001; 2001US-00881823.
XX
PR 20-AUG-1999; 99US-00378577.
XX
PS (SHIW/) SHI W.
PA (MORR/) MORRISON S L.
PA (TRIN/) TRINH K.
PA (WIMS/) WIMS L.
PA (CHEN/) CHEN L.
PA (ANDE/) ANDERSON M H.
XX
PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;
XX
WPI; 2002-565838/60.
DR N-PSDB; ABN84611.
XX
PT Treatment and prevention of dental caries in mammals, in particular
PT humans by orally administering genetically engineered or purified
PT antibodies that bind to surface antigens of carcinogenic organisms.
XX
PS Claim 14; Fig 3B; 30pp; English.
XX
CC The present sequence is the protein sequence of the heavy chain variable
CC region (VH) of the murine monoclonal antibody SWLA3 (IgG), which binds
CC specifically to the surface antigens of cariogenic type c Streptococcus
CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC
CC HB 12558) hybridoma cells. In an example from the invention, chimeric
CC monoclonal antibody TEFE was produced comprising SWLA3 variable regions
CC and human antibody constant regions. Such chimeric monoclonal antibodies
CC can be used to prevent or treat dental caries in humans. The antibodies
CC engage the effector apparatus of the human immune system when they bind
CC to cariogenic organisms, resulting in their destruction. The chimeric
CC antibodies may be produced in edible plants, in transgenic animals, or in
CC chicken eggs for oral ingestion
XX
SQ Sequence 144 AA;

Query Match 77.5%; Score 562.5; DB 5; Length 144;
Best Local Similarity 75.4%; Pred. No. 2.6e-44;
Matches 107; Conservative 18; Mismatches 14; Indels 3; Gaps 1;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPFGASLKLSCAASGFSFNGYMSWVRQTS 60
DB 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPFGASLKLSCAASGFTFSNGYMSWVRQIP 60
QY 61 DKRLWVASISTGGANTFPDVKGRFTISRANKNTLYLQMSLSKSDTALYFCARDSH 120
DB 61 DKRLWVASIRSGGRTYSDNVKGRFTISRANKNTLYLQMSLSKSDTAMYYCRRDDG 120

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Qy 121 SVGWFAT--WGQGLTVTSA 139  
Db 121 SYGSIYYANDYWGQGLTVTSS 142

Search completed: May 25, 2005, 15:47:22  
Job time : 66.427 secs

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Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 17.3265 Seconds  
(without alignments)  
598.864 Million cell updates/sec

Title: US-10-006-773A-17  
Perfect score: 726  
Sequence: 1 MNGLSLIFLVVLKGVQCE.....HSVGCWFMWGQGLTVTUSA 139

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	542.5	74.7	138	1 US-08-053-171-7	Sequence 7, Appli
2	542.5	74.7	138	1 US-08-053-171-11	Sequence 11, Appl
3	542.5	74.7	135	3 US-08-579-378A-16	Sequence 16, Appl
4	541.5	74.6	136	3 US-08-976-183A-33	Sequence 33, Appl
5	540.5	74.4	136	3 US-08-976-183A-31	Sequence 31, Appl
6	537.5	74.0	136	3 US-08-976-183A-32	Sequence 32, Appl
7	536.5	73.9	136	3 US-08-976-183A-34	Sequence 34, Appl
8	535.5	73.8	136	1 US-08-253-877C-57	Sequence 57, Appl
9	535.5	73.8	136	1 US-08-452-164A-57	Sequence 57, Appl
10	534	73.6	139	1 US-08-129-930B-96	Sequence 96, Appl
11	534	73.6	139	3 US-08-134-346A-51	Sequence 51, Appl
12	534	73.6	139	3 US-08-976-288A-96	Sequence 96, Appl
13	533	73.4	135	3 US-08-579-378A-20	Sequence 20, Appl
14	530.5	73.1	247	5 PCT-US94-07659-2	Sequence 2, Appli
15	522.5	72.0	140	3 US-08-836-561-23	Sequence 23, Appl
16	522.5	72.0	140	4 US-09-434-122-23	Sequence 23, Appl
17	521.5	71.8	138	2 US-08-379-057-14	Sequence 14, Appl
18	517.5	71.3	158	2 US-08-653-402B-6	Sequence 6, Appli
19	501.5	69.1	158	2 US-08-653-402B-10	Sequence 10, Appl
20	493	67.9	124	4 US-09-518-737-2	Sequence 2, Appli
21	491	67.6	120	4 US-09-232-290-42	Sequence 42, Appl
22	491	67.6	456	4 US-09-495-880A-11	Sequence 11, Appl
23	489	67.4	135	5 PCT-US95-07302-8	Sequence 8, Appli
24	489	67.4	159	2 US-08-653-402B-2	Sequence 2, Appli
25	481	66.3	135	3 US-08-619-491-8	Sequence 8, Appli
26	479.5	66.0	130	4 US-09-225-322B-8	Sequence 8, Appli
27	479.5	66.0	130	4 US-09-764-304-8	Sequence 8, Appli

28	477.5	65.8	130	4 US-09-225-322B-18	Sequence 18, Appl
29	477.5	65.8	130	4 US-09-764-304-18	Sequence 18, Appl
30	477.5	65.7	135	3 US-08-619-491-4	Sequence 4, Appli
31	477	65.7	135	5 PCT-US95-07302-4	Sequence 4, Appli
32	476	65.6	255	2 US-07-690-192-4	Sequence 2, Appli
33	475.5	65.5	464	4 US-09-472-087-2	Sequence 2, Appli
34	475.5	65.5	464	4 US-09-472-087-66	Sequence 66, Appl
35	474.5	65.4	119	2 US-08-475-000-16	Sequence 16, Appl
36	474.5	65.4	119	2 US-08-483-199-16	Sequence 16, Appl
37	474.5	65.4	119	2 US-08-484-508-16	Sequence 16, Appl
38	473	65.2	123	1 US-08-356-272-3	Sequence 3, Appli
39	470.5	64.8	125	1 US-08-331-398A-65	Sequence 65, Appl
40	470.5	64.8	125	2 US-08-331-397B-65	Sequence 65, Appl
41	470.5	64.8	125	2 US-08-759-804A-64	Sequence 64, Appl
42	469.5	64.7	170	2 US-08-652-558-40	Sequence 40, Appl
43	467	64.3	251	1 US-08-398-612A-30	Sequence 30, Appl
44	467	64.3	251	1 US-08-398-611A-30	Sequence 30, Appl
45	467	64.3	251	2 US-08-491-334A-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1  
US-08-053-171-7  
; Sequence 7, Application US/08053171  
; Patent No. 5562903  
; GENERAL INFORMATION:  
; APPLICANT: Co, Loibner  
; TITLE OF INVENTION: Antibody Derivatives  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,171  
; FILING DATE: 22-APR-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-54-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 328-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 138 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-053-171-7

Query Match	74.7%	Score 542.5;	DB 1;	Length 138;
Best Local Similarity	77.0%;	Pred. No. 4.6e-51;		
Matches 107;	Conservative 10;	Mismatches 21;	Indels 1;	Gaps 1;
Oy	1	MNFGLSLIFLVVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSFSNYGMSVWRTS	60	
Db	1	MNGLSLIFLVVLKGVQCEVKLVESGGGLVQPGSLLKLSCATSGFTSDIYMYWVRQTP	60	
Oy	61	DKLEWVASISTGGANTFYDPNVKGRFTISRENAKNTLYLQMSLSKSEDTALYFCARDSH	120	
Db	61	EKLEWVAYISNGGSHYVDSVKGRFTISRDNKNTLYLQMSRLSRSDTAMVHCAR-GM	119	

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RESULT 3
US-08-579-378A-16
; Sequence 16, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew

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RESULT 4  
US-08-976-183A-33  
; Sequence 33, Application US/08976183A  
; Patent No. 6307026  
; GENERAL INFORMATION:  
; APPLICANT: King, David J.  
; APPLICANT: Adair, John R.  
; APPLICANT: Owens, Raymond J.  
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33  
; TITLE OF INVENTION: ANTIGEN  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARNER  
; STREET: 3000 K. Street, N.W., Suite 500  
; CITY: Washington, D.C.

```

; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183A-33

Query Match 74.6%; Score 541.5; DB 3; Length 136;
Best Local Similarity 77.0%; Pred. No. 5.8e-51;
Matches 107; Conservative 15; Mismatches 14; Indels 3; Gaps 1;

QY 1 MNFGLSLIFLVILKGVQCEKLVESGGDLMPGASLKLSCAASGFFSFNYGMSWVQRTS 60
Db 1 MNFGLSLIFLVILKGVQCEKLVESGGDLMPGASLKLSCAASGFFSFNYGMSWVQRT 60
QY 61 DKLEWVASISTGGANTFYDNDVKGRFTISRENAKNTLYLQWSSLKSGEDTALYFCARDSH 120
Db 61 EKELEWVATISSGGSYTYILDSVKGRFTISRDSARNTLYLQWSSLSRSEDALYYCA---P 117
QY 121 SVGCWFPATWGQGLTVTVSA 139
Db 118 TTVPVPAYMGOGTLTVTSA 136

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RESULT 5
US-08-976-183A-31
; Sequence 31, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,183A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/595,848
FILING DATE: 02-FEB-1996
APPLICATION NUMBER: PCT/GB93/02529
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9225853.2
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9315249.4
FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bernhard D. Saxe
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/151/CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-183A-31

Query Match 74.4%; Score 540.5; DB 3; Length 136;
Best Local Similarity 76.3%; Pred. No. 7.5e-51;
Matches 106; Conservative 16; Mismatches 14; Indels 3;

QY 1 MNFGSLIFLVLVLKGVQCEVKLVESGGDLNNPGASLKLSCAASGFSPSNYGMGMA
DB 1 MNFGSLIFLVLVLILKGVQCEVKLVESGGGLVKPGGSLKLSCAASGFAPFTYDYM
QY 61 DKLEWVASITGCGANTFYDNNVKGRFTISRENAKNTLYLQMSSLKSGEDTALYI
DB 61 EKLEWVATISSGGSYYIYLDVSKGRFTISRDSARNTLYLQMSSLRSEDALYI
QY 121 SGCWCFAWGQGLTVTVSA 139
DB 118 TTVVPFAYWGQGLTVTVSA 136

RESULT 6
US-08-976-183A-32
Sequence 32, Application US/08976183A
Patent No. 6307026
GENERAL INFORMATION:
APPLICANT: King, David J.
APPLICANT: Adair, John R.
APPLICANT: Owens, Raymond J.
TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K. Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/976,183A

FILING DATE: 02-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/595,848

FILING DATE: 02-FEB-1996

APPLICATION NUMBER: PCT/GB93/02529

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA: GB 9225853.2

APPLICATION NUMBER: 9315249.4

FILING DATE: 22-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Bernhard D. Saxe

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 40283/151/CARA

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:

LENGTH: 136 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-976-183A-32

Query Match 74.0%; Score 537.5; DB 3; Length 136;

Best Local Similarity 76.3%; Pred. No. 1.6e-50;

Matches 106; Conservative 15; Mismatches 15; Indels 3; Gaps 1;

QY 1 MNFGSLFLVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFSGNYGMSWVRQTS 60

Db 1 MNFGSLFLVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFSGNYGMSWVRQTP 60

QY 61 DKRLWVASISTGGANTFYPDNVKGRTTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120

Db 61 EKRLWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSLSRSEDALYYCA---P 117

QY 121 SVGCWFPATWGQGLTVTUSA 139

Db 118 TTVVPFAYWGQGLTVTUSA 136

RESULT 7

US-08-976-183A-34

Sequence 34, Application US/08976183A

Patent No. 6307026

GENERAL INFORMATION:

APPLICANT: King, David J.

APPLICANT: Adair, John R.

APPLICANT: Owens, Raymond J.

TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

TITLE OF INVENTION: ANTIGEN

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K. Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,183A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/595,848

FILING DATE: 02-FEB-1996

APPLICATION NUMBER: PCT/GB93/02529

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9225853.2

FILING DATE: 10-DEC-1993

APPLICATION NUMBER: 9315249.4

FILING DATE: 22-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Bernhard D. Saxe

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 40283/151/CARA

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 136 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-976-183A-34

Query Match 73.9%; Score 536.5; DB 3; Length 136;

Best Local Similarity 75.5%; Pred. No. 2e-50;

Matches 105; Conservative 16; Mismatches 15; Indels 3; Gaps 1;

QY 1 MNFGSLFLVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFSGNYGMSWVRQTS 60

Db 1 MNFGSLFLVLKGVQCEVKLVESGGDLMNPGASLKLSCAASGFSGNYGMSWVRQTP 60

QY 61 DKRLWVASISTGGANTFYPDNVKGRTTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120

Db 61 EKRLWVATISSGGSYTYLDSVKGRFTISRDSARNTLYLQMSLSRSEDALYYCA---P 117

QY 121 SVGCWFPATWGQGLTVTUSA 139

Db 118 TTVVPFAYWGQGLTVTUSA 136

RESULT 8

US-08-253-877C-57

Sequence 57, Application US/08253877C

Patent No. 5773001

GENERAL INFORMATION:

APPLICANT: Hamann, Philip R.

APPLICANT: Hinman, Lois

APPLICANT: Hollander, Irwin

APPLICANT: Holcomb, Ryan

APPLICANT: Hallett, William

APPLICANT: Tsou, Hwei-Ru

APPLICANT: Weiss, Martin J.

TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor

TITLE OF INVENTION: Agents and Intermediates for Their Synthesis

NUMBER OF SEQUENCES: 73

CORRESPONDENCE ADDRESS:

ADDRESSEE: American Cyanamid Company

STREET: One Cyanamid Plaza

CITY: Wayne

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07470-8426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30



```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253.877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-253-877C-57

Query Match 73.8%; Score 535.5; DB 1; Length 136;
Best Local Similarity 75.5%; Pred. No. 2.6e-50;
Matches 105; Conservative 16; Mismatches 15; Indels 3; Gaps 1;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSESNYGMWVROTS 60
Db 1 MNFGLSLFLVLKGVQCEVKLVESGGGLVPGGSLKLSCAASGFASFSTYDMSWVRQTP 60

Qy 61 DKRLWVASISTGGANTFYDPNVKGRFTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 EKRLWVATISSGGSYTYLLDSVKGRFTISRDSRNTLYLQMSLSRSEDTALYYCA---P 117

Qy 121 SVGCWFATWGGTTLVTUSA 139
Db 118 TTVVPFAYWGGTTLVTUSA 136

RESULT 9
US-08-452-164A-57
; Sequence 57, Application US/08452164A
; Patent No. 5877296
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452.164A
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2158

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253.877C
; FILING DATE: 03-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhard, Elizabeth M.
; REGISTRATION NUMBER: 31,088
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-253-877C-57

Query Match 73.8%; Score 535.5; DB 1; Length 136;
Best Local Similarity 75.5%; Pred. No. 2.6e-50;
Matches 105; Conservative 16; Mismatches 15; Indels 3; Gaps 1;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLNMPGASLKLSCAASGFSESNYGMWVROTS 60
Db 1 MNFGLSLFLVLKGVQCEVKLVESGGGLVPGGSLKLSCAASGFASFSTYDMSWVRQTP 60

Qy 61 DKRLWVASISTGGANTFYDPNVKGRFTISRANAKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 EKRLWVATISSGGSYTYLLDSVKGRFTISRDSRNTLYLQMSLSRSEDTALYYCA---P 117

Qy 121 SVGCWFATWGGTTLVTUSA 139
Db 118 TTVVPFAYWGGTTLVTUSA 136

RESULT 10
US-08-129-930B-96
; Sequence 96, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.
; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129.930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-129-930B-96

Query Match 73.6%; Score 534; DB 1; Length 139;
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Best Local Similarity 69.8%; Pred. No. 3.9e-50;
Matches 97; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQTS 60
Db 1 MDFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQAP 60

QY 61 DKRELEWASISTGCANTFYPDNVKGRFTTSRENKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 GKGLEWVAEISSGGNAYYQDTVTGRTTSRDNKNTLYLQMSLSRAEDTAVYVCAREDY 120

QY 121 SVGCWFATWGQGLTVTVSS 139
Db 121 GIPANFAYWGQGLTVTVSS 139

RESULT 11
US-08-134-346A-51
; Sequence 51, Application US/08134346A
; Patent No. 6281335
; GENERAL INFORMATION:
; APPLICANT: do Couto, F.J.R.
; APPLICANT: Ceriani, R.L.C.
; APPLICANT: Petersen, J.A.
; TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrager, Chong & Flaherty
; STREET: 300 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10022-7499
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,346A
; FILING DATE: 08-OCT-1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Onofrio, Dara L.
; REGISTRATION NUMBER: 34,889
; REFERENCE/DOCKET NUMBER: CLT 149,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-826-6565
; TELEFAX: 212-826-5909
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-134-346A-51

Query Match 73.6%; Score 534; DB 3; Length 139;
Best Local Similarity 69.8%; Pred. No. 3.9e-50;
Matches 97; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQTS 60
Db 1 MDFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQAP 60

QY 61 DKRELEWASISTGCANTFYPDNVKGRFTTSRENKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 GKGLEWVAEISSGGNAYYQDTVTGRTTSRDNKNTLYLQMSLSRAEDTAVYVCAREDY 120

QY 121 SVGCWFATWGQGLTVTVSS 139
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Db 121 GIPANFAYWGQGLTVTVSS 139

RESULT 12
US-08-976-288A-96
; Sequence 96, Application US/08976288A
; Patent No. 6315997
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination and
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder & Poplawski
; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976-288A
; FILING DATE: No. 6315997ember 21, 1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/129,930
; FILING DATE: September 30, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. 6315997ember 16, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-976-288A-96

Query Match 73.6%; Score 534; DB 3; Length 139;
Best Local Similarity 69.8%; Pred. No. 3.9e-50;
Matches 97; Conservative 22; Mismatches 20; Indels 0; Gaps 0;

QY 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQTS 60
Db 1 MDFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFNGMSWVRQAP 60

QY 61 DKRELEWASISTGCANTFYPDNVKGRFTTSRENKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 GKGLEWVAEISSGGNAYYQDTVTGRTTSRDNKNTLYLQMSLSRAEDTAVYVCAREDY 120

QY 121 SVGCWFATWGQGLTVTVSS 139
Db 121 GIPANFAYWGQGLTVTVSS 139
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RESULT 13
US-08-579-378A-20
; Sequence 20, Application US/08579378A
; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: L-Selectin
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8
; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebescheutz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-378A-20

Query Match 73.4%; Score 533; DB 3; Length 135;
Best Local Similarity 75.5%; Pred. No. 4.8e-50;
Matches 105; Conservative 15; Mismatches 15; Indels 4; Gaps 2;

Qy 1 MNFGLSLFLVLVLKGVQCEVKLVESGGLMNPGLSKLSCAASGFSFNYSNMGSMVRQTS 60
Db 1 MNFGLSLFLVLVLKGVQCEVKLVESGGLMNPGLSKLSCAASGFSFNYSNMGSMVRQTP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120
Db 61 DKRLWVASISTGG-STYYPDSVKGRFTISRDNKNTLYLQMSLSKSDTAVYYCARDYD 119

Qy 121 SVGCWFPATWGQGLTVTVSA 139
Db 120 G--YFDWVGQGLTVTVSS 135

RESULT 14
PCT-US94-07659-2
; Sequence 2, Application PC/TUS9407659
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; APPLICANT: Gross, Mitchell
; APPLICANT: Jonak, Zdenka L.
; APPLICANT: Theisen, Timothy
; APPLICANT: Hurlle, Mark
; APPLICANT: Jackson, Jeffrey R.
; TITLE OF INVENTION: Recombinant and Humanized Il-1 beta
; TITLE OF INVENTION: Antibodies for Treatment of Il-1 Mediated Inflammatory
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation - Corp.
; ADDRESSEE: Intellectual Property
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07659
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/090,534
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50171-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 270-5024
; TELEFAX: (610) 270-5090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07659-2

Query Match 73.1%; Score 530.5; DB 5; Length 247;
Best Local Similarity 74.8%; Pred. No. 1.9e-49;
Matches 104; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

Qy 1 MNFGLSLFLVLVLKGVQCEVKLVESGGLMNPGLSKLSCAASGFSFNYSNMGSMVRQTS 60
Db 1 MNFGLSLFLVLVLKGVQCEVKLVESGGLMNPGLSKLSCAASGFSFNYSNMGSMVRQTP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120
Db 61 EKRLDWAVYISSGGGTYPDYVTKGRFTISRDNKNTLYLQMSLSKSDTAMVHCARGGV 120

Qy 121 SVGCWFPATWGQGLTVTVSA 139
Db 121 RRG-YFDWVGAGTTVTVSS 138

RESULT 15
US-08-836-561-23
; Sequence 23, Application US/08836561
; Patent No. 6018032
; GENERAL INFORMATION:
; APPLICANT: KOIKE, Masamichi
; APPLICANT: FURUYA, Akiko
; APPLICANT: NAKAMURA, Kazuyasu
; APPLICANT: IIDA, Akihiro
; APPLICANT: ANAZAWA, Hideharu
; APPLICANT: HANA1, No. 6018032uo
```

APPLICANT: TAKATSU, Kiyoshi  
TITLE OF INVENTION: Antibody Against Human Interleukin-5  
TITLE OF INVENTION: Receptor Alpha Chain  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,561  
FILING DATE: 09-MAY-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 232384/95  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, III, Stanton T  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-115-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-836-561-23

Query Match 72.0%; Score 522.5; DB 3; Length 140;  
Best Local Similarity 71.6%; Pred. No. 6.9e-49;  
Matches 101; Conservative 20; Mismatches 17; Indels 3; Gaps 2;  
QY 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASIKLSCAASGFSFNYGMSWVRQTS 60  
DB 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASIKLSCAASGFSFNYGMSWVRQTS 60  
QY 61 DKRLWVASISTGGANTFYDPNVKGRFTISRENKNTLYLQMSLSKSEDTALYFCARDSH 120  
DB 61 DKRLWVASISTGGANTFYDPNVKGRFTISRENKNTLYLQMSLSKSEDTALYFCARDSH 120  
QY 121 SVGCWFAT--WGQGLTVTVSA 139  
DB 121 -YGNRYAMDYWGQGLTVTVSS 140

Search completed: May 25, 2005, 15:58:27  
Job time : 18.3265 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.



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; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-010-942B-4

Query Match
Best Local Similarity 79.7%; Score 578.5; DB 14; Length 138;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFPSNYGMSWVRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFPSNYGMSWVRQNS 60
Qy 61 DKLEWASISTGCANTFYDNNVKGRTTISRANKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 DKLEWASIRSGGRTTYSNDNVKGRFTISRANKNTLYLQMSLSKSEDTALYFCVRDYH 120
Qy 121 SVGCWFATWQGGTLVTVSA 139
Db 121 YSGS-SDYWGQGTIVTVSS 138

RESULT 6
US-10-388-389-4
; Sequence 4, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-388-389-4

Query Match
Best Local Similarity 79.7%; Score 578.5; DB 15; Length 138;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFPSNYGMSWVRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFPSNYGMSWVRQNS 60
Qy 61 DKLEWASISTGCANTFYDNNVKGRTTISRANKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 DKLEWASIRSGGRTTYSNDNVKGRFTISRANKNTLYLQMSLSKSEDTALYFCVRDYH 120
Qy 121 SVGCWFATWQGGTLVTVSA 139
Db 121 YSGS-SDYWGQGTIVTVSS 138

RESULT 7
US-10-703-713-4
; Sequence 4, Application US/10703713
; Publication No. US20040171815A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/703,713
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-703-713-4

Query Match
Best Local Similarity 79.7%; Score 578.5; DB 16; Length 138;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFPSNYGMSWVRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFPSNYGMSWVRQNS 60
Qy 61 DKLEWASISTGCANTFYDNNVKGRTTISRANKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 DKLEWASIRSGGRTTYSNDNVKGRFTISRANKNTLYLQMSLSKSEDTALYFCVRDYH 120
Qy 121 SVGCWFATWQGGTLVTVSA 139
Db 121 YSGS-SDYWGQGTIVTVSS 138

RESULT 8
US-10-704-070-4
; Sequence 4, Application US/10704070
; Publication No. US20040171816A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/704,070
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-704-070-4

Query Match
Best Local Similarity 79.7%; Score 578.5; DB 16; Length 138;
Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFPSNYGMSWVRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFPSNYGMSWVRQNS 60
Qy 61 DKLEWASISTGCANTFYDNNVKGRTTISRANKNTLYLQMSLSKSEDTALYFCARDSH 120
Db 61 DKLEWASIRSGGRTTYSNDNVKGRFTISRANKNTLYLQMSLSKSEDTALYFCVRDYH 120
Qy 121 SVGCWFATWQGGTLVTVSA 139
Db 121 YSGS-SDYWGQGTIVTVSS 138

```

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; EDUCATION NO: 052000401161351
;
; GENERAL INFORMATION:
; APPLICANT: Basl, Gurik
; APPLICANT: Saldanha, Jose
;
; Query Match 79.7%; Score 578.5; DB 16; Length 138;
; Best Local Similarity 82.7%; Pred. No. 9.3e-46;
; Matches 115; Conservative 6; Mismatches 17; Indels 1; Gaps 1

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US-10-275-180A-23

Query Match      74.7%; Score 542.5; DB 14; Length 464;
Best Local Similarity 75.9%; Pred. No. 7.2e-42;
Matches 107; Conservative 16; Mismatches 13; Indels 5; Gaps 2;

Qy      1 MNFGLSLIFVLVLKGVQCEVKLVESGGDLNMPGSLKLSCAASGSPFSNYGHSWVRQTS 60
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MNFGLSLIFVLVLKGVQCEVNLVESGGGLVKPGGSLKLSCAASGFTFSSYVMSWVRQP 60
         |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      61 DKRLIEWASISTGGANTYPPDNVKGRFTISRNAKNTLYLQMSLSKSEDTALYFCARDSH 120
         :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 EKRLIEWATISGGSYTYPPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAMYVCARRGD 120
         :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      121 SVGCWFAT--WGQGTFLVTVA 139
         |:|:|||||:|||||:
Db      121 SM---ITTDYWGQGTTLTVSS 138
         |:|:|||||:|||||:

RESULT 15
US-10-010-942B-8
; Sequence 8, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:

```

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; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: BETA AMYLOID PEPTIDE
; CURRENT APPLICATION NUMBER: US/10/010,942B
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-010-942B-8

```

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Query Match      73.8%; Score 534.5; DB 14; Length 138;
Best Local Similarity 74.8%; Pred. No. 1.1e-41;
Matches 104; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY      1 MNEGLSLIFLVLVKGVQCEVKLVESGGDLMPGASLKLSCAASGFSNNGMSWVRQTS 60
Db      1 MNEGLSLIFLVLVKGVQCEVKLVESGGDLMPGASLKLSCAASGFSNNGMSWVRQAP 60

QY      61 DKLEWVASISTGGANTFYDPNVKGRFTISRENAKNTLYLQMSLKSXEDTALYFCARDSH 120
Db      61 GKLEWVASIRSGGRTFYSDNVKGRFTISRDNAKNSLYLQMSLRAEDTALYVCVRD 120

QY      121 SVGCWFATWGQGTTLTVSA 139
Db      121 YSGS-SDYWGQGTTLTVSS 138

```

Search completed: May 25, 2005, 16:06:54  
Job time : 65.259 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 19.654 Seconds  
(without alignments)  
680.480 Million cell updates/sec

Title: US-10-006-773A-17  
Perfect score: 726  
Sequence: 1 MNFGLSLIFLVVLKGVQCE.....HSVGCWFATWGQGLTVTUSA 139

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: Pir1.\*  
2: Pir2.\*  
3: Pir3.\*  
4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578.5	79.7	138	2 S09258	Ig heavy chain V r
2	547.5	75.4	142	2 C34903	Ig heavy chain pre
3	534.5	73.6	152	2 B26471	Ig heavy chain pre
4	528	72.7	139	2 S38808	Ig heavy chain - m
5	506	69.7	117	1 HVMS84	Ig heavy chain pre
6	503	69.3	117	1 HVMS34	Ig heavy chain pre
7	500	68.9	140	2 S70442	Ig heavy chain pre
8	495	68.2	117	1 HVMS39	Ig heavy chain pre
9	491	67.6	139	2 S31674	Ig heavy chain V r
10	491	67.6	254	2 B31790	Ig heavy chain V r
11	489.5	67.4	140	2 S31588	Ig heavy chain V r
12	488.5	67.3	138	2 S31666	Ig heavy chain V r
13	487	67.1	548	2 S38864	Ig epsilon chain C
14	481.5	66.3	140	2 A30532	Ig heavy chain pre
15	480.5	66.2	136	2 S31615	hypothetical prote
16	479.5	66.0	134	2 S31699	Ig heavy chain V r
17	479	66.0	117	1 HVMS57	Ig heavy chain pre
18	477.5	65.8	134	2 S31679	Ig heavy chain V r
19	477.5	65.8	140	2 S31686	Ig heavy chain V r
20	476	65.6	117	1 HVMS3F	Ig heavy chain pre
21	475	65.4	137	2 S31701	Ig heavy chain V r
22	472	65.0	141	2 S31669	Ig heavy chain V r
23	471.5	64.9	140	2 S22657	Ig heavy chain pre
24	469.5	64.7	139	2 I37781	Ig variable region
25	469.5	64.7	160	2 S05271	Ig heavy chain pre
26	468	64.5	136	2 S31587	Ig heavy chain V r
27	467.5	64.4	130	2 PL0058	Ig heavy chain pre
28	467.5	64.4	135	2 S31598	Ig heavy chain V r
29	464.5	64.0	132	2 S31603	Ig heavy chain V r

30	463	63.8	135	2	I37778	Ig variable region
31	463	63.8	151	2	A60943	Ig heavy chain pre
32	462	63.6	121	2	D27888	Ig heavy chain V r
33	458.5	63.2	136	2	S60296	Ig heavy-chain var
34	458	63.1	147	2	I37780	Ig variable region
35	456	62.8	136	1	GIMS21	Ig heavy chain pre
36	453.5	62.5	136	2	SI6847	Ig heavy chain V r
37	453.5	62.5	138	2	A30561	Ig heavy chain pre
38	453	62.4	137	2	S78054	Ig heavy chain pre
39	452	62.3	145	2	S11239	Ig heavy chain V r
40	451	62.1	119	2	D27889	Ig heavy chain V r
41	451	62.1	119	2	D27888	Ig heavy chain V r
42	451	62.1	128	2	PH0094	Ig heavy chain V r
43	450	62.0	119	2	PH1531	Ig H chain V regio
44	449.5	61.9	122	2	E27888	Ig heavy chain V r
45	448	61.7	118	2	PL0254	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S09258  
Ig heavy chain V region precursor - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 29-Jan-1993 #sequence\_revision 29-Jan-1993 #text\_change 23-Jul-1999  
C/Accession: S09258  
R/Hamada, H.; Maezawa, K.; Tsuruo, T.  
Nucleic Acids Res. 18, 1900, 1990  
A/Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK  
A/Reference number: S09258; MUID:90245594; PMID:2110659  
A/Accession: S09258  
A/Molecule type: DNA  
A/Residues: 1-138 <HAM>  
A/Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545  
A/Genetics:  
A/Introns: 16/1  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 578.5; DB 2; Length 138;  
Best Local Similarity 79.9%; Pred. No. 2.4e-45;  
Matches 111; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

Qy	1	MNFGLSLIFLVVLKGVQCEVLSGGDIWNPGLKSLCAASGFSFNYSWVQRTS	60
Db	1	MNFGLSLIFLVVLKGVQCEVLSGGDIWNPGLKSLCAASGFSFNYSWVQRTS	60
Qy	61	DKRLWVASITGANTFFPDNVKGRFTISRENAKNTLYLQMSLSKSEDTALYFCARDSH	120
Db	61	EKRLEWATISSGGNTYYPDNVKGRFTISRDNAKNNLYLQMSLSKSEDTALYFCAR	119
Qy	121	SVGCWFATWGQGLTVTUSA	139
Db	120	RYEAWFASWGQGLTVTUSA	138

RESULT 2

C34903  
Ig heavy chain precursor V region (5-27) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 16-Aug-1996  
C/Accession: C34903  
R/Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A/Title: Active site structure and antigen binding properties of idiotypically cross-reac  
A/Reference number: A34903; MUID:90094387; PMID:2104617  
A/Accession: C34903  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-142 <BED>  
C/Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin  
F;34-119/Domain: immunoglobulin homology <IMM>

Query Match 75.4%; Score 547.5; DB 2; Length 142;  
Best Local Similarity 76.2%; Pred. No. 1.6e-42;  
Matches 109; Conservative 12; Mismatches 17; Indels 5; Gaps 3;

QY 1 MNFGSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60  
DB 1 MNFGSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTP 60

QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRANAKNTLYQMSSLSKSEDTALFYFCAR 117  
DB 61 EKRLWVASFGNKPTG-RTYTPDSVKGRFTISRDNARNLYLQMSLSASEDTAMYICAR 119

QY 118 DSHV-GCWFATWGQTLTVSA 139  
DB 120 GGYTGGYWFAYWGQTLTVSA 142

RESULT 3

B26471  
Ig heavy chain precursor V region (MAK33) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 23-Jul-1999  
C;Accession: B26471; S70410  
R;Buckel, P.; Hubner-Parajoz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.  
Gene 51, 13-19, 1987  
A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine  
A;Reference number: A91572; MUID:87248058; PMID:3110009  
A;Accession: B26471  
A;Molecule type: mRNA  
A;Residues: 1-152 <BUC>  
A;Cross-references: GB:M1613; NID:g195405; PIDN:AAA38292.1; PID:g195406  
R;Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 172, 1717-1727, 1990  
A;Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary  
A;Reference number: S70410; MUID:91079775; PMID:2258702  
A;Accession: S70410  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-19 <LEB>  
A;Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476  
C;Genetics: 16/1  
A;Introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 534.5; DB 2; Length 152;  
Best Local Similarity 74.6%; Pred. No. 2.6e-41;  
Matches 106; Conservative 14; Mismatches 19; Indels 3; Gaps 1;

QY 1 MNFGSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60  
DB 1 MNFGSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTP 60

QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRANAKNTLYQMSSLSKSEDTALFYFCAR 120  
DB 61 EKRLWVASISDGSYTYTPDSVKGRFTISRDNARNLYLQMSLSASEDTAMYICAR 120

QY 121 SVGCW---FATWGQTLTVSA 139  
DB 121 YGNYGDAMDYWGQTSVTSS 142

RESULT 4

S38808  
Ig heavy chain - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 21-Jan-2000

C;Accession: S38808  
R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.  
Immunogenetics 36, 15-21, 1992  
A;Title: Molecular characterization of the variable regions of a mouse polyreactive IgG  
A;Reference number: S38807; MUID:92267566; PMID:1587549  
A;Accession: S38808  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-139 <SEQ>  
A;Cross-references: EMBL:X53400  
A;Note: The authors translated the codon GAG for residue 117 as Lys  
A;Note: the sequence of residues 134-139 and the corresponding nucleotide sequence are  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 528; DB 2; Length 139;  
Best Local Similarity 72.9%; Pred. No. 9.1e-41;  
Matches 105; Conservative 14; Mismatches 13; Indels 12; Gaps 3;

QY 1 MNFGSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60  
DB 1 MNFGSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTP 60

QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRANAKNTLYQMSSLSKSEDTALFYFCAR 120  
DB 61 EKRLWVASISRG-TTYTPDSVKGRFTISRDNARNLYLQMSLSASEDTAMYICAR 117

QY 121 SVGCWFA-----TWGQTLTV 137  
DB 118 --GIYYGALYGM DYWGQTSVT 139

RESULT 5

HWS84  
Ig heavy chain precursor V region (5-84) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: JT0505  
R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A;Reference number: JT0501; MUID:89279149; PMID:2499654  
A;Accession: JT0505  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-117 <LEV>  
A;Cross-references: UNIPROT:P18525  
A;Experimental source: strain BALB/cJ  
A;Note: this sequence belongs to the VH7183 subfamily  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>  
F;41-115/Disulfide bonds: #status predicted

Query Match 69.7%; Score 506; DB 1; Length 117;  
Best Local Similarity 82.9%; Pred. No. 7.4e-39;  
Matches 97; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MNFGSLIFLVVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTS 60  
DB 1 MNFGSLIFLVVLKGVCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMWVRQTP 60

QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRANAKNTLYQMSSLSKSEDTALFYFCAR 117  
DB 61 EKRLWVASISNGGSGTYTPDVTKGRFTISRDNARNLYLQMSLSASEDTAMYICAR 117

RESULT 6  
HWS34  
Ig heavy chain precursor V region (345) - mouse  
C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C;Accession: J70502  
J;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A;Reference number: J70501; MUID:89279149; PMID:2499654  
A;Accession: J70502  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-117 <LEV>  
A;Cross-references: UNIPROT:P18526  
A;Experimental source: strain BALB/cJ  
A;Note: this sequence belongs to the VH7183 subfamily  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>  
F;41-115/Diulfide bonds: #status predicted

Query Match 69.3%; Score 503; DB 1; Length 117;  
Best Local Similarity 81.2%; Pred. No. 1.4e-38;  
Matches 95; Conservative 12; Mismatches 10; Indels 0; Gaps 0;  
Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFSNYGMSWVRQTS 60  
Db 1 MNFGLRLFLVLTLKGVKCEVQLVESGGGLVKPGGSLKLSCAASGFAFSYDMSWVRQTP 60  
Qy 61 DKRLWVASISTGGANTFYPDNVKGRTTISRENKNTLYLQMSLSKSEDTALYFCAR 117  
Db 61 EKRLWVAIISGGGTYPTVTKGRTTISRDNKNTLYLQMSLSKSEDTALYFCAR 117

## RESULT 7

S70442  
Ig heavy chain precursor V region (mu) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: S70442  
R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.  
Mol. Immunol. 29, 1363-1373, 1992  
A;Title: IGM kappa/Iambda EBV human B cell clone: an early step of differentiation of fe  
A;Reference number: S70442; MUID:93024508; PMID:1383695  
A;Accession: S70442  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-140 <CUI>  
A;Cross-references: UNIPROT:O8WUK1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 68.9%; Score 500; DB 2; Length 140;  
Best Local Similarity 68.6%; Pred. No. 3.1e-38;  
Matches 96; Conservative 21; Mismatches 21; Indels 2; Gaps 2;  
Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFSNYGMSWVRQTS 60  
Db 1 MEFGLSWFLVALLRGVQCQVQLVESGGVQVPGPSRLSLSCAASGFTFSNYGMHWVRQAP 60  
Qy 61 DKRLWVASISTGGANTFYPDNVKGRTTISRENKNTLYLQMSLSKSEDTALYFCARDSH 120  
Db 61 GKLEWVAFIRYDGSNKYADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYYCARD-H 119

Qy 121 SVGC-WFATWGGTTLVTUSA 139  
Db 120 IVGATPYDYGQGTTLVTVSS 139

## RESULT 8

HWS39  
Ig heavy chain precursor V region (7-39) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004

C;Accession: J70507  
J;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A;Reference number: J70501; MUID:89279149; PMID:2499654  
A;Accession: J70507  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-117 <LEV>  
A;Cross-references: UNIPROT:P18530  
A;Experimental source: strain BALB/cJ  
A;Note: this sequence belongs to the VH7183 subfamily  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-117/Product: Ig heavy chain V region (7-39) #status predicted <MAT>  
F;34-117/Domain: immunoglobulin homology <IMM>  
F;41-115/Diulfide bonds: #status predicted

Query Match 68.2%; Score 495; DB 1; Length 117;  
Best Local Similarity 81.2%; Pred. No. 7.3e-38;  
Matches 95; Conservative 10; Mismatches 12; Indels 0; Gaps 0;  
Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFSNYGMSWVRQTS 60  
Db 1 MNFGLSLFLVLKGVQCEVKLVESGGGVKPGGSLKLSCEASGFTFSNYGMSWVRQTP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRTTISRENKNTLYLQMSLSKSEDTALYFCAR 117  
Db 61 EKRLWVASISGGVSYTYYPDSVKGRFTISRDNKNTLYLQMSLSKSEDTALYFCAR 117

## RESULT 9

S31674  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31674  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31674  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-139 <CUI>  
A;Cross-references: EMBL:Z14204; NID:g30967; PIDN:CAA78573.1; PID:g30968  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.6%; Score 491; DB 2; Length 139;  
Best Local Similarity 66.2%; Pred. No. 2e-37;  
Matches 92; Conservative 22; Mismatches 25; Indels 0; Gaps 0;  
Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSFSNYGMSWVRQTS 60  
Db 1 MEFGLSWFLVALLRGVQCQVQLVESGGVQVPGPSRLSLSCAASGFTFSNYGMHWVRQAP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRTTISRENKNTLYLQMSLSKSEDTALYFCARDSH 120  
Db 61 CKGLEWVAIVSYDGSNKYADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYYCAKAGL 120

Qy 121 SVGC-WFATWGGTTLVTUSA 139  
Db 121 GFFNWFDPWGGTTLVTVSS 139

## RESULT 10

B31790  
Ig heavy chain V region (17/9) - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 23-May-1997

C;Accession: B31790  
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilsson, I.A.  
J. Biol. Chem. 263, 17100-17105, 1988  
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an ar  
A;Reference number: A92686; MUID:89034213; PMID:3182835  
A;Accession: B31790  
A;Molecule type: mRNA  
A;Residues: 1-254 <SCH>  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.6%; Score 491; DB 2; Length 254;  
Best Local Similarity 79.2%; Pred. No. 3.8e-37;  
Matches 95; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

QY 20 EVKLVEGGDLMPGASLKSCAASGFSFNSYGMWVROTSDKRLWVASISTGGANTPY 79  
Db 1 EVQLVEGGDLVKGPGSLKSLCAASGFSFSSYGMWVROTSDKRLWVASISGGGYTY 60  
QY 80 PDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSHSVGCFATWGQTLVTVSA 139  
Db 61 PDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSHSVGCFATWGQTLVTVSA 120

RESULT 11  
S31588  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31588  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31588  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-140 <CUI>  
A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.4%; Score 489.5; DB 2; Length 140;  
Best Local Similarity 65.7%; Pred. No. 2.8e-37;  
Matches 92; Conservative 26; Mismatches 21; Indels 1; Gaps 1;

QY 1 MNFGLSLIFLVLRGQCEVKLVESGGDLMPGASLKSLCAASGFSFNSYGMWVROTSD 60  
Db 1 MEFGLSWLFVAILRGVQCEVKLVESGGDLMPGASLKSLCAASGFSFNSYGMWVROTSD 60  
QY 61 DKRLWVASISGGANTFYPDNVKGRTISRDNKNTLYLQMSLSKSDTALYFCARD-S 119  
Db 61 GRGLEWVASISGGSGTYADSVKGRFTISRDSKNTLYLQMSLSRAEDTAVYYCAKDH 120

RESULT 12  
S31666  
Ig heavy chain V region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C;Accession: S31666  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A;Reference number: S31585  
A;Accession: S31666  
A;Status: preliminary

A;Molecule type: mRNA  
A;Residues: 1-138 <CUI>  
A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 488.5; DB 2; Length 138;  
Best Local Similarity 66.4%; Pred. No. 3.4e-37;  
Matches 93; Conservative 23; Mismatches 21; Indels 3; Gaps 2;

QY 1 MNFGLSLIFLVLRGQCEVKLVESGGDLMPGASLKSLCAASGFSFNSYGMWVROTSD 60  
Db 1 MEFGLSWLFVAILRGVQCEVKLVESGGDLMPGASLKSLCAASGFSFNSYGMWVROTSD 60  
QY 61 DKRLWVASISGGANTFYPDNVKGRTISRDNKNTLYLQMSLSKSDTALYFCARDSH 120  
Db 61 GRGLEWVASISGGSGTYADSVKGRFTISRDSKNTLYLQMSLSRAEDTAVYYCAK--A 118

QY 121 SVGCW-FATWGQTLVTVSA 139  
Db 119 RTGYWYFDLWGRGTLVTVSS 138

RESULT 13  
S38864  
Ig epsilon chain C region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 24-May-2001  
C;Accession: S38864  
R;Kipp, B.; Becker, W.; Schlaak, M.  
submitted to the EMBL Data Library, November 1993  
A;Description: Combination of a defined specificity and desired isotype by cloning of a  
A;Reference number: S38864  
A;Accession: S38864  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-548 <KIP>  
A;Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
F;353-421/Domain: immunoglobulin homology <IMM>

Query Match 67.1%; Score 487; DB 2; Length 548;  
Best Local Similarity 77.5%; Pred. No. 1.9e-36;  
Matches 93; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 20 EVKLVEGGDLMPGASLKSLCAASGFSFNSYGMWVROTSDKRLWVASISTGGANTPY 79  
Db 1 QVKLLEGGDLVKGPGSLKSLCAASGSLTFSSYGMWVROTSDKRLWVASISGGGYTY 60  
QY 80 PDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSHSVGCFATWGQTLVTVSA 139  
Db 61 PDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCARDSHSVGCFATWGQTLVTVSA 120

RESULT 14  
A30532  
Ig heavy chain precursor V-III region (38) - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1989 #sequence\_revision 31-Dec-1989 #text\_change 18-Oct-1996  
C;Accession: A30532  
R;Weeker, T.C.; Grimaldi, J.C.; O'Rourke, R.; Loeb, J.; Juliusson, G.; Einhorn, S.  
J. Immunol. 141, 3994-3998, 1988  
A;Title: Lack of detectable somatic hypermutation in the V region of the Ig H chain gen  
A;Reference number: A30532; MUID:89035542; PMID:3141510  
A;Accession: A30532  
A;Molecule type: DNA  
A;Residues: 1-140 <MEE>  
A;Cross-references: GB:M23110  
C;Genetics: 16/1  
A;introns: 16/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

E:20-140/Product: Ig heavy chain V-III region 38 #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 481.5; DB 2; Length 140;  
Best Local Similarity 66.4%; Pred. No. 1.5e-36;  
Matches 93; Conservative 21; Mismatches 25; Indels 1; Gaps 1;  
Qy 1 MNFGLSLIFLVLLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMGNVVRQTS 60  
Db 1 MEFGSLWLFVAILKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMGNVVRQAP 60  
Qy 61 DKRLWVASISTGGANTFYPDNVKGRTTISRNAKNTLYLQWSSLKSEDTALYFCARDSH 120  
Db 61 KGLEWSSISGSGGTYYTASVGRFTTISRDNKNTLYLQWSSLKSEDTALYFCARDSH 120  
Qy 121 SVGCW-FATWGGTGLVTVSA 139  
Db 121 DIRLPLAYWGGTGLVTVSS 140

## RESULT 15

S31615  
hypothetical protein - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 23-Jul-1999  
C:Accession: S31615  
R:Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.  
submitted to the EMBL Data Library, April 1991  
A:Description: Immunoglobulin variable heavy and light chain cDNA sequences for antidiox  
A:Reference number: S31615  
A:Accession: S31615  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-136 <REC>  
A:Cross-references: EMBL:X58884; NID:g51824; PIDN:CAA41688.1; PID:g51825  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 66.2%; Score 480.5; DB 2; Length 136;  
Best Local Similarity 66.2%; Pred. No. 1.8e-36;  
Matches 94; Conservative 20; Mismatches 19; Indels 9; Gaps 3;  
Qy 1 MNFGLSLIFLVLLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMGNVVRQTS 60  
Db 1 MNFGLSLIFLVLLKGVQCEVKLVESGGDLMPGASLKLSCAASGFSPSNYGMGNVVRQTP 60  
Qy 61 DKRLWVASISTGGANTFYPDNVKGRTTISRNAKNTLYLQWSSLKSEDTALYFCARDSH 120  
Db 61 EKRLWVATITGGGTYYTIPDSVGRFTTISRDNARDTLNLHMTNLKSEDTAMYYC----- 115  
Qy 121 SVG-CWF--ATWGGTGLVTVSA 139  
Db 116 -LGYWYDGTWGGTGLVISA 136

Search completed: May 25, 2005, 16:48:41  
Job time : 20.654 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 67.7544 Seconds  
(without alignment)  
1050.544 Million cell updates/sec

Title: US-10-006-773A-17

Perfect score: 726

Sequence: 1 MNFGLSLIFLVVLKGVQCE.....HSVCCWFWTQGGTLVTVSA 139

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	549	75.6	487	Q99KA4	Q99ka4 mus musculus
2	528.5	72.8	486	Q91Z07	Q91z07 mus musculus
3	516.5	70.1	479	Q91WP5	Q91wp5 mus musculus
4	509	71.1	196	Q65ZL8	Q65zl8 mus musculus
5	506	69.7	117	HV54_MOUSE	P18525 mus musculus
6	503	69.3	117	HV55_MOUSE	P18526 mus musculus
7	497.5	68.5	119	Q920E7	Q920e7 mus musculus
8	495	68.2	117	HV59_MOUSE	P18530 mus musculus
9	486.5	67.0	480	Q91XE1	Q91xe1 mus musculus
10	483.5	66.6	470	Q6PJ44	Q6pja4 homo sapien
11	483	66.5	613	Q8WUK1	Q8wuk1 homo sapien
12	479	66.0	117	HV58_MOUSE	P18529 mus musculus
13	476	65.6	117	HV53_MOUSE	P18524 mus musculus
14	475.5	65.5	597	Q96BB9	Q96bb9 homo sapien
15	475	65.4	473	Q91Z05	Q91z05 mus musculus
16	469.5	64.7	485	Q6PDB8	Q6pdb8 mus musculus
17	467.5	64.4	464	Q6MZU6	Q6mzu6 homo sapien
18	466	64.2	475	Q6MZQ6	Q6mzq6 homo sapien
19	465.5	64.1	499	Q8N5K4	Q8n5k4 homo sapien
20	462	63.6	478	Q96K68	Q96k68 homo sapien
21	461.5	63.6	474	Q6PI81	Q6pi81 homo sapien
22	459	63.2	606	Q6GMV2	Q6gmv2 homo sapien
23	457.5	63.0	493	Q6GMX2	Q6gmx2 homo sapien
24	457	62.9	465	Q6P6C4	Q6p6c4 homo sapien
25	456	62.8	136	HV16_MOUSE	P17183 mus musculus
26	455.5	62.7	255	Q6KB05	Q6kb05 mus musculus
27	452	62.3	573	Q8WUJ38	Q8wu38 homo sapien
28	451	62.1	544	Q6PJ95	Q6pj95 homo sapien
29	447.5	61.6	466	Q6IN78	Q6in78 homo sapien
30	444.5	61.2	493	Q6NCU6	Q6ncu6 homo sapien
31	443	61.0	117	HV3C_HUMAN	P01764 homo sapien

32	442.5	61.0	472	2	Q6N089	Q6n089 homo sapien
33	442	60.9	479	2	Q6MZV6	Q6mzv6 homo sapien
34	441	60.7	473	2	Q6MZV7	Q6mzv7 homo sapien
35	438	60.3	487	2	Q6ZVX0	Q6zvx0 homo sapien
36	432.5	59.6	470	2	Q7Z5W1	Q7z5w1 homo sapien
37	432.5	59.6	480	2	Q6N094	Q6n094 homo sapien
38	430.5	59.3	248	2	Q65ZQ7	Q65zq7 mus sp. b3(
39	427.5	58.9	466	2	Q6N096	Q6n096 homo sapien
40	423	58.3	494	2	Q6ZW64	Q6zww4 homo sapien
41	421.5	58.1	493	2	Q68CN4	Q68cn4 homo sapien
42	419	57.7	483	2	Q6MZX9	Q6mzx9 homo sapien
43	415.5	57.2	487	2	Q80Z17	Q80zi7 mus musculu
44	415	57.2	473	2	Q6P055	Q6p055 homo sapien
45	413	56.9	122	2	Q9UL84	Q9ul84 homo sapien

#### ALIGNMENTS

RESULT 1  
Q99KA4  
ID Q99KA4 PRELIMINARY; PRT; 487 AA.  
AC Q99KA4;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Igh-VJ558 protein.  
GN Name=Igh-VJ558;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C2ECH II; TISSUE=Mammary tumor;  
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
SEQUENCE FROM N.A.  
STRAIN=C2ECH II; TISSUE=Mammary tumor;  
RA Director MGC Project;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
EMBL; BC004786; AAH04786.1; -.  
DR HSSP; P01810; 2FBJ.  
DR MGD; MGI:96486; Igh-VJ558.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; IG\_LIKE; 4.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN 2.  
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

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Query Match           75.5%; Score 549; DB 2; Length 487;					
Best Local Similarity   75.5%; Pred. No. 2.9e-46;					
Matches 108; Conservative 14; Mismatches 17; Indels 4; Gaps 2					
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QY	1	MNFGLSLFLVLVVGVOCEVKLVESGGDLMPGASLKLSCAASGFSGFNGMSWVRQT	60		
DB	1	MNFGLSLFLVLVVGVOCEVKLVESGGDLMPGASLKLSCAASGFSGFNGMSWVRQT	60		
<hr/>					
QY	61	KRLEWVASISTGGANTPYDPNVKGRFTISRENAKNLYLQMSLSKSEDTALFYCCARD--	118		
DB	61	KRLEWVASISDGSYTYPPDNVKGRTISRDKAKNLYLQMSHLKSEDTAMYYCARGD	120		
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QY	119	SHSVCCW--PATWGCGHLLVTISA	139		
DB	121	GSPGYGSRFDYWGQGTTITVSS	143		
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RESULT 2					
QY1207		PRELIMINARY; PRT; 486 AA.			
ID	Q91207				
AC	Q91207				
DT	01-DEC-2001 (TrEMBLrel. 19, Created)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
DE	Igh-VJ558 protein.				
GN	Name=Igh-VJ558;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RP	[1]				
RC	SEQUENCE FROM N.A.				
RC	STRAIN=CZECH II; TISSUE=Mammary tumor;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Strausberg R.L., Fengold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T.I., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,				
RA	Krzywinski M.I., Skalska U., Smalus D.E., Schnerch A., Schein J.E.,				
RA	Jones S.J., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CZECH II; TISSUE=Mammary tumor;				
DR	Director MGC Project;				
DR	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC010324; AAA10324.1; -.				
DR	HSSP; P01789; IMCP.				
DR	Pfam; PF07654; CI-set; 2.				
DR	SMART; SM00406; IGV; 1.				
DR	PROSITE; PS00835; IG LIKE; 4.				
DR	PROSITE; PS00290; IG MHG; UNKNOWN 2.				
SQ	SEQUENCE 486 AA; 52681 MW; 4FEF835125DA870B CRC64;				
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Query Match           72.8%; Score 528.5; DB 2; Length 486;					
Best Local Similarity   70.6%; Pred. No. 3.2e-44;					
Matches 101; Conservative 18; Mismatches 19; Indels 5; Gaps 2					
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QY	1	MNFGLSLFLVLVVGVOCEVKLVESGGDLMPGASLKLSCAASGFSGFNGMSWVRQT	60		

```

Qy 121 SVGCWFATWGQGTTLVTVSA 139
Db 118 --GGYFDVWGAGTAVTVSS 134

RESULT 4
Q65ZL8 PRELIMINARY; PRT; 196 AA.
AC Q65ZL8;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE VH183-DSP2-JH3-CHI protein (Fragment).
GN Name=VH183-DSP2-JH3-CHI;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95362300; PubMed=7635518;
RA Komori T., Sugiyama H.;
RT "An aberrant splicing using a 3' cryptic splice site within the CHI
RL exon induces truncated mu-chain production.";
RL Immunology 85:166-170(1995).
DR EMBL; S79401; AAB35023.2; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 196
SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;

Query Match 70.1%; Score 509; DB 2; Length 196;
Best Local Similarity 82.8%; Pred. No. 9.8e-43;
Matches 96; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVLVESGGDLMPGASLKLSCAASGFSPSYGMSWVRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVLVESGGGLVKPGGSLKLSCAASGFTSSYMSWVRQTP 60
Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCA 116
Db 61 EKRLWVATISSGGSYTYPDNVKGRFTISRDNKNTLYLQMSLSKSDTAMYYCA 116

RESULT 5
HV54 MOUSE
ID HV54 MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RL primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
DR HSSP; P01810; 2FBJ.

Query Match 69.3%; Score 503; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 2.1e-42;
Matches 95; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

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DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON TER 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 69.7%; Score 506; DB 1; Length 117;
Best Local Similarity 82.9%; Pred. No. 1.1e-42;
Matches 97; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVQCEVLVESGGDLMPGASLKLSCAASGFSPSYGMSWVRQTS 60
Db 1 MNFGLSLIFLVVLKGVQCEVLVESGGGLVKPGGSLKLSCAASGFTSSYMSWVRQTP 60
Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSDTALYFCA 117
Db 61 EKRLWVATISSGGSYTYPDNVKGRFTISRDNKNTLYLQMSLSKSDTAMYYCAR 117

RESULT 6
HV55 MOUSE
ID HV55 MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RL primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
DR HSSP; P01783; 1IGC.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 19
FT DOMAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON TER 117
SQ SEQUENCE 117 AA; 12902 MW; 49380B4627ACA99A CRC64;

Query Match 69.3%; Score 503; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 2.1e-42;
Matches 95; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

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CC -!- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.
DR PIR; JT0507; HWS39.
DR HSP; P18529; I18K.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 68.2%; Score 495; DB 1; Length 117;
Best Local Similarity 81.2%; Pred. No. 1.3e-41;
Matches 95; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNFGLSLFLVLVKGQCEVKLVESGGDLMPGASLKLSCAASGFSFSGNYGMSWVRQTS 60
DB 1 MNFGLSLFLVLVKGQCEVKLVESGGDLMPGASLKLSCAASGFSFSGNYGMSWVRQTP 60
QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSEDTALYFCAR 117
DB 61 EKRLWVASISGGSVTYPPDSVKGRFTISRDNKNTLYLQMSLSKSEDTALYFCAR 117

RESULT 9
Q91XE1 PRELIMINARY; PRT; 480 AA.
AC Q91XE1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-VJ558 protein (Fragment).
GN Name=Igh-VJ558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
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QY 1 MNFGLSLFLVLVKGQCEVKLVESGGDLMPGASLKLSCAASGFSFSGNYGMSWVRQTS 60
DB 1 MNFGLSLFLVLVKGQCEVKLVESGGDLMPGASLKLSCAASGFSFSGNYGMSWVRQTP 60
QY 61 DKRLWVASISTGGANTFYPDNVKGRFTISRDNKNTLYLQMSLSKSEDTALYFCAR 117
DB 61 EKRLWVASISGGSVTYPPDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCAR 117

RESULT 7
Q920E7 PRELIMINARY; PRT; 119 AA.
AC Q920E7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309337; AL09421.1; -.
DR PIR; C25913; C25913.
DR HSP; P01783; I1GC.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1 1
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

Query Match 68.5%; Score 497.5; DB 2; Length 119;
Best Local Similarity 80.2%; Pred. No. 7.7e-42;
Matches 97; Conservative 13; Mismatches 8; Indels 3; Gaps 2;

QY 20 EVKLVSSEGGDLMPGASLKLSCAASGFSFSGNYGMSWVRQTS DKRLWVASISTGGANTFY 79
DB 1 EVKLVSSEGGDLMPGASLKLSCAASGFSFSGNYGMSWVRQTPDKRLWVASISGGSVTYV 60
QY 80 PDNVKGRFTISRDNKNTLYLQMSLSKSEDTALYFCAR-DSHVSVCWFPATWGQTLTVTS 138
DB 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARHGDYDVG--PAYWGQTLTVTS 118

QY 139 A 139
DB 119 A 119

RESULT 8
HV59 MOUSE
ID HV59 MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response."
RL J. Exp. Med. 169:2007-2019 (1989).
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RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018798; AAH10798.1; -.
DR HSSP; P01789; 1MCP.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT NON TER 1
SQ SEQUENCE 480 AA; 51936 MW; 20B9234BEF2B41ED CRC64;

Query Match 67.0%; Score 486.5; DB 2; Length 480;
Best Local Similarity 68.8%; Pred. No. 5e-40; Indels 3; Gaps 1;
Matches 95; Conservative 17; Mismatches 23;

Qy 2 NFGSLIFLVLVKGVQCEVKLVESGGLMNPGLASLKLSCAASGFSFNSYMSWVROTSD 61
Db 1 NFGSLIFLVLVKGVQCEVKLVESGGLVFGGSLRLSCAASGFSFNSYMSWVROTPE 60

Qy 62 KRLWVASISTGGANTFYPDNVKGRFTISRNAKNTLYLQMSLSKSDTALYFCARDSHS 121
Db 61 KRLWVATISNSGVATHYPDSMKGRFTISRDAQNTVLLQMTLSNSEDVAVYCTRGDY- 119

Qy 122 VGCWFATWGQGLTVTUSA 139
Db 120 --WYFDVNGAGTTVTVSS 135

RESULT 10
Q6PJA4 PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
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DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 66.6%; Score 483.5; DB 2; Length 470;
Best Local Similarity 65.7%; Pred. No. 9.7e-40;
Matches 92; Conservative 20; Mismatches 27; Indels 1; Gaps 1;

Qy 1 NFGSLIFLVLVKGVQCEVKLVESGGLMNPGLASLKLSCAASGFSFNSYMSWVROTSD 60
Db 1 MELGLSWFLVAILDEGVQCEVKLVESGGLVQPGSLRLSCVSGFTFSSYMSWVROAP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRNAKNTLYLQMSLSKSDTALYFCARDSH 120
Db 61 GKGLWVANIKQDGESEKYYVDSVKGRFTISRDAKNSLYLQMSLSRAEDTAVYCARDGS 120

Qy 121 S-VGCWFATWGQGLTVTUSA 139
Db 121 SWYRDWFDPMGQGLTVTVSS 140

RESULT 11
Q8WUK1 PRELIMINARY; PRT; 613 AA.
ID Q8WUK1
AC Q8WUK1;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR HSSP; P36005; F36005.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
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DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
GN IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAHL5760.1; -.
DR PIR; S05271; S05271.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.C1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS0290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD88CE263D9 CRC64;

Query Match 65.5%; Score 475.5; DB 2; Length 597;
Best Local Similarity 63.2%; Pred. No. 8e-39;
Matches 91; Conservative 26; Mismatches 22; Indels 5; Gaps 2;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGLMNPGLASLKLSCAASGFSFSGMSWVRQTS 60
Db 1 MEFGLSWFLVAILKGVQCEVKLVESGGLVQPGSLRLSCAASGFSFSSYAMNWRQAP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRENKNTLYLQMSLSKSDTALYFCARD-- 118
Db 61 GKGLWVASISGGSGTGYADSVKGRFTISRDNRSRTLYLQMSLRADTAVYYCAKDPK 120

Qy 119 SHVGCWFAT---WGQGLTVTVSA 139
Db 121 GYSASGNTREDYWGQGLTVTVSS 144

RESULT 15
Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Expressed sequence AU044919.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAHL0327.1; -.
DR PIR; S68213; S68213.
DR HSSP; P01783; IIGC.
DR MGD; MGI:2144967; AU044919.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS0290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 65.4%; Score 475; DB 2; Length 473;
Best Local Similarity 64.1%; Pred. No. 6.9e-39;
Matches 91; Conservative 21; Mismatches 22; Indels 8; Gaps 2;

Qy 1 MNFGLSLFLVLKGVQCEVKLVESGGLMNPGLASLKLSCAASGFSFSGMSWVRQTS 60
Db 1 MDSLELVFLVLILKGVQCEVKLVESGGLVQPGSLRLSCAASGFTFSDYGMHWVRQAP 60

Qy 61 DKRLWVASISTGGANTFYPDNVKGRFTISRENKNTLYLQMSLSKSDTALYFCARDSH 120
Db 61 EKGLWVAYISGSGTIIYADTVKGRFTISRDNKNTLYLQMTSLRSEDYATYYCARE-- 118

Qy 121 SVGCWFAT---WGQGLTVTVSA 139
Db 119 ---LWLRRIDYWGQGLTVTVSS 137

Search completed: May 25, 2005, 15:56:07
Job time : 68.7544 secs
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**BEST AVAILABLE COPY**



May 26 09:14:26 2005

GenCore - 2005  
(c) 1993  
62.1321 Seconds  
alignments)  
5 Million cell updates/sec

CGGK-19-0009-1A residues  
May 25, 2005, 15:35...CGGKSYPTFGGKLSIKR.132

Run on: US-10-006-773a-19.rag  
Gen parameters: 2105692

Title: score: 100  
Perfect score: 100  
Sequence: ch 100%  
Scoring table: 100%  
First 45 summaries

Search results  
Total: 16Dec04: \*  
Genesep1980s: \*  
Genesep2000s: \*  
Genesep2001s: \*  
Genesep2002s: \*  
Genesep2003as: \*  
7: Genesep2003bs: \*  
8: Genesep2004s: \*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Match	Length	ID	Description
1	689	100.0	132	6	ABG74248 Mouse ant
2	669	97.1	128	8	ADI26648 Mouse ant
3	664	96.4	127	2	AAW01145 MAB 10.1
4	663	96.2	135	7	ABR82783 Hybridoma
5	663	96.2	135	7	ABR82893 Hybridoma
6	649	94.2	136	2	AAW01632 Ber-H2 he
7	643	93.3	136	4	AAW01632 Ber-H2 he
8	634	92.0	136	8	ADO47803 AF2 antib
9	623	90.4	127	3	AAW71545 Mouse AF2
10	600	87.1	121	2	AAW47085 Mouse J59
11	600	87.1	121	2	AAW90370 J591 mono
12	600	87.1	121	2	AAW90370 J591 mono
13	567	82.3	109	2	AAW36222 Murine mo
14	562	81.6	107	2	AAW47086 Mouse J59
15	562	81.6	107	2	AAW90374 J591 mono
16	562	81.6	107	2	AAW36225 Monoclonal
17	562	81.6	107	3	AAW10444 Murine mo
18	551	80.0	107	8	ADW71777 Anti-VAP-
19	534	77.5	101	5	ABB07176 Mouse 09
20	534	77.5	101	8	ADI26668 Mouse ant
21	532	77.2	133	2	AAW21934 Variable
22	532	77.2	133	2	AAW05264 Antibody
23	532	77.2	133	5	ABG98315 Murine hu
24	530	76.9	133	2	AAW21936 Variable
25	530	76.9	133	2	AAW05266 Antibody

26	530	76.9	133	5	ABG98317	Abg98317 Murine wi
27	527	76.5	133	2	AAW21933	Aaw21933 Variable
28	527	76.5	133	2	AAW05263	Aaw05263 Antibody
29	527	76.5	133	5	ABG98314	Abg98314 Murine hu
30	517	75.0	132	2	AAW56961	Aaw56961 MAB A33 1
31	514	74.6	108	2	AAW00828	Aaw00828 Variable
32	512	74.3	145	8	ADL27476	Adl27476 Amino aci
33	511	74.2	133	7	ADC24968	Adc24968 Murine G2
34	511	74.2	133	7	ADK51723	Adk51723 Murine G2
35	511	74.2	260	8	ADL65425	Adl65425 DNA gyrase
36	505	73.3	147	2	AAW19576	Aaw19576 Mouse ant
37	503	73.0	107	6	ABO10727	Abol10727 Variable
38	503	73.0	107	6	ABR44618	AbR44618 Murine J4
39	503	73.0	107	6	ABR44618	AbR44618 Murine J4
40	503	73.0	131	2	AAW62187	Aaw62187 Mouse ant
41	503	73.0	131	2	AAW02545	Aaw02545 L Chain V
42	496	72.0	238	5	AAE27930	Aae27930 Human C5E
43	496	72.0	238	6	ABB82839	Abb82839 Antibody
44	495.5	71.9	132	2	AAW65169	Aaw65169 PRIA3 ant
45	493	71.6	128	3	AAW71547	Aaw71547 Humanised

ALIGNMENTS

RESULT 1  
ABG74248  
ID ABG74248 standard; protein; 132 AA.  
XX  
AC ABG74248;  
XX  
DT 22-APR-2003 (first entry)  
XX  
DB Mouse antibody 3E11 light chain variable region.

XX T-cell receptor; cytostatic; dermatological; neuroprotective;  
KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;  
KW 3E11; prostate-specific membrane antigen; zeta signalling chain;  
KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;  
KW small cell lung cancer; light chain variable region; mouse.  
XX Mus sp.  
XX  
XX US2002132983-A1.  
XX  
XX 19-SEP-2002.  
XX  
XX 10-DEC-2001; 2001US-00006773.  
XX  
XX 30-NOV-2000; 2000US-0250087P.  
XX 30-NOV-2000; 2000US-0250089P.  
XX (JUNG/) JUNGHANS R P.  
XX Junghans RP;  
XX WPI; 2003-208946/20.  
XX N-PSDB; ABX16574.  
XX  
XX New chimeric molecule useful in treating patients with disorders, such as  
XX melanoma, neuroendocrine disorders, prostate and small cell lung cancer  
XX comprises GD3 and/or PSMA binding domains of antibody.

XX Disclosure; Page 18; 35pp; English.  
XX The invention relates to a chimeric molecule comprising the GD3  
XX (ganglioside antigen) binding domain of antibody MB3.6, with any of 3  
XX variable gene sequences, or the PSMA (prostate-specific membrane antigen)  
XX binding domain of antibody 3D8, 4D4 and 3E11, with variable gene  
XX sequences, the zeta signalling chain of the T cell receptor and an  
XX intervening CDSalpha hinge in which cysteine residues have been mutated.  
XX The chimeric molecules expressed in T cells or NK cells or other  
XX effector cells are useful in treating patients with cancers expressing



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XX OS Mus musculus.
XX FH Key
XX FT Binding-site
XX FT Binding-site
XX FT Binding-site
XX FT Binding-site
XX PN WO9620959-A1.
XX PD 11-JUL-1996.
XX PP 27-DEC-1995; 95WO-JP002714.
XX PR 29-DEC-1994; 94JP-00340006.
XX PA (YAMA ) YAMANOUCHI PHARM CO LTD.
XX PI Kawauchi Y, Takasaki J, Yasunaga T, Masuho Y;
XX DR WPI; 1996-333946/33.
XX DR N-PSDB; AAT40805.
XX PT Monoclonal antibody inhibiting type II phospholipase A2 activity - for
XX PT treatment of myocardial and cerebral infarction.
XX PS Claim 6; Fig 13; 69pp; Japanese.
XX CC Monoclonal antibodies which inhibit type II phospholipase A2 are useful
XX CC in the treatment of myocardial infarction, cerebral infarction, acute
XX CC kidney failure, chronic rheumatism, cardiac shock, pancreatitis, adult
XX CC respiratory distress syndrome and colitis. The antibodies were generated
XX CC by immunising Balb/C mice with recombinant human type II phospholipase
XX CC A2. Spleen cells from the mice were fused with mouse myeloma P3U1
XX CC (P3x63Ag8.U1) and the hybridomas obtained were screened for phospholipase
XX CC A2 inhibitory activity. Active clones were isolated including 12H5, 1.4
XX CC and 10.1. These were cultured and the antibody isolated from the culture
XX CC supernatant by precipitation with ammonium sulphate and purification on a
XX CC column of protein A-Sepharose CL4B. Because the antibody acts on the
XX CC primate and mouse forms of enzyme as well as human it is particularly
XX CC suitable for preclinical testing
XX SQ Sequence 127 AA;

Query Match 96.4%; Score 664; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 5.9e-45;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVVSWYQOKP 64
DB 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVVSWYQOKP 60

QY 65 EQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGG 124
DB 61 EQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGG 120

QY 125 GTKLEIK 131
DB 121 GTKLEIK 127

RESULT 4
ABR82783
ID ABR82783 standard; protein; 135 AA.
XX AC ABR82783;
XX DT 18-DEC-2003 (first entry)
XX DE Hybridoma HB22-196 anti-CD22 MAb kappa light chain V-J junction.

XX CD22; B-cell malignancy; anti-CD22 antibody; cytostatic; human; HB22-196.
XX Homo sapiens.
XX PN WO2003072036-A2.
XX PD 04-SEP-2003.
XX PF 20-FEB-2003; 2003WO-US005323.
XX PR 21-FEB-2002; 2002US-0359419P.
XX PR 21-OCT-2002; 2002US-0420472P.
XX PA (UYDU-) UNIV DUKE.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Tedder T, Tuscano J;
XX DR WPI; 2003-712652/67.
XX DR N-PSDB; ACF36433.
XX PT Treating a human patient diagnosed with a B-cell malignancy by
XX PT administering a blocking anti-CD22 monoclonal antibody binding to the
XX PT first two Ig-like domains of native human CD22 (hCD22).
XX PS Claim 32; Fig 23; 72pp; English.
XX CC The invention relates to treating a human patient diagnosed with a B-cell
XX CC malignancy. The method involves (a) administering to the human patient a
XX CC blocking anti-CD22 monoclonal antibody binding to the first two Ig-like
XX CC domains, or to an epitope within the first two Ig-like domains of native
XX CC human CD22 (hCD22) (ABR82771) and (b) monitoring the response of the
XX CC malignancy to the treatment. The method is useful for treating a human
XX CC patient diagnosed with a B-cell malignancy comprising Hodgkin's lymphoma,
XX CC Burkitt's lymphoma, multiple myeloma, chronic lymphocytic leukemia, hairy
XX CC cell leukemia or prolymphocytic leukemia. The present sequence represents
XX CC the amino acid sequence for kappa light chain V-J junction for anti-CD22
XX SQ antibody from hybridoma HB22-196
XX SQ Sequence 135 AA;

Query Match 96.2%; Score 663; DB 7; Length 135;
Best Local Similarity 99.2%; Pred. No. 7.6e-45;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVVSWYQOKP 64
DB 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVVSWYQOKP 60

QY 65 EQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGG 124
DB 61 EQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEDLADYHCGQGSYPYTFGG 120

QY 125 GTKLEIKR 132
DB 121 GTKLEIKR 128

RESULT 5
ABR82893
ID ABR82893 standard; protein; 135 AA.
XX AC ABR82893;
XX DT 18-DEC-2003 (first entry)
XX DE Hybridoma HB22-196 anti-CD22 MAb kappa light chain V-J junction.
XX CD22; autoimmune disease; anti-CD22 antibody; immunosuppressive;
XX cytostatic; nephrotropic; dermatological; antinflammatory; anti-ulcer;
XX antirheumatic; antiarthritic; antipsoriatic; thyromimetic; antianemic;
XX antidiabetic; antiallergic; gene therapy; HB22-196.

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XX OS Homo sapiens.
XX PN WO2003072736-A2.
XX PD 04-SEP-2003.
XX PF 21-FEB-2003; 2003WO-US005549.
XX PR 21-FEB-2002; 2002US-0359419P.
XX PR 21-OCT-2002; 2002US-0420472P.
XX PA (UYDU-) UNIV DUKE.
XX PI Tedder TF;
XX DR WPI; 2003-721765/68.
XX DR N-PSDB; ACF36501.
XX PT Treating an autoimmune disease or a B-cell malignancy in a human patient
XX PT comprises administering an amount of an anti-CD22 monoclonal antibody to
XX PT the patient and monitoring the response of the disease to the treatment.
XX PS Claim 4; Fig 23; 69pp; English.
XX CC The invention relates to treating a human patient diagnosed with an
XX CC autoimmune disease. The method involves administering to the patient an
XX CC amount of a blocking anti-CD22 monoclonal antibody and monitoring the
XX CC response of the autoimmune disease to the treatment. The method is useful
XX CC in treating autoimmune diseases (e.g. glomerulonephritis, systemic lupus
XX CC erythematosus, rheumatoid arthritis, psoriasis, ulcerative colitis,
XX CC Hashimoto's thyroiditis, autoimmune haemolytic anemias, diabetes or
XX CC allergies) or B-cell malignancies (e.g. lymphomas or leukemias). The
XX CC present sequence represents the amino acid sequence for kappa light chain
XX CC V-J junction for anti-CD22 antibody from hybridoma HB22-196
XX SQ Sequence 135 AA;
XX
Query Match 96.2%; Score 663; DB 7; Length 135;
Best Local Similarity 99.2%; Pred. No. 7.6e-45;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 MESQTQVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKCKASENVVTVSWYQQKP 64
Db 1 MESQTQVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKCKASENVVTVSWYQQKP 60
QY 65 EQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGG 124
Db 61 EQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGG 120
QY 125 GTKLEIKR 132
Db 121 GTKLEIKR 128
XX
RESULT 6
AAW01632
ID AAW01632 standard; protein; 136 AA.
XX
XX AAW01632;
XX
XX 22-JUL-1997 (first entry)
XX
XX Ber-H2 heavy kappa chain.
XX
XX CD30; immunoglobulin; variable region; CDR; cancer; diagnosis; therapy;
XX Ber-H2.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Peptide 1..29
XX FT /label= sig_peptide

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FT Protein 30..136
FT /label= mat_protein
XX PN DE19543039-C1.
XX PD 21-NOV-1996.
XX PF 08-NOV-1995; 95DE-01043039.
XX PR 08-NOV-1995; 95DE-01043039.
XX PA (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAEPARATE.
XX PI Ziegler A, Stein H;
XX DR WPI; 1996-507017/51.
XX DR N-PSDB; AAT58329.
XX PT DNA mola. encoding CD30-specific immunoglobulin variable regions - useful
XX PT for cancer diagnosis or therapy.
XX PS Claim 15; Page 15; 20pp; German.
XX CC The ligands are useful for diagnosis or therapy of CD30 expressing
XX CC cancers, esp. Hodgkinson's disease. Cytoplasmic RNA was isolated from
XX CC cells of the mouse myeloma hybrid line Ber-H2. cDNA was isolated using
XX CC reverse transcriptase. A VHDJ fragment contg. band was cut from a gel and
XX CC purified. DNA corresponding to VK and Vgamma was isolated and cloned into
XX CC vectors. Oligonucleotides used are given in AAT58331 to AAT58340
XX SQ Sequence 136 AA;
XX
Query Match 94.2%; Score 649; DB 2; Length 136;
Best Local Similarity 95.4%; Pred. No. 9.8e-44;
Matches 125; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MGIKMESQTLVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKCKASENVTVVSWY 60
Db 6 MGIKMESQTLVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKCKASENVTVVSWY 65
QY 61 QOKPEQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPY 120
Db 66 QOKPEQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPY 125
QY 121 TFGGGTKLEIK 131
Db 126 TFGGGTKLEIK 136
XX
RESULT 7
AAB69693
ID AAB69693 standard; protein; 136 AA.
XX
XX AAB69693;
XX
XX 30-APR-2001 (first entry)
XX
XX Murine AF2 antibody light chain SEQ ID NO: 99.
XX
XX Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;
XX KW light chain; graft versus host disease; transplant; autoimmune disease;
XX KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
XX KW myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.
XX
XX Mus sp.
XX
XX US6180370-B1.
XX
XX 30-JAN-2001.
XX
XX 07-JUN-1995; 95US-00484537.
XX
XX 28-DEC-1988; 88US-00290975.

```

```
PR 13-FEB-1989; 89US-00310252.
PR 28-SEP-1990; 90US-00590274.
PR 19-DEC-1990; 90US-00634278.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Queen CL, Selick HE;
XX
XX WPI; 2001-190856/19.
XX N-PSDB; AAF58757.
XX
XX Producing humanized immunoglobulin, involves producing a cell containing
XX DNA segments encoding humanized heavy and light chain variable regions,
XX and expressing the DNA segments in the cell.
XX
XX Example 9; Fig 43; 145pp; English.
XX
XX The present invention describes a method of producing humanised
XX immunoglobulins involving expressing in a cell a nucleic acid encoding a
XX humanised version of an immunoglobulin. This is obtained by comparing a
XX donor and human immunoglobulin and producing a combined antibody which
XX contains part of each. These are useful in the treatment of graft-versus-
XX host disease, transplant rejection, autoimmune diseases such as diabetes,
XX rheumatoid arthritis, myaschenia gravis, multiple sclerosis and systemic
XX lupus erythematosus, herpes infections, CMV virus infections and myeloid
XX leukaemia. The present sequence is an antibody used to demonstrate the
XX method of the invention
XX
XX Sequence 136 AA;
XX
XX Query Match 93.3%; Score 643; DB 4; Length 136;
XX Best Local Similarity 93.1%; Pred. No. 2.9e-43;
XX Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 MGIKMESQTLVFISILLWLYGADGNIVMTQSPKSMVSGRVTLTCKASENVVTVYSWY 60
XX 6 MGIKMESQTLVFISILLWLYGADGNIVMTQSPKSMVSGRVTLTCKASENVVTVYSWY 65
XX
XX 61 QQRPEQSPKLLIYGASNRYTGVPRFTGSGSATDFTLTISVQAEADLADYHCGGQSYVPY 120
XX 66 QQRPEQSPKLLIYGASNRYTGVPRFTGSGSATDFTLTISVQAEADLADYHCGGQSYVPY 125
XX
XX 121 TFGSGTKLEIK 131
XX 126 TFGSGTKLEIK 136
XX
XX RESULT 8
XX ADO47803
XX ID ADO47803. standard; protein; 136 AA.
XX
XX AC ADO47803;
XX
XX 15-JUL-2004 (first entry)
XX
XX AF2 antibody light chain variable region.
XX
XX humanised immunoglobulin; Ig; immunoglobulin; framework; acceptor Ig;
XX donor Ig; CDR; complementarity determining region; interleukin-2; IL-2;
XX IL-2 receptor; T-cell mediated disorder; Af2 antibody;
XX light chain variable region.
XX
XX Unidentified.
XX
XX US2004058414-A1.
XX
XX 25-MAR-2004.
XX
XX 30-MAY-2003; 2003US-00452357.
XX
XX 28-DEC-1988; 88US-00290975.
XX 13-FEB-1989; 89US-00310252.
XX 28-SEP-1990; 90US-00590274.
XX
```

```
PR 07-JUN-1995; 95US-00484537.
PR 22-NOV-2000; 2000US-00718993.
XX
XX (QUEB/) QUEEN C L.
XX (COMS/) CO M S.
XX (SCHN/) SCHNEIDER W P.
XX (LAND/) LANDOLFI N F.
XX (COEL/) COELINGH K L.
XX (SELI/) SELICK H E.
XX
XX Queen CL, Co MS, Schneider WP, Landolfi NF, Coelingh KL;
XX Selick HE;
XX
XX WPI; 2004-304235/28.
XX N-PSDB; ADO47802.
XX
XX Designing humanized immunoglobulin chain comprises substituting human
XX framework amino acids of acceptor immunoglobulin with corresponding amino
XX acid from donor immunoglobulin at position in immunoglobulin.
XX
XX Disclosure; Fig 54; 130pp; English.
XX
XX The invention describes a method of designing a humanised immunoglobulin
XX (Ig) chain. The method comprises substituting human framework amino acids
XX of the acceptor Ig with a corresponding amino acid from the donor Ig at a
XX position in the Igs, where the amino acid is immediately adjacent to one
XX of the CDR's or the amino acid is predicted to have a side chain atom
XX whose Van der Waals surface is 3 angstroms from the CDR's in three-
XX dimensional Ig model and is capable of interacting with the antigen or
XX with the CDR's of the humanised Ig that when the chain is a heavy chain,
XX substituted amino acid(s) is capable of interacting with CDR's 2 or 3.
XX Also described are: an Ig comprising two light/heavy chains; a DNA
XX sequence which upon expression encodes a humanised Ig chain; a
XX polynucleotide composition comprising a DNA sequence coding for a
XX humanised Ig; a composition comprising a pure humanised immunoglobulin
XX capable of inhibiting binding of human interleukin-2 (IL-2) to a human IL
XX -2 receptor; treating T-cell mediated disorders in a human patient
XX comprising administering to the patient a therapeutic dose of an Ig; and
XX a composition comprising a pure humanised Ig reactive with the p75 chain
XX of the human IL-2 receptor. The method is used for designing a humanised
XX immunoglobulin chain, useful for treating T-cell mediated disorders in a
XX human patient. The invented method produces an Ig chain that is easily
XX and economically produced. This is the amino acid sequence of Af2
XX antibody light chain variable region, residues of which can be replaced
XX with residues from a mouse antibody light chain variable region to create
XX a humanised antibody.
XX
XX Sequence 136 AA;
XX
XX Query Match 92.0%; Score 634; DB 8; Length 136;
XX Best Local Similarity 92.4%; Pred. No. 1.5e-42;
XX Matches 121; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 MGIKMESQTLVFISILLWLYGADGNIVMTQSPKSMVSGRVTLTCKASENVVTVYSWY 60
XX 6 MGIKMESQTLVFISILLWLYGADGNIVMTQSPKSMVSGRVTLTCKASENVVTVYSWY 65
XX
XX 61 QQRPEQSPKLLIYGASNRYTGVPRFTGSGSATDFTLTISVQAEADLADYHCGGQSYVPY 120
XX 66 QQRPEQSPKLLIYGASNRYTGVPRFTGSGSATDFTLTISVQAEADLADYHCGGQSYVPY 125
XX
XX 121 TFGSGTKLEIK 131
XX 126 TFGSGTKLEIK 136
XX
XX RESULT 9
XX AAY71545
XX ID AAY71545 standard; protein; 127 AA.
XX
XX AC AAY71545;
XX
XX 12-OCT-2000 (first entry)
XX
```

XX Mouse AF2 antibody light chain variable region (AF2-VL).

DE Humanised antibody; HuZAF; mouse AF2 antibody; human EU antibody; AF2-VL;  
 XX light chain variable region; VL; heavy chain variable region; VH; IgG2b;  
 KW gamma-interferon; IFN; complementarity determining region; CDR; FR;  
 KW framework region; immunosuppressive; antiinflammatory; antisclerotic;  
 KW gastrointestinal; antiidiabetic; antiarthritic; dermatological; inhibitor;  
 KW autoimmune disease; graft versus host disease; organ transplant;  
 KW multiple sclerosis; Type I diabetes; rheumatoid arthritis; psoriasis;  
 KW systemic lupus erythematosus; SLE; Crohn's disease.

XX Mus sp.

XX Location/Qualifiers

EH Key

FT Peptide

FT 1..20 /note= "N-terminal peptide"

FT Protein

FT 21..127

FT /note= "Mature mouse antibody AF2 light chain variable  
 region (AF2-VL)"

FT Region

FT 44..54 /label= CDR

FT /note= "Complementarity determining region"

FT Region

FT 70..76 /label= CDR

FT /note= "Complementarity determining region"

FT Region

FT 109..117 /label= CDR

FT /note= "Complementarity determining region"

XX WO200032634-A1.

XX 08-JUN-2000.

XX 29-NOV-1999; 99WO-US028195.

XX 01-DEC-1998; 98US-0110523P.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Vasquez M, Landolfi NF, Tsurushita N, Queen CL;  
 PI WPI; 2000-412292/35.  
 DR N-PSDB; AAD01345.

XX Humanized murine AF2 immunoglobulins, useful for inhibiting gamma-  
 PT interferon for the treatment of autoimmune diseases, e.g. multiple  
 PT sclerosis and diabetes.

XX Claim 1; Fig 1A; 32pp; English.

XX The present amino acid sequence is the mouse AF2 antibody, light chain  
 CC variable region (AF2-VL). It has IgG2b isotype and kappa light chain. It  
 CC is used for the construction of humanised version of mouse AF2 antibody  
 CC HuZAF, that comprises mouse antibody AF2 complementarity determining  
 CC regions (CDRs), functionally joined to the human acceptor antibody EU  
 CC framework region (FR). HuZAF antibody specifically binds to and  
 CC neutralises gamma-interferon (IFN). They can also block the binding of  
 CC mouse AF2 immunoglobulin to gamma-IFN. HuZAF does not contain sequences  
 CC that are immunogenically active in humans and remains unaffected by  
 CC immune responses, that may reduce its activity or circulating half-life.  
 CC HuZAF may be administered to treat autoimmune diseases such as graft  
 CC versus host disease following organ transplant, Type I diabetes, multiple  
 CC sclerosis, rheumatoid arthritis, psoriasis, systemic lupus erythematosus  
 CC (SLE), Hashimoto's thyroiditis, primary biliary cirrhosis and  
 CC inflammatory bowel disease like, Crohn's disease

XX Sequence 127 AA;

SQ Query Match 90.4%; Score 623; DB 3; Length 127;  
 Best Local Similarity 92.9%; Pred. No. 1e-41;  
 Matches 118; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVLTCTKASENVVTVSWYQKP 64  
 |||||  
 Db 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMVVSIGERVLTLSCKASENVDTVSWYQKP 60  
 |||||

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCCQGSYPYTFGG 124  
 |||||  
 Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCCQGSYPYTFGS 120  
 |||||

QY 125 GTKLEIK 131  
 |||||  
 Db 121 GTKLEIK 127  
 |||||

RESULT 10  
 AAW47085  
 ID AAW47085 standard; protein; 121 AA.  
 XX  
 AC AAW47085;  
 XX  
 DT 26-JUN-1998 (first entry)  
 XX  
 DE Mouse J591 monoclonal antibody light chain.  
 XX  
 KW Mouse; monoclonal antibody; J591; prostate specific membrane antigen;  
 KW cancer; vascular endothelial cell; metastatic adenocarcinoma.  
 XX  
 OS Mus sp.  
 XX WO9803873-A1.  
 XX 29-JAN-1998.  
 XX  
 XX 17-JUL-1997; 97WO-US012035.  
 XX  
 PR 18-JUL-1996; 96US-0022125P.  
 PR 09-APR-1997; 97US-00838682.  
 XX  
 PA (CORR ) CORNELL RES FOUND INC.  
 XX  
 PI Bander NH;  
 XX  
 DR WPI; 1998-120937/11.  
 DR N-PSDB; AAV13951.  
 XX  
 PT Destroying cancer cells with agent that binds to prostate specific  
 PT membrane antigen - on vascular endothelial cells near the cancer, or on  
 PT normal, hypertrophic or cancerous prostatic cells, also used for  
 PT diagnosis.

XX Example 12; Page 57; 94pp; English.

XX The present sequence represents the mouse J591 monoclonal antibody light  
 CC chain from an example of the present invention. The present invention  
 CC describes the elimination of cancer cells by treating vascular  
 CC endothelial cells (VEC) close to the cancer with an agent (A) able to  
 CC bind to the extracellular domain (ECD) of prostate specific membrane  
 CC antigen (PSMA). (A) both binds to the VEC and destroys the cancer cells.  
 CC Also described are: (1) the detection of cancer tissue by detecting  
 CC binding of labelled (A) to VEC close to, or within, a cancer tissue; (2)  
 CC eliminating or detecting normal, benignly hyperplastic or cancerous  
 CC prostate epithelial cells using optionally labelled (A); (3) hybridomas  
 CC that produce a monoclonal antibody (Mab) that binds to PSMA. The method  
 CC is used to treat renal, urothelial, colon, lung, rectal or breast cancers  
 CC and metastatic adenocarcinoma of the liver. The diagnostic method is  
 CC particularly used to detect recurrence of prostatic disease or to monitor  
 CC the effect of treatments for prostate cancer (presence of PSMA in the  
 CC serum indicates that prostate cells are being lysed). (A) binds to an  
 CC epitope of PSMA expressed on live cells (contrast antibody 7E11 which  
 CC only binds after cell lysis), allowing targeting of live, unfixed cells  
 CC and thus providing more efficient treatment and diagnosis. Both cancer  
 CC cells themselves and the VEC on which they depend are killed. All VEC  
 CC close to cancer cells express PSMA, whatever the type of cancer, but  
 CC normal VEC do not

```

XX SQ Sequence 121 AA;
Query Match      87.1%; Score 600; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.4e-40;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTITSSVQAEDLADYHCGQGSYPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTITSSVQAEDLADYHCGQGSYPYTFGGGTKLEIKR 114

RESULT 11
AAY90370
ID AAY90370 standard; protein; 121 AA.
XX AC AAY90370;
XX DT 15-JAN-2001 (first entry)
XX DE J591 monoclonal antibody kappa light chain protein sequence #1.
XX KW J591 monoclonal antibody; extracellular domain; diagnosis; therapy;
XX KW prostate specific membrane antigen; prostate cancer; kappa light chain.
XX OS Homo sapiens.
XX FN US6107090-A.
XX PD 22-AUG-2000.
XX PF 09-APR-1997; 97US-00838682.
XX PR 06-MAY-1996; 96US-0016976P.
XX PR 18-JUL-1996; 96US-0022125P.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PI Bander NH;
XX WPI; 1998-120937/11.
XX DR N-PSDB; AAA37832.
XX PT Destroying cancer cells with agent that binds to prostate specific
XX PT membrane antigen - on vascular endothelial cells near the cancer, or on
XX PT normal, hypertrophic or cancerous prostatic cells, also used for
XX PT diagnosis.
XX PS Example 12; Fig 10; 33pp; English.
XX CC This sequence is the kappa light chain of the monoclonal antibody J591.
XX CC The invention relates to an isolated antibody or its antigen binding
XX CC portion (I) which binds to an extracellular domain of prostate specific
XX CC membrane antigen and which does not require cell lysis to bind to the
XX CC extracellular domain. The antibody or its antigen binding portion is
XX CC selected for its ability to bind to live cells. (I) is useful for
XX CC diagnosis of diseases associated with the presence of normal, benign
XX CC hyperplastic, and cancerous epithelial cells or portions. Also it can be
XX CC used for identifying the recurrence of such diseases, particularly when
XX CC the disease is localised in a particular biological material of the
XX CC patient for e.g. recurrence of prostatic disease. They can also be used
XX CC alone or bound to a substance effective to kill cancerous prostate
XX CC epithelial cells as a therapy for prostate cancer. Binding and
XX CC internalising of the antibody with the prostate specific membrane
XX CC antigen, permits the therapeutic use of intracellularly acting cytotoxic
XX CC agents. (I) targets only prostate epithelial cells and other tissue are
XX CC spared which provides safer treatment particularly for elderly patients.
XX CC The antibodies bind to living prostate cells and treatments using these
XX CC antibodies are more effective than those which target lysed prostate

CC cells
XX SQ Sequence 121 AA;
Query Match      87.1%; Score 600; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.4e-40;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTITSSVQAEDLADYHCGQGSYPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTITSSVQAEDLADYHCGQGSYPYTFGGGTKLEIKR 114

RESULT 12
AAB36222
ID AAB36222 standard; protein; 121 AA.
XX AC AAB36222;
XX DT 15-FEB-2001 (first entry)
XX DE Murine monoclonal antibody J591 kappa light chain #1.
XX KW Mouse; antibody; heavy chain; prostate cancer; biological agent.
XX OS Mus sp.
XX FN US6136311-A.
XX PD 24-OCT-2000.
XX PF 17-JUL-1997; 97US-00895914.
XX PR 06-MAY-1996; 96US-0016976P.
XX PR 18-JUL-1996; 96US-0022125P.
XX PR 09-APR-1997; 97US-00838682.
XX PA (CORR ) CORNELL RES FOUND INC.
XX PI Bander NH;
XX WPI; 1998-120937/11.
XX DR N-PSDB; AAC66542.
XX PT Destroying cancer cells with agent that binds to prostate specific
XX PT membrane antigen - on vascular endothelial cells near the cancer, or on
XX PT normal, hypertrophic or cancerous prostatic cells, also used for
XX PT diagnosis.
XX PS Example 12; Fig 10; 35pp; English.
XX CC The present invention describes a method of killing cancer cells,
XX CC particularly prostate cancer cells, by directing a biological agent to
XX CC the cells which then binds to a prostate specific membrane antigen and
XX CC causes the molecule to be internalised. The internalisation of the agent,
XX CC which may be bound to a drug or which may act to kill the cell alone,
XX CC then leads to the death of the cell. The present sequence forms part of
XX CC an antibody which may be used as the biological agent of the invention.
XX CC In addition to prostate cancer, the method can be used with renal,
XX CC urothelial, colon, renal, lung and breast cancer cells, and cancerous
XX CC cells of metastatic adenocarcinoma to the liver

CC cells
XX SQ Sequence 121 AA;
Query Match      87.1%; Score 600; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.4e-40;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQQKPEQSPKLLIYGASNR 78

```



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Db      1  LYGADGNVMTQSPKSMNSVGERVTLTCKASENVVTVSVYQKPEQSPKLLIYGASNR 60
      79  YTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIKR 132
      61  YTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIKR 114

RESULT 13
AAR27144
ID  AAR27144 standard; protein; 109 AA.
AC  AAR27144;
XX
XX  09-SEP-2004 (revised)
DT  25-MAR-2003 (revised)
DT  20-MAY-1998 (first entry)
XX
XX  1E6 kappa light chain variable region.
XX
XX  Chimeric; heavy chain; variable region; monoclonal antibody;
KW  lymphocyte function associated antigen-3; LFA-3; inflammation;
KW  autoimmune disease; immunomodulation; systemic lupus erythematosus;
KW  rheumatoid arthritis; thyroiditis.
XX
XX  Homo sapiens.
OS  Unidentified.
XX
XX  Key Location/Qualifiers
FH Domain 24..34
FT /note= "CDR1"
FT Domain 50..56
FT /note= "CDR2"
FT Domain 89..97
FT /note= "CDR3"
XX
XX  EP503646-A1.
XX
XX  16-SEP-1992.
XX
XX  12-MAR-1992; 92EP-00104318.
XX
XX  12-MAR-1991; 91US-00667975.
XX
XX  (BIOJ ) BIOGEN INC.
XX
XX  Sato VL, Chisholm PL, Wallner BP;
PI
XX
XX  WPI; 1992-309758/38.
DR  N-PSDB; AAQ28653.
XX
XX  Monoclonal antibodies active against lymphocyte function associated
FT  antigen-3 - for treating inflammation and autoimmune diseases, and for
PT  detecting LFA-3 protein in a sample.
XX
XX  Claim 19; Page 14; 30pp; English.
XX
XX  Light and heavy chain variable region sequences were deduced from the DNA
CC  sequences obt'd. by PCR of DNA sequences obt'd. from the hybridoma cell
CC  line 1E6-2C12 (ATCC HB 10693). The light and heavy chain regions may be
CC  used to construct a monoclonal antibody active against LFA-3 which blocks
CC  adhesion of LFA-3 expressing cells to lymphocytes. The antibody may be
CC  used in the treatment and diagnosis of acute and chronic inflammation,
CC  autoimmune diseases and for immuno- modulation including systemic lupus
CC  erythematosus, rheumatoid arthritis and thyroiditis. See also AAR27145.
CC  (Updated on 25-MAR-2003 to correct PN field.)
XX
XX  Revised record issued on 09-SEP-2004 : Correction to feature Table Key
CC
XX  Sequence 109 AA;
SQ

Query Match 82.3%; Score 567; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2.3e-37;

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Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      25  NIVMTQSPKSMNSVGERVTLTCKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 84
      |||||
DB      1  NIVMTQSPKSMNSVGERVTLTCKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60
      |||||
QY      85  RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIKR 132
      |||||
DB      61  RFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYPTFGGTTKLEIKR 108
      |||||

RESULT 14
AAW47086
ID  AAW47086 standard; protein; 107 AA.
XX
XX  AAW47086;
AC
XX
XX  26-JUN-1998 (first entry)
DT
XX
XX  Mouse J591 monoclonal antibody light chain variable region.
DE
XX
XX  Mouse; monoclonal antibody; J591; prostate specific membrane antigen;
KW  cancer; vascular endothelial cell; metastatic adenocarcinoma.
XX
XX  Mus sp.
OS
XX
XX  WO9803873-A1.
PN
XX
XX  29-JAN-1998.
PD
XX
XX  17-JUL-1997; 97WO-US012035.
PF
XX
XX  18-JUL-1996; 96US-0022125P.
PR
XX
XX  09-APR-1997; 97US-00838682.
XX
XX  (CORR ) CORNELL RES FOUND INC.
PA
XX
XX  Bander NH;
PI
XX
XX  WPI; 1998-120937/11.
DR  N-PSDB; AAV13952.
XX
XX  Destroying cancer cells with agent that binds to prostate specific
PT  membrane antigen - on vascular endothelial cells near the cancer, or on
PT  normal, hypertrophic or cancerous prostatic cells, also used for
PT  diagnosis.
XX
XX  Example 12; Page 60; 94pp; English.
XX
XX  The present sequence represents the mouse J591 monoclonal antibody light
CC  chain variable region from an example of the present invention. The
CC  present invention describes the elimination of cancer cells by treating
CC  vascular endothelial cells (VEC) close to the cancer with an agent (A)
CC  able to bind to the extracellular domain (ECD) of prostate specific
CC  membrane antigen (PSMA). (A) both binds to the VEC and destroys the
CC  cancer cells. Also described are: (1) the detection of cancer tissue by
CC  detecting binding of labelled (A) to VEC close to, or within, a cancer
CC  tissue; (2) eliminating or detecting normal, benignly hyperplastic or
CC  cancerous prostate epithelial cells using optionally labelled (A); (3)
CC  hybridomas that produce a monoclonal antibody (MAB) that binds to PSMA.
CC  The method is used to treat renal, urothelial, colon, lung, rectal or
CC  breast cancers and metastatic adenocarcinoma of the liver. The diagnostic
CC  method is particularly used to detect recurrence of prostatic disease or
CC  to monitor the effect of treatments for prostate cancer (presence of PSMA
CC  in the serum indicates that prostate cells are being lysed). (A) binds to
CC  an epitope of PSMA expressed on live cells (contrast antibody 7E11 which
CC  only binds after cell lysis), allowing targeting of live, unfixed cells
CC  and thus providing more efficient treatment and diagnosis. Both cancer
CC  cells themselves and the VEC on which they depend are killed. All VEC
CC  close to cancer cells express PSMA, whatever the type of cancer, but
CC  normal VEC do not
XX
XX  Sequence 107 AA;
SQ

```



Query Match 81.6%; Score 562; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-37;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 NIVMTQSPKSMSSVGERVTLTCKASENVVTVVSWYQOKPEQSPKLLIYGASNRYTGVPD 84  
 Db 1 NIVMTQSPKSMSSVGERVTLTCKASENVVTVVSWYQOKPEQSPKLLIYGASNRYTGVPD 60

Qy 85 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYSPYTFGGGTGLEIK 131  
 Db 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYSPYTFGGGTGLEIK 107

RESULT 15

AA90374  
 ID AA90374 standard; protein; 107 AA.  
 AC AAY90374;  
 DT 15-JAN-2001 (first entry)  
 DE J591 monoclonal antibody light chain protein sequence fragment.  
 KW J591 monoclonal antibody; extracellular domain; diagnosis; therapy;  
 KW prostate specific membrane antigen; prostate cancer; light chain.  
 OS Homo sapiens.  
 PN US6107090-A.  
 PD 22-AUG-2000.  
 PF 09-APR-1997; 97US-00838682.  
 PR 06-MAY-1996; 96US-0016976P.  
 PR 18-JUL-1996; 96US-0022125P.  
 PA (CORR ) CORNELL RES FOUND INC.  
 PI Bander NH;  
 DR WPI; 1998-120937/11.  
 DR N-PSDB; AAA37834.  
 PT Destroying cancer cells with agent that binds to prostate specific  
 PT membrane antigen - on vascular endothelial cells near the cancer, or on  
 PT normal, hypertrophic or cancerous prostatic cells, also used for  
 PT diagnosis.

Example 12; Col 22; 33pp; English.

This sequence is a fragment of the light chain of the monoclonal antibody  
 J591. The invention relates to an isolated antibody or its antigen  
 binding portion (I) which binds to an extracellular domain of prostate  
 specific membrane antigen and which does not require cell lysis to bind  
 to the extracellular domain. The antibody or its antigen binding portion  
 is selected for its ability to bind to live cells. (i) is useful for  
 diagnosis of diseases associated with the presence of normal, benign  
 hyperplastic, and cancerous epithelial cells or portions. Also it can be  
 used for identifying the recurrence of such diseases, particularly when  
 the disease is localised in a particular biological material of the  
 patient for e.g. recurrence of prostatic disease. They can also be used  
 alone or bound to a substance effective to kill cancerous prostate  
 epithelial cells as a therapy for prostate cancer. Binding and  
 internalising of the antibody with the prostate specific membrane  
 antigen, permits the therapeutic use of intracellularly acting cytotoxic  
 agents. (i) targets only prostate epithelial cells and other tissue are  
 spared which provides safer treatment particularly for elderly patients.  
 The antibodies bind to living prostate cells and treatments using these  
 antibodies are more effective than those which target lysed prostate  
 cells

CC

SQ Sequence 107 AA;

Query Match 81.6%; Score 562; DB 2; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-37;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 NIVMTQSPKSMSSVGERVTLTCKASENVVTVVSWYQOKPEQSPKLLIYGASNRYTGVPD 84  
 Db 1 NIVMTQSPKSMSSVGERVTLTCKASENVVTVVSWYQOKPEQSPKLLIYGASNRYTGVPD 60

Qy 85 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYSPYTFGGGTGLEIK 131  
 Db 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYSPYTFGGGTGLEIK 107

Search completed: May 25, 2005, 15:47:24  
 Job time : 64.1321 secs



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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 16.454 Seconds  
(without alignments)  
598.864 Million cell updates/sec

Title: US-10-006-773A-19

Perfect score: 689

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	643	93.3	136	1	US-07-634-278-99
2	643	93.3	136	1	US-08-477-728-99
3	643	93.3	136	1	US-08-474-040-99
4	643	93.3	136	1	US-08-487-200-99
5	643	93.3	136	3	US-08-484-537-99
6	623	90.4	127	3	US-09-450-520A-2
7	600	87.1	121	3	US-08-838-682-11
8	600	87.1	121	3	US-08-895-914-11
9	600	87.1	121	3	US-09-357-710A-11
10	600	87.1	121	4	US-09-357-707-11
11	600	87.1	121	4	US-09-357-708-11
12	567	82.3	109	5	PCT-US92-02044-2
13	562	81.6	107	3	US-08-838-682-16
14	562	81.6	107	3	US-08-895-914-16
15	562	81.6	107	3	US-09-357-710A-16
16	562	81.6	107	4	US-09-357-707-16
17	562	81.6	107	4	US-09-357-708-16
18	523	75.9	132	1	US-08-253-877C-55
19	523	75.9	132	2	US-08-452-164A-55
20	523	75.9	132	3	US-08-976-183A-36
21	518	75.2	132	3	US-08-976-183A-37
22	505	73.3	147	2	US-08-653-402B-4
23	503	73.0	131	4	US-09-269-921-104
24	495.5	71.9	132	2	US-08-602-725-38
25	493	71.6	128	3	US-09-450-520A-6
26	487	70.7	131	1	US-08-202-047-5
27	487	70.7	131	3	US-08-964-690-5

Sequence 14, Appl  
Sequence 14, Appl  
Sequence 14, Appl  
Sequence 65, Appl  
Sequence 36, Appl  
Sequence 27, Appl  
Sequence 49, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 58, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 28, Appl  
Sequence 28, Appl

28 477 69.2 131 2 US-08-822-028-14  
29 477 69.2 131 3 US-08-479-285-14  
30 477 69.2 131 4 US-09-503-653A-14  
31 476 69.1 127 3 US-08-525-539A-65  
32 475 68.9 154 3 US-08-513-968-36  
33 473 68.7 127 3 US-08-646-265A-27  
34 457 66.3 127 3 US-08-525-539A-49  
35 454 65.9 107 3 US-08-554-840-4  
36 454 65.9 107 4 US-08-925-339-4  
37 454 65.9 107 4 US-09-332-595-4  
38 453 65.7 133 3 US-08-579-378A-2  
39 453 65.7 133 5 PCT-US93-11612-2  
40 452 65.6 134 4 US-08-961-309-58  
41 449 65.2 107 3 US-08-554-840-2  
42 449 65.2 107 4 US-08-925-339-2  
43 449 65.2 107 4 US-09-332-595-2  
44 448 65.0 126 2 US-08-822-028-28  
45 448 65.0 126 3 US-08-479-285-28

## ALIGNMENTS

RESULT 1  
US-07-634-278-99  
; Sequence 99, Application US/07634278  
; Patent No. 5530101  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

MOLECULE TYPE: protein  
US-07-634-278-99

Query Match 93.3%; Score 643; DB 1; Length 136;  
Best Local Similarity 93.1%; Pred. No. 2.2e-57;  
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVTVTSWY 60  
|||||  
Db 6 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMYSIGERVTLTKKASENVTVTSWY 65  
|||||

QY 61 QQRPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYYPY 120  
|||||  
Db 66 QQRPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYNPY 125  
|||||

QY 121 TFGGGTKLEIK 131  
|||||  
Db 126 TFGGGTKLEIK 136  
|||||

RESULT 2  
US-08-477-728-99  
; Sequence 99, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-477-728-99

Query Match 93.3%; Score 643; DB 1; Length 136;  
Best Local Similarity 93.1%; Pred. No. 2.2e-57;  
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVTVTSWY 60  
|||||  
Db 6 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMYSIGERVTLTKKASENVTVTSWY 65  
|||||

QY 61 QQRPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYYPY 120  
|||||  
Db 66 QQRPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYNPY 125  
|||||

QY 121 TFGGGTKLEIK 131  
|||||  
Db 126 TFGGGTKLEIK 136  
|||||

RESULT 3  
US-08-474-040-99  
; Sequence 99, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas P.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-474-040-99

Query Match 93.3%; Score 643; DB 1; Length 136;

Best Local Similarity 93.1%; Pred. No. 2.2e-57;  
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGIRMESQTLVPISILLWLYGADGNIVMTQSPKSMGSGRVTLTCKASENVVTVSWY 60  
Db 6 MGIRMESQTLVPISILLWLYGADGNIVMTQSPKSMGSGRVTLTCKASENVVTVSWY 65

Qy 61 QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 120  
Db 66 QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 125

Qy 121 TFGGQTKLEIK 131  
Db 126 TFGSGTKLEIK 136

RESULT 4

US-08-487-200-99  
; Sequence 99, Application US/08487200  
; Patent No. 5693762  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO. Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487.200  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002610  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-487-200-99

Query Match 93.3%; Score 643; DB 1; Length 136;

Best Local Similarity 93.1%; Pred. No. 2.2e-57;  
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MGIRMESQTLVPISILLWLYGADGNIVMTQSPKSMGSGRVTLTCKASENVVTVSWY 60  
Db 6 MGIRMESQTLVPISILLWLYGADGNIVMTQSPKSMGSGRVTLTCKASENVVTVSWY 65

Qy 61 QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 120  
Db 66 QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQGSYPY 125

Qy 121 TFGGQTKLEIK 131  
Db 126 TFGSGTKLEIK 136

RESULT 5

US-08-484-537-99  
; Sequence 99, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO. Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,537  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-484-537-99

Query Match 93.3%; Score 643; DB 3; Length 136;

Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGKMSQTLVFTSILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVSWY 60  
|||||  
Db 6 MGKMSQTLVFTSILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVSWY 65  
|||||

QY 61 QKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPY 120  
|||||  
Db 66 QKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQSYNYPF 125  
|||||

QY 121 TFGGKLEIK 131  
|||||  
Db 126 TFGGKLEIK 136  
|||||

RESULT 6  
US-09-450-520A-2  
; Sequence 2, Application US/09450520A  
; Patent No. 6329511  
; GENERAL INFORMATION:  
; APPLICANT: Vasequez, Maximiliano  
; APPLICANT: Landolfi, Nicholas F.  
; APPLICANT: Tsurushita, Naoya  
; APPLICANT: Queen, Cary L.  
; APPLICANT: Protein Design Labs, Inc.  
; TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon  
; FILE REFERENCE: 011823-008110US  
; CURRENT APPLICATION NUMBER: US/09/450,520A  
; PRIOR FILING DATE: 1999-11-29  
; PRIOR APPLICATION NUMBER: 60/110,523  
; PRIOR FILING DATE: 1998-12-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Mus sp.  
; FEATURE:  
; OTHER INFORMATION: AF2 VL  
US-09-450-520A-2

Query Match 90.4%; Score 623; DB 3; Length 127;  
Best Local Similarity 92.9%; Pred. No. 2.1e-55;  
Matches 118; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 5 MESQTLVFTSILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVSWYQKP 64  
|||||  
Db 1 MESQTLVFTSILLWLYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVSWYQKP 60  
|||||

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 124  
|||||  
Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQSYNYPF 120  
|||||

QY 125 GTKLEIK 131  
|||||  
Db 121 GTKLEIK 127  
|||||

RESULT 7  
US-08-838-682-11  
; Sequence 11, Application US/08838682  
; Patent No. 6107090  
; GENERAL INFORMATION:  
; APPLICANT: Bander M.D., Neil H.  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.

ZIP: 14603-1051  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,682  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/016,976  
FILING DATE: 06-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/022,125  
FILING DATE: 18-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1172  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-838-682-11

Query Match 87.1%; Score 600; DB 3; Length 121;  
Best Local Similarity 100.0%; Pred. No. 4.1e-53;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNR 78  
|||||  
Db 1 LYGADGNIVMTQSPKSMMSGVGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNR 60  
|||||

QY 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGTKLEIKR 132  
|||||  
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGTKLEIKR 114  
|||||

RESULT 8  
US-08-895-914-11  
; Sequence 11, Application US/08895914  
; Patent No. 6136311  
; GENERAL INFORMATION:  
; APPLICANT: Bander, Neil H.  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603-1051  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/895,914  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/016,976  
; FILING DATE: 06-MAY-1996  
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 60/022,125
; FILING DATE: 18-JUL-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/838,682
; FILING DATE: 09-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldman, Michael L.
; REGISTRATION NUMBER: 30,727
; REFERENCE/DOCKET NUMBER: 19603/1173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1304
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-895-914-11

Query Match      87.1%; Score 600; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.1e-53;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 114

RESULT 9
US-09-357-710A-11
; Sequence 11, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/025
; CURRENT APPLICATION NUMBER: US/09/357,710A
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-710A-11

Query Match      87.1%; Score 600; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.1e-53;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 114

RESULT 10
US-09-357-7107-11
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; Sequence 11, Application US/09357707
; Patent No. 6649163
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/078
; CURRENT APPLICATION NUMBER: US/09/357,707
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/895,914
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-707-11

Query Match      87.1%; Score 600; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.1e-53;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 114

RESULT 11
US-09-357-708-11
; Sequence 11, Application US/09357708
; Patent No. 6770450
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/357,708
; CURRENT FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/895,914
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-708-11

Query Match      87.1%; Score 600; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.1e-53;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQQKPEQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTKASENVVTVSVYQQKPEQSPKLLIYGASNR 60

Qy 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGTKLEIKR 114
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Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGGKLEIKR 114

## RESULT 12

PCT-US92-02044-2  
; Sequence 2, Application PC/TUS9202044  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; APPLICANT: SATO, Vicki L.  
; APPLICANT: CHISHOLM, Patricia L.  
; APPLICANT: WALLNER, Barbara P.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES RECOGNIZING  
; TITLE OF INVENTION: LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN-3  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: c/o FISH & NEAVE  
; STREET: 875 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/02044  
; FILING DATE: 19920312  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/667,975  
; FILING DATE: 12-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HALEY Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B150CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 715-0600  
; TELEFAX: (212) 715-0673  
; TELEX: 14-8367  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 109 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US92-02044-2

Query Match 82.3%; Score 567; DB 5; Length 109;

Best Local Similarity 100.0%; Pred. No. 7.7e-50; Mismatches 0; Indels 0; Gaps 0;  
Matches 108; Conservative 0

QY 25 NIVMTQSPKSMMSVGERVTLTKASENVVTVSWYQQKPEQSPKLLIYGASNRYTGVPD 84

Db 1 NIVMTQSPKSMMSVGERVTLTKASENVVTVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

QY 85 RTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGGKLEIKR 132

Db 61 RFTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGGKLEIKR 108

## RESULT 13

US-08-838-682-16  
; Sequence 16, Application US/08838682  
; Patent No. 6107090  
; GENERAL INFORMATION:  
; APPLICANT: Bander M.D., Neil H.  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE  
; TITLE OF INVENTION: CANCER  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP

; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603-1051  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,682  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/016,976  
; FILING DATE: 06-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/022,125  
; FILING DATE: 18-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/1172  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1304  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-838-682-16

Query Match 81.6%; Score 562; DB 3; Length 107;

Best Local Similarity 100.0%; Pred. No. 2.4e-49; Mismatches 0; Indels 0; Gaps 0;  
Matches 107; Conservative 0

QY 25 NIVMTQSPKSMMSVGERVTLTKASENVVTVSWYQQKPEQSPKLLIYGASNRYTGVPD 84

Db 1 NIVMTQSPKSMMSVGERVTLTKASENVVTVSWYQQKPEQSPKLLIYGASNRYTGVPD 60

QY 85 RTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGGKLEIK 131

Db 61 RFTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGGKLEIK 107

## RESULT 14

US-08-895-914-16  
; Sequence 16, Application US/08895914  
; Patent No. 6136311  
; GENERAL INFORMATION:  
; APPLICANT: Bander, Neil H.  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603-1051  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/895,914  
; FILING DATE:  
; CLASSIFICATION: 435



Search completed: May 25, 2005, 15:58:28  
Job time : 17.454 secs

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/016,976  
;; FILING DATE: 06-MAY-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/022,125  
;; FILING DATE: 18-JUL-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/838,682  
;; FILING DATE: 09-APR-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Goldman, Michael L.  
;; REGISTRATION NUMBER: 30,727  
;; REFERENCE/DOCKET NUMBER: 19603/1173  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (716) 263-1304  
;; TELEFAX: (716) 263-1600  
;; INFORMATION FOR SEQ ID NO: 16:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 107 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-895-914-16

Query Match 81.6%; Score 562; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred.No. 2.4e-49;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 25 NIVMTQSPKSMVSGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVDP 84  
Db 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVDP 60  
QY 85 RFTGSGSATDFTLTISVQAEDLDADYHCGQGYSPYTFGGGTKLEIK 131  
Db 61 RFTGSGSATDFTLTISVQAEDLDADYHCGQGYSPYTFGGGTKLEIK 107

RESULT 15  
US-09-357-710A-16  
; Sequence 16, Application US/09357710A  
; Patent No. 6290956  
; GENERAL INFORMATION:  
; APPLICANT: Bander, Neil H.  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER  
; FILE REFERENCE: Lois M. Kwasigroch: BZL 242/025  
; CURRENT APPLICATION NUMBER: US/09/357,710A  
; CURRENT FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: US 08/838,682  
; PRIOR FILING DATE: 1997-04-09  
; PRIOR APPLICATION NUMBER: US 60/016,976  
; PRIOR FILING DATE: 1996-05-06  
; PRIOR APPLICATION NUMBER: US 60/022,125  
; PRIOR FILING DATE: 1996-07-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-357-710A-16

Query Match 81.6%; Score 562; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred.No. 2.4e-49;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 25 NIVMTQSPKSMVSGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVDP 84  
Db 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSWYQKPEQSPKLLIYGASNRYTGVDP 60  
QY 85 RFTGSGSATDFTLTISVQAEDLDADYHCGQGYSPYTFGGGTKLEIK 131  
Db 61 RFTGSGSATDFTLTISVQAEDLDADYHCGQGYSPYTFGGGTKLEIK 107

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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 60.9042 Seconds  
(without alignments)  
724:991 Million cell updates/sec

Title: US-10-006-773A-19  
Perfect score: 689  
Sequence: 1 MGIMESQTLVFSILLWLY.....GGQSYPTFGGKLEIKR 132

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Gap 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	689	100.0	132	13	US-10-006-773-19
2	669	97.1	128	14	US-10-010-729-70
3	663	96.2	135	15	US-10-372-481-31
4	663	96.2	135	15	US-10-371-797-31
5	661	95.9	128	8	US-08-779-784-34
6	634	92.0	136	15	US-10-452-357-99
7	627	91.0	136	15	US-10-389-155-84
8	627	91.0	136	15	US-10-389-417-84
9	623	90.4	127	9	US-09-992-524-2
10	600	87.1	121	10	US-09-929-665-11
11	600	87.1	121	10	US-09-929-546-11
12	562	81.6	107	10	US-09-929-665-16
13	562	81.6	107	10	US-09-929-546-16

14	534	77.5	101	14	US-10-010-729-21	Sequence 21, Appl
15	532	77.2	133	10	US-09-874-141-47	Sequence 47, Appl
16	530	76.9	133	10	US-09-874-141-51	Sequence 51, Appl
17	527	76.5	133	10	US-09-874-141-45	Sequence 45, Appl
18	512	74.3	145	15	US-10-326-795-17	Sequence 17, Appl
19	511	74.2	132	15	US-10-365-123-53	Sequence 53, Appl
20	503	73.0	107	14	US-10-160-506-48	Sequence 48, Appl
21	503	73.0	107	16	US-10-449-379-48	Sequence 48, Appl
22	503	73.0	107	16	US-10-688-015-48	Sequence 48, Appl
23	503	73.0	131	10	US-09-269-921-104	Sequence 104, Appl
24	503	73.0	131	10	US-09-509-098-2	Sequence 2, Appl
25	503	73.0	131	14	US-10-218-253-104	Sequence 104, Appl
26	493	71.6	128	9	US-09-992-524-6	Sequence 6, Appl
27	493	71.6	128	15	US-10-440-202-1	Sequence 1, Appl
28	490	71.1	107	14	US-10-160-506-64	Sequence 64, Appl
29	490	71.1	107	14	US-10-160-506-65	Sequence 65, Appl
30	490	71.1	107	16	US-10-449-379-64	Sequence 64, Appl
31	490	71.1	107	16	US-10-449-379-65	Sequence 65, Appl
32	490	71.1	107	16	US-10-688-015-64	Sequence 65, Appl
33	490	71.1	107	16	US-10-688-015-65	Sequence 65, Appl
34	487	70.7	107	14	US-10-160-506-66	Sequence 66, Appl
35	487	70.7	107	16	US-10-449-379-66	Sequence 66, Appl
36	487	70.7	107	16	US-10-688-015-66	Sequence 66, Appl
37	485	70.4	107	14	US-10-160-506-63	Sequence 63, Appl
38	485	70.4	107	16	US-10-449-379-63	Sequence 63, Appl
39	485	70.4	107	16	US-10-688-015-63	Sequence 63, Appl
40	484	70.2	107	14	US-10-160-506-50	Sequence 50, Appl
41	484	70.2	107	14	US-10-160-506-67	Sequence 67, Appl
42	484	70.2	107	14	US-10-160-506-68	Sequence 68, Appl
43	484	70.2	107	16	US-10-449-379-50	Sequence 50, Appl
44	484	70.2	107	16	US-10-449-379-67	Sequence 67, Appl
45	484	70.2	107	16	US-10-449-379-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1

US-10-006-773-19  
; Sequence 19, Application US/10006773  
; Publication No. US20020132983A1  
; GENERAL INFORMATION:  
; APPLICANT: Junghans, Richard P.  
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti  
; FILE REFERENCE: 003  
; CURRENT APPLICATION NUMBER: US/10/006,773  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/250,089  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 132  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-006-773-19

Query Match 100.0%; Score 689; DB 13; Length 132;  
Best Local Similarity 100.0%; Pred. No. 4.2e-56;  
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGIMESQTLVFSILLWLYGADGNI	VMTQSPKMSMSVGERVLTTCASENVVTVSWY	60
Db	1	MGIMESQTLVFSILLWLYGADGNI	VMTQSPKMSMSVGERVLTTCASENVVTVSWY	60
Qy	61	QQRPEQSKLLIYGASNRYTGVDP	FTGSGSATDFTLTISVQAEADLADYHCGGGSYPY	120
Db	61	QQRPEQSKLLIYGASNRYTGVDP	FTGSGSATDFTLTISVQAEADLADYHCGGGSYPY	120
Qy	121	TFGGGTXLEIKR	132	
Db	121	TFGGGTXLEIKR	132	

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RESULT 2
US-10-010-729-70
; Sequence 70, Application US/10010729
; Publication No. US20030185827A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Pease, Larry R.
; TITLE OF INVENTION: Human IGM Antibodies and Diagnostic and
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous
; TITLE OF INVENTION: System
; FILE REFERENCE: 1199-1-005CIP2
; CURRENT APPLICATION NUMBER: US/10/010,729
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/730,473
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 09/580,787
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: 09/322,862
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/779,784
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 08/692,084
; PRIOR FILING DATE: 1996-08-08
; PRIOR APPLICATION NUMBER: 08/236,520
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-010-729-70
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Query Match 97.1%; Score 669; DB 14; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.9e-54;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MESQTLVFTISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSVYQKP 64
Db 1 MESQTLVFTISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSVYQKP 60

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 124
Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 120

QY 125 GTKLEIKR 132
Db 121 GTKLEIKR 128
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RESULT 3
US-10-372-481-31
; Sequence 31, Application US/10372481
; Publication No. US20030202975A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F.
; TITLE OF INVENTION: REAGENTS AND TREATMENT METHODS FOR AUTOIMMUNE DISEASES
; FILE REFERENCE: 5405.306
; CURRENT APPLICATION NUMBER: US/10/372,481
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05549
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 135
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-372-481-31

Query Match 96.2%; Score 663; DB 15; Length 135;
Best Local Similarity 99.2%; Pred. No. 1.1e-53;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 MESQTLVFTISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSVYQKP 64
Db 1 MESQTLVFTISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSVYQKP 60

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 124
Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 120

QY 125 GTKLEIKR 132
Db 121 GTKLEIKR 128
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RESULT 4
US-10-371-797-31
; Sequence 31, Application US/10371797
; Publication No. US20040001828A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TUSCANO, Joseph
; APPLICANT: TEDDER, Thomas
; TITLE OF INVENTION: TREATMENT METHODS USING ANTI-CD22
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 39754-0951
; CURRENT APPLICATION NUMBER: US/10/371,797
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 60/420,472
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/359,419
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 135
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-371-797-31
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```
Query Match 96.2%; Score 663; DB 15; Length 135;
Best Local Similarity 99.2%; Pred. No. 1.1e-53;
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 MESQTLVFTISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSVYQKP 64
Db 1 MESQTLVFTISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSVYQKP 60

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 124
Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 120

QY 125 GTKLEIKR 132
Db 121 GTKLEIKR 128
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RESULT 5
US-08-779-784-34
; Sequence 34, Application US/08779784
; Publication No. US20020164325A1
; GENERAL INFORMATION:
; APPLICANT: Rodriguez, Moses
; APPLICANT: Miller, David J.
; APPLICANT: Asakura, Kunihiko
; TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
; TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
; NUMBER OF SEQUENCES: 37
```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: David A. Jackson, Esq.  
;; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
;; CITY: Hackensack  
;; STATE: New Jersey  
;; COUNTRY: USA  
;; ZIP: 07601  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.30  
;; CURRENT APPLICATION NUMBER: US/08/779,784  
;; FILING DATE: 07-JAN-1997  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; PRIOR APPLICATION NUMBER: US 08/692,084  
;; FILING DATE: 08-AUG-1996  
;; PRIOR APPLICATION DATA:  
;; PRIOR APPLICATION NUMBER: US 08/236,520  
;; FILING DATE: 29-APR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Jackson Esq., David A.  
;; REGISTRATION NUMBER: 26,742  
;; REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-487-5800  
;; TELEFAX: 201-343-1684  
;; INFORMATION FOR SEQ ID NO: 34:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 128 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; FRAGMENT TYPE: N-terminal  
;; ORIGINAL SOURCE:  
;; ORGANISM: Mus musculus  
;; US-08-779-784-34

Query Match 95.9%; Score 661; DB 8; Length 128;  
Best Local Similarity 99.2%; Pred. No. 1.6e-53;  
Matches 127; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 5 MESQTLVPISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVVSWYQOKP 64  
Db 1 MESQTLVPISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVVSWYQOKP 60  
  
Qy 65 EQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFGG 124  
Db 61 EQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPYTFRG 120  
  
Qy 125 GTKLEIKR 132  
Db 121 GTKLEIKR 128

RESULT 6  
US-10-452-357-99  
; Sequence 99, Application US/10452357  
; Publication No. US20040058414A1  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary  
; APPLICANT: Co, Man Sung  
; APPLICANT: Schneider, William  
; APPLICANT: Landolfi, Nicholas  
; APPLICANT: Coelingh, Kathleen  
; APPLICANT: Selick, Harold  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; FILE REFERENCE: 05882.0078.CNUS01

;; CURRENT APPLICATION NUMBER: US/10/452,357  
;; CURRENT FILING DATE: 2003-05-30  
;; PRIOR APPLICATION NUMBER: 09/718,993  
;; PRIOR FILING DATE: 2000-11-22  
;; PRIOR APPLICATION NUMBER: 09/487,200  
;; PRIOR FILING DATE: 1995-06-07  
;; PRIOR APPLICATION NUMBER: 07/634,278  
;; PRIOR FILING DATE: 1990-12-19  
;; PRIOR APPLICATION NUMBER: 07/590,275  
;; PRIOR FILING DATE: 1990-09-28  
;; PRIOR APPLICATION NUMBER: 07/310,252  
;; PRIOR FILING DATE: 1989-02-13  
;; PRIOR APPLICATION NUMBER: 07/290,975  
;; PRIOR FILING DATE: 1988-12-28  
;; NUMBER OF SEQ ID NOS: 113  
;; SOFTWARE: Patent in version 3.2  
;; SEQ ID NO 99  
;; LENGTH: 136  
;; TYPE: PRT  
;; ORGANISM: Artificial  
;; FEATURE:  
;; OTHER INFORMATION: AF2 light chain antibody  
;; US-10-452-357-99

Query Match 92.0%; Score 634; DB 15; Length 136;  
Best Local Similarity 92.4%; Pred. No. 5.4e-51;  
Matches 121; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
  
Qy 1 MGKQESQTLVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVVSWY 60  
Db 6 MGKQESQTLVFIISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVVSWY 65  
  
Qy 61 QOKPEQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPY 120  
Db 66 QOKPEQSPKLLIYGASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPY 125  
  
Qy 121 TFGSGTKLEIK 131  
Db 126 TFGSGTKLEIK 136

RESULT 7  
US-10-389-155-84  
; Sequence 84, Application US/10389155  
; Publication No. US20030229208A1  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary L.  
; Co, Man Sung  
; Schneider, William P.  
; Landolfi, Nicholas F.  
; Coelingh, Kathleen L.  
; Selick, Harold E.  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/389,155  
; FILING DATE: 13-Mar-2003  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/325,000  
; FILING DATE: 01-JUN-1999  
; APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 08/484,537  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-002650US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 84:  
US-10-389-155-84

Query Match 91.0%; Score 627; DB 15; Length 136;  
Best Local Similarity 91.6%; Pred. No. 2.4e-50;  
Matches 120; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMYSVGERVTLTCKASENVTVVSWY 60  
Db 6 MGKMSQTLVFIISILLWLYGAGNIVMTQSPKSMYSVIGERVTLSCASENVDTVSWY 65  
QY 61 QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGSYPY 120  
Db 66 QOKPEQSPKLLIYGASNRVTGVHDFRTGSGSATDFTLTSSVQAEADLADYHCGQGSYNYPF 125  
QY 121 TFGGGTKLEIK 131  
Db 126 TFGSGTKLEIK 136

RESULT 8  
US-10-389-417-84  
Sequence 84, Application US/10389417  
Publication No. US20040049014A1  
GENERAL INFORMATION:  
APPLICANT: Queen, Cary L.  
Co, Man Sung  
Schneider, William P.  
Landolfi, Nicholas F.  
Coeligh, Kathleen L.  
Sclick, Harold E.  
TITLE OF INVENTION: Improved Humanized Immunoglobulins  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/389,417  
FILING DATE: 13-Mar-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/325,000

FILING DATE: 01-JUN-1999  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 08/484,537  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-002650US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 84:  
US-10-389-417-84

Query Match 91.0%; Score 627; DB 15; Length 136;  
Best Local Similarity 91.6%; Pred. No. 2.4e-50;  
Matches 120; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGKMSQTLVFIISILLWLYGADGNIVMTQSPKSMYSVGERVTLTCKASENVTVVSWY 60  
Db 6 MGKMSQTLVFIISILLWLYGAGNIVMTQSPKSMYSVIGERVTLSCASENVDTVSWY 65  
QY 61 QOKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGSYPY 120  
Db 66 QOKPEQSPKLLIYGASNRVTGVHDFRTGSGSATDFTLTSSVQAEADLADYHCGQGSYNYPF 125  
QY 121 TFGGGTKLEIK 131  
Db 126 TFGSGTKLEIK 136

RESULT 9  
US-09-992-524-2  
Sequence 2, Application US/09992524  
Patent No. US20020091240A1  
GENERAL INFORMATION:  
APPLICANT: Vasquez, Maximiliano  
Landolfi, Nicholas F.  
APPLICANT: Tsurushita, Naoya  
APPLICANT: Queen, Cary L.  
APPLICANT: Protein Design Labs, Inc.  
TITLE OF INVENTION: Humanized Antibodies To Gamma-Interferon  
FILE REFERENCE: 011823-008110US  
CURRENT APPLICATION NUMBER: US/09/992,524  
CURRENT FILING DATE: 2001-11-13  
PRIOR APPLICATION NUMBER: 09/450,520  
PRIOR FILING DATE: 1999-11-29  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 127  
TYPE: PRT  
ORGANISM: Mus sp.  
FEATURE:  
OTHER INFORMATION: AF2 VL  
US-09-992-524-2

Query Match 90.4%; Score 623; DB 9; Length 127;  
Best Local Similarity 92.9%; Pred. No. 5.2e-50;  
Matches 118; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKP 64
Db 1 MESQTLVFISILLWLYGADGNIVMTQSPKSMYVSGERVTLTCKASENVTVSVWYQKP 60
QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGG 124
Db 61 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQSYNYPFTFGS 120
QY 125 GTKLEIK 131
Db 121 GTKLEIK 127

RESULT 10
US-09-929-665-11
; Sequence 11, Application US/09929665
; Publication No. US20030003101A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-11

Query Match 87.1%; Score 600; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.6e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNR 60
QY 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIKR 114

RESULT 11
US-09-929-546-11
; Sequence 11, Application US/09929546
; Publication No. US20030031673A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
US-09-929-546-11

Query Match 87.1%; Score 600; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.6e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNR 60
QY 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIKR 114
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; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-546-11

Query Match 87.1%; Score 600; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.6e-48;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNR 78
Db 1 LYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNR 60
QY 79 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIKR 132
Db 61 YTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIKR 114

RESULT 12
US-09-929-665-16
; Sequence 16, Application US/09929665
; Publication No. US20030003101A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/024
; CURRENT APPLICATION NUMBER: US/09/929,665
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,704
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; PRIOR APPLICATION NUMBER: US 60/016,976
; PRIOR FILING DATE: 1996-05-06
; PRIOR APPLICATION NUMBER: US 60/022,125
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-929-665-16

Query Match 81.6%; Score 562; DB 10; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 NIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNRVTGVPD 84
Db 1 NIVMTQSPKSMMSVGERVTLTCKASENVVTVSVWYQKPQSPKLLIYGASNRVTGVPD 60
QY 85 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIK 131
Db 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYTFGGGKLEIK 107

RESULT 13
US-09-929-546-16
; Sequence 16, Application US/09929546
; Publication No. US20030031673A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil H.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
; FILE REFERENCE: Lois M. Kwasiogoch: BZL 242/028
; CURRENT APPLICATION NUMBER: US/09/929,546
; CURRENT FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/357,708
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: US 08/838,682
; PRIOR FILING DATE: 1997-04-09
; SOFTWARE: PatentIn version 3.0
US-09-929-546-16
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; PRIOR FILING DATE: 1996-05-06  
; PRIOR APPLICATION NUMBER: US 60/022,125  
; PRIOR FILING DATE: 1996-07-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-929-546-16

Query Match 81.6%; Score 562; DB 10; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.9e-44;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 25 NIWMTQSPKMSMSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 84  
DB 1 NIWMTQSPKMSMSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60  
QY 85 RFTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGGKLEIK 131  
DB 61 RFTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGGKLEIK 107

## RESULT 14

US-10-010-729-21  
; Sequence 21, Application US/10010729  
; Publication No. US2003018587A1  
; GENERAL INFORMATION:  
; APPLICANT: Rodriguez, Moses  
; APPLICANT: Miller, David J.  
; APPLICANT: Pease, Larry R.  
; TITLE OF INVENTION: Human Igm Antibodies and Diagnostic and  
; TITLE OF INVENTION: Therapeutic Uses Thereof Particularly in the Central Nervous  
; TITLE OF INVENTION: System  
; FILE REFERENCE: 1199-1-005CIP2  
; CURRENT APPLICATION NUMBER: US/10/010,729  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: 09/730,473  
; PRIOR FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: 09/580,787  
; PRIOR FILING DATE: 2000-05-30  
; PRIOR APPLICATION NUMBER: 09/322,862  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 08/779,784  
; PRIOR FILING DATE: 1997-01-07  
; PRIOR APPLICATION NUMBER: 08/692,084  
; PRIOR FILING DATE: 1996-08-08  
; PRIOR APPLICATION NUMBER: 08/236,520  
; PRIOR FILING DATE: 1994-04-29  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-010-729-21

Query Match 77.5%; Score 534; DB 14; Length 101;  
Best Local Similarity 100.0%; Pred. No. 7e-42;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 25 NIWMTQSPKMSMSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 84  
DB 1 NIWMTQSPKMSMSVGERVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRYTGVPD 60  
QY 85 RFTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGG 125  
DB 61 RFTGSGSATDFTLTSSVQAEADLADYHCGGYSYPYTFGGG 101

## RESULT 15

US-09-874-141-47

; Sequence 47, Application US/09874141  
; Publication No. US20030012781A1  
; GENERAL INFORMATION:  
; APPLICANT: ANDERSON, DARRELL  
; APPLICANT: PAN, LI-ZHEN  
; APPLICANT: HANNA, NABIL  
; APPLICANT: RASTETTER, WILLIAM H.  
; APPLICANT: KLOETZER, WILLIAM S.  
; TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS  
; TITLE OF INVENTION: CONTAINING, AND THERAPEUTIC USE THEREOF  
; FILE REFERENCE: 037003-0280632  
; CURRENT APPLICATION NUMBER: US/09/874,141  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 60/209,584  
; PRIOR FILING DATE: 2000-06-06  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: humanized VL#2 amino acid  
US-09-874-141-47

Query Match 77.2%; Score 532; DB 10; Length 133;  
Best Local Similarity 75.8%; Pred. No. 1.4e-41;  
Matches 100; Conservative 13; Mismatches 19; Indels 0; Gaps 0;  
QY 1 MGKIMESQTLVFIISILLWLYGADGNIVMTQSPKMSMSVGERVTLTKKASENVTVVSWY 60  
DB 1 MGFKMESQFLAFVAFFLWLSGVDGIVMTQSPDSLAVSLGERATINCKASQNVITAVMY 60  
QY 61 QOKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCGGYSYPY 120  
DB 61 QOKPEQSPKLLIYGASNRYTGVPDRFSGSGGTDTLTLTSSVQAEADVADYFCQYNSYPY 120  
QY 121 TFGGCTKLEIKR 132  
DB 121 TFGGCTKLEIKR 132

Search completed: May 25, 2005, 16:06:55  
Job time : 62.0292 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 18.6642 Seconds  
(without alignments)  
680.480 Million cell updates/sec

Title: US-10-006-773A-19

Perfect score: 689

Sequence: 1 MGIKMESQTLVFIISILLWL.....GGGYSPYTFGGYKLEIKR 132

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	666	96.7	136	1 KWMS21	Ig kappa chain pre
2	615	89.3	118	2 I33932	Ig kappa chain pre
3	556	80.7	111	2 D37266	Ig kappa chain v r
4	515	74.7	107	2 S33132	Ig kappa chain v r
5	496	72.0	149	1 KWMS11	Ig kappa chain pre
6	495	71.8	152	2 S30751	Ig kappa chain pre
7	494	71.7	107	2 S38713	Ig light chain v r
8	474	68.8	128	2 A47159	Ig lambda chain v r
9	471	68.4	127	2 S04577	Ig kappa chain pre
10	470	68.2	131	2 P0207	anti-idiotypic ant
11	467	67.8	135	2 S38807	Ig light chain v-j
12	465	67.5	117	2 S42466	Ig kappa chain v r
13	459	66.6	107	2 P0268	Ig kappa chain v r
14	454	65.9	96	2 P1070	Ig light chain v r
15	447	64.9	240	2 S06084	Ig kappa chain pre
16	446.5	64.8	91	2 P1071	Ig light chain v r
17	445	64.6	108	2 P10204	anti-DNA autoantib
18	442	64.2	134	2 P1214	Ig kappa chain pre
19	441	64.0	134	1 K4HUI7	Ig kappa chain pre
20	436	63.3	119	2 P00265	Ig kappa chain v r
21	435	63.1	134	2 S49531	anti-Sm antibody v r
22	432	62.7	107	2 S32192	Ig kappa chain v r
23	430	62.4	145	2 P10014	Ig kappa chain pre
24	429.5	62.3	133	2 P50023	Ig kappa chain pre
25	428.5	62.2	133	1 K4HUI1	Ig kappa chain pre
26	427	62.0	107	2 S32191	Ig kappa chain v r
27	426.5	61.9	225	2 S37484	Ig kappa chain - m
28	422	61.2	132	2 S46373	Ig kappa chain v-j
29	419	60.8	129	2 S52793	Ig kappa chain v r

#### ALIGNMENTS

##### RESULT 1

KWMS21

Ig kappa chain precursor V region (MOPC 21) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1980 #sequence\_revision 02-Apr-1982 #text\_change 09-Jul-2004

C:Accession: A93736; A90262; B49982; A01917

R:Hamlyn, P.H.; Gait, M.J.; Milstein, C.

Nucleic Acids Res. 9, 4485-4494, 1981

A:Title: Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxy

A:Reference number: A93736; MUID:82059477; PMID:6170937

A:Accession: A93736

A:Molecule type: mRNA

A:Residues: 1-136 <HAM>

A:Cross-references: UNIPROT:P01634

R:Swasti, J.; Milstein, C.

Biochem. J. 128, 427-444, 1972

A:Title: The complete amino acid sequence of a mouse kappa light chain.

A:Reference number: A90262; MUID:73053310; PMID:4638343

A:Contents: myeloma protein MOPC 21

A:Accession: A90262

A:Molecule type: protein

A:Residues: 30-136 <SVA>

R:Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R.

J. Biol. Chem. 269, 2805-2813, 1994

A:Title: Topology of an amiloride-binding protein.

A:Reference number: A49982; MUID:94132051; PMID:8300613

A:Accession: B49982

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 30-136 <LIN>

A:Cross-references: GB:L24803; NID:G452098; PIDN:AAC37684.1; PID:G452099

A:Experimental source: Clone BA7.1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-29/Domain: signal sequence #status predicted <SIG>

F:30-136/Product: Ig kappa chain V region (MOPC 21) #status experimental <MAT>

F:45-119/Domain: immunoglobulin homology <IMM>

F:125-136/Region: J segment (JK2)

F:52-117/Disulfide bonds: #status predicted

Query Match 96.7%; Score 666; DB 1; Length 136;

Best Local Similarity 98.5%; Pred. No. 4.2e-49;

Matches 129; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MGIKMESQTLVFIISILLWLVCAGDNIVMTQSPKSMVSGVRVLTCTCKASENVVTVYSWY 60

Db 6 MGIKMESHTLVFIISILLCLVCGADGNIVMTQSPKSMVSGVRVLTCTCKASENVVTVYSWY 65

Qy 61 QOKPEQSKLLIYGASNRYTGVDPDRFTGSGSATDFTLTITSSVQAEADLADYHCGGYSPY 120

Db 66 QOKPEQPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGQGYSPY 125

QY 121 TFGGGTKLEIK 131  
 Db 126 TFGGGTKLEIK 136

RESULT 2

I33932  
 Ig kappa chain precursor V region (E7) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 21-Jan-2000  
 C:Accession: I33932  
 R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989  
 A:Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-line  
 A:Reference number: A33932; MUID:89282823; PMID:2499887  
 A:Accession: I33932  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-118 <BAC>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 89.3%; Score 615; DB 2; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-45;  
 Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GIKMESQTLVFISILLMLYGADGNIVMTQSPKSMMSGVGVTLTKKASENVVTVYSWYQ 61  
 Db 1 GIKMESQTLVFISILLMLYGADGNIVMTQSPKSMMSGVGVTLTKKASENVVTVYSWYQ 60  
 QY 62 QKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGQGYSP 119  
 Db 61 QKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGQGYSP 118

RESULT 3

D37266  
 Ig kappa chain V region (129) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 21-Jan-2000  
 C:Accession: D37266  
 R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.  
 J. Biol. Chem. 266, 6607-6613, 1991  
 A:Title: Heavy and light chain variable region sequences and antibody properties of anti  
 A:Reference number: A38740; MUID:91177923; PMID:1706720  
 A:Accession: D37266  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-111 <RUF>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 556; DB 2; Length 111;  
 Best Local Similarity 98.1%; Pred. No. 5.8e-40;  
 Matches 106; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 25 NIVMTQSPKSMMSGVGVTLTKKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 84  
 Db 4 DIVMTQIPKSMMSGVGVTLTKKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 63  
 QY 85 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIKR 132  
 Db 64 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIKR 111

RESULT 4

S33132  
 Ig kappa chain V region - mouse (fragment)  
 C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: S33132  
 R:Tempest, P.R.; Barbanti, E.; Bremner, P.; Carr, F.J.; Ghislieri, M.; Rifaldi, B.; Mar  
 submitted to the EMBL Data Library, May 1993  
 A:Description: A humanized anti-tumor necrosis factor alpha monoclonal antibody that act  
 A:Reference number: S33131  
 A:Accession: S33132  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-107 <TEM>  
 A:Cross-references: EMBL:222670; NID:G297473; PIDN:CAA80379.1; PID:G297474  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 74.7%; Score 515; DB 2; Length 107;  
 Best Local Similarity 92.5%; Pred. No. 1.6e-36;  
 Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 25 NIVMTQSPKSMMSGVGVTLTKKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 84  
 Db 1 NIVMTQSPKSMMSGVGVTLTKKASENVVTVYSWYQKPEQSPKLLIYGASNRVTGVPD 60  
 QY 85 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 131  
 Db 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 107

RESULT 5

KWS11  
 Ig kappa chain precursor V region (MPC11) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 09-Jul-2004  
 A:Accession: A90823; A90753; A90298; A01916  
 R:Kelley, D.E.; Coleclough, C.; Perry, R.P.  
 Cell 29, 681-689, 1982  
 A:Title: Functional significance and evolutionary development of the 5'-terminal region  
 A:Reference number: A90823; MUID:83001944; PMID:6288267  
 A:Accession: A90823  
 A:Molecule type: DNA  
 A:Residues: 1-71 <REL>  
 A:Cross-references: UNIPROT:P01633  
 A:Note: the sequence was determined from the differentiated gene  
 R:Rabbits, T.H.; Hamlyn, P.H.; Matthysens, G.; Roe, B.A.  
 Can. J. Biochem. 58, 176-187, 1980  
 A:Title: The variability, arrangement, and rearrangement of immunoglobulin genes.  
 A:Reference number: A90753; MUID:80176554; PMID:6245773  
 A:Accession: A90753  
 A:Molecule type: mRNA  
 A:Residues: 41-149 <RAB>  
 R:Smith, G.P.  
 Biochem. J. 171, 337-347, 1978  
 A:Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC 11.  
 A:Reference number: A90298; MUID:78186617; PMID:418775  
 A:Contents: myeloma protein MPC11  
 A:Accession: A90298  
 A:Molecule type: protein  
 A:Residues: 30-149 <SMI>  
 A:Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not d  
 C:Comment: The mature chain has 12 additional residues at its amino end, due to a tandem  
 42 corresponds to the amino-terminal residue of typical kappa chains.  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
 chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: duplication; heterotetramer; immunoglobulin  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:30-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>  
 F:57-131/Domain: immunoglobulin homology <IMM>  
 F:64-129/Disulfide bonds: #status predicted

Query Match 72.0%; Score 496; DB 1; Length 149;  
 Best Local Similarity 70.1%; Pred. No. 8.5e-35;  
 Matches 101; Conservative 10; Mismatches 21; Indels 12; Gaps 1;

QY	1	MGIKMESQTLVFIISILLWL-----YGADGNIWMTQSPKSMMSVGERVTLTKC	48
Db	6	MGIKMESQIQVFEVFLWLSGVGDGIWMTQFAGVGDGIWMTQSHKFMSTSVGDRVSITCK	65
QY	49	ASENNVTVVSWYQOKPQSPKLLIYGASNRVTGVPDRFTGGSGATDFTLTISVQASDLA	108
Db	66	ASQDVSTVAVYQOKPQSPKLLIYSASRYTGVDPDRFTGGSGTDFFTTISVQASDLA	125
QY	109	DYHCGQGSYPYTFGGGTKLEIKR	132
Db	126	VYVCOQHYSPTPTFGGCTKLEIKR	149
RESULT 6			
S30751	Ig kappa chain precursor V region - mouse		
C;Species:	Mus musculus (house mouse)		
C;Date:	31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000		
C;Accession:	S30751		
R;Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.			
Nucleic Acids Res.	15, 5496, 1987		
A;Title:	Improved RNA sequencing method to determine immunoglobulin mRNA sequence.		
A;Reference number:	S30751; MUID:87260030; PMID:3601683		
A;Accession:	S30751		
A;Molecule type:	mRNA		
A;Residues:	1-152 <GRA>		
A;Cross-references:	EMBL:X05877; NID:952195; PIDN:CAA29301.1; PID:952196		
C;Superfamily:	immunoglobulin V region; immunoglobulin homology		
C;Keywords:	heterotetramer; immunoglobulin		
F;45-119/Domain:	immunoglobulin homology <IMW>		
F;138-152/Domain:	C region (C-kappa) (fragment) #status predicted <CRE>		
Query Match	71.8%; Score 495; DB 2; Length 152;		
Best Local Similarity	72.7%; Pred. No. 1e-34;		
Matches	96; Conservative 14; Mismatches 22; Indels 0; Gaps 0;		
QY	1	MGIKMESQTLVFIISILLWLYGADGNIWMTQSPKSMMSVGERVTLTKCASNVTYVSWY	60
Db	6	MGIKMESQIQAFVFLWLSGVGDGIWMTQSHRPMSTSVGDRVSITCKASQDVTTAVSWY	65
QY	61	QOKPEQSPKLLIYGASNRVTGVPDRFTGGSGATDFTLTISVQASDLADYHCGQGSYPY	120
Db	66	QOKPEQSPKLLIFWASRHTGVDPDRFTGGSGTDTYTLTISVQASDLALYCCQHYSTPL	125
QY	121	TFGGGCTKLEIKR	132
Db	126	TFGAGTKLEIKR	137
RESULT 7			
S38713	Ig light chain V region - mouse		
C;Species:	Mus musculus (house mouse)		
C;Date:	06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000		
C;Accession:	S38713		
R;Cimanis, A.V.			
submitted to the EMBL Data Library, November 1993			
A;Reference number:	S38713		
A;Accession:	S38713		
A;Status:	preliminary		
A;Molecule type:	mRNA		
A;Residues:	1-107 <CIM>		
A;cross-references:	EMBL:X76019; NID:9416090; PIDN:CAA53606.1; PID:gl333952		
C;Superfamily:	immunoglobulin V region; immunoglobulin homology		
C;Keywords:	immunoglobulin		
F;16-90/Domain:	immunoglobulin homology <IMW>		
Query Match	71.7%; Score 494; DB 2; Length 107;		
Best Local Similarity	88.8%; Pred. No. 9e-35;		
Matches	95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;		
QY	25	NIWMTQSPKSMMSVGERVTLTKCASNVTYVSWYQOKPEQSPKLLIYGASNRVTGVPD	84

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYSPYTFGG 124  
 Db 61 GQSPKLLIYGASNRVTGVPDRFTGSGSGTDFTLTISVQAEADLADYHCGQSYSPYTFGG 120  
 QY 125 GTKLEIK 131  
 Db 121 GTKLEIK 127

RESULT 10  
 PL0207  
 anti-Idiotypic antibody E225, kappa chain V region precursor - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
 C:Accession: PL0207  
 R:Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.  
 Mol. Immunol. 27, 429-433, 1990  
 A:Title: Nucleotide sequence of the VH, VL regions of an anti-idiotypic antibody reacting  
 A:Reference number: PL0207; MUID:90309764; PMID:1973259  
 A:Accession: PL0207  
 A:Molecule type: mRNA  
 A:Residues: 1-131 <SOU>  
 A>Note: This sequence corresponds to subgroup V mouse immunoglobulin light chain  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:36-110/Domain: immunoglobulin homology <IMM>  
 F:44-54/Region: complementarity-determining 1  
 F:70-76/Region: complementarity-determining 2  
 F:109-117/Region: complementarity-determining 3  
 F:116-127/Region: J region

Query Match 68.2%; Score 470; DB 2; Length 131;  
 Best Local Similarity 71.1%; Pred. No. 1.le-32;  
 Matches 91; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSWYQKQP 64  
 Db 1 METKQVFFYMLLWSGVEGDIVMTQSHKFMSTVGDVSIICKASQDVRIAVAWYQKQP 60

QY 65 EQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYSPYTFGG 124  
 Db 61 GQSPKLLIYGASNRVTGVPDRFTGSGSGTDFTLTISVQAEADLADYHCGQSYSPYTFGG 120

QY 125 GTKLEIK 132  
 Db 121 GTKLEIK 128

RESULT 11  
 S39807  
 Ig light chain V-J region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
 C:Accession: S39807  
 R:Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.  
 Immunogenetics 36, 15-21, 1992  
 A:Title: Molecular characterization of the variable regions of a mouse polyreactive IgG2  
 A:Reference number: S39807; MUID:92267566; PMID:1587549  
 A:Accession: S39807  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-135 <SEQ>  
 A:Cross-references: EMBL:X59816  
 A>Note: the authors translated the codon GGC for residue 1 as Ala and TGT for residue 21  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 F:38-118/Domain: immunoglobulin homology <IMM>

Query Match 67.8%; Score 467; DB 2; Length 135;  
 Best Local Similarity 66.9%; Pred. No. 2.le-32;  
 Matches 89; Conservative 19; Mismatches 19; Indels 6; Gaps 1;

QY 4 KMESQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVV-----TVV 57

Db 2 KMESQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSWYQKQP 61  
 QY 58 SWYQKQPSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSY 117  
 Db 62 AWYQKQPSPKLLIYGASNRVTGVPDRFTGSGSGTDFTLTISVQAEADLADYHCGQSY 121  
 QY 118 YPYTFGGGKLEIK 130  
 Db 122 YPYTFGGGKLEIK 134

RESULT 12  
 S42466  
 Ig kappa chain V region - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 21-Jan-2000  
 C:Accession: S42466  
 R:Shiyanov, P.A.; Bespalov, I.A.; Terletskaia, H.N.; Deyev, S.M.  
 submitted to the EMBL Data Library, March 1994  
 A:Reference number: S42466  
 A:Accession: S42466  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-117 <SHI>  
 A:Cross-references: EMBL:X78108; NID:g460824; PID:CAA54998.1; PID:g460825  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 67.5%; Score 465; DB 2; Length 117;  
 Best Local Similarity 76.9%; Pred. No. 2.7e-32;  
 Matches 90; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 15 ILLWLYGADGNIVMTQSPKSMMSVGERVTLTKKASENVVTVSWYQKQPSPKLLIYG 74  
 Db 1 MLLWLSGVEGDIVMTQSHKFMSTVGDVSIICKASQDVRIAVAWYQKQPSPKLLIYG 60

QY 75 ASNRVTGVPDRFTGSGSATDFTLTISVQAEADLADYHCGQSYSPYTFGGGKLEIK 131  
 Db 61 ASNRVTGVPDRFTGSGSGTDFTLTISVQAEADLADYHCGQSYSPYTFGGGKLEIK 117

RESULT 13  
 PL0268  
 Ig kappa chain V region (anti-DNA, DP9VK and DP17VK) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
 C:Accession: PL0268  
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J.  
 J. Exp. Med. 171, 265-297, 1990  
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
 A:Reference number: PL0231; MUID:90111618; PMID:2104919  
 A:Accession: PL0268  
 A:Molecule type: mRNA  
 A:Residues: 1-107 <SHL>  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-23/Region: framework 1  
 F:16-90/Domain: immunoglobulin homology <IMM>  
 F:24-34/Region: complementarity-determining 1  
 F:35-49/Region: framework 2  
 F:50-56/Region: complementarity-determining 2  
 F:57-88/Region: framework 3  
 F:89-97/Region: complementarity-determining 3  
 F:98-107/Region: framework 4

Query Match 66.6%; Score 459; DB 2; Length 107;  
 Best Local Similarity 82.2%; Pred. No. 7.8e-32;  
 Matches 88; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 25 NIWMTQSPKSMMSVGERVTLTKKASENVVTVSWYQKQPSPKLLIYGASNRVTGVPD 84

UY 119 PYTFGGT KLETKR 132



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 64.3423 Seconds  
(without alignments)  
1050.544 Million cell updates/sec

Title: US-10-006-773A-19

Perfect score: 699

Sequence: 1 MGKMSQTLVFISILLWL.....GGQSYYPYTRGGGTYKLEIKR 132

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	666	96.7	136	1 KV5B MOUSE	P01634 mus musculus
2	496	72.0	149	1 KV5A MOUSE	P01633 mus musculus
3	442	64.2	134	1 KV4C HUMAN	P06314 homo sapien
4	428.5	62.2	133	1 KV4B HUMAN	P06313 homo sapien
5	411	59.7	108	2 QSVIJO	Q8vi10 mus musculus
6	408	59.2	114	1 KV1A MOUSE	P01632 mus musculus
7	403	58.5	236	2 QGMMW1	Q6gmw1 homo sapien
8	401	58.2	131	1 KV3I MOUSE	P01661 mus musculus
9	401	58.2	255	2 Q6KB05	Q6kb05 mus musculus
10	400	58.1	236	2 Q6GMX8	Q6gmx8 homo sapien
11	399	57.9	236	2 Q6GMX0	Q6gmx0 homo sapien
12	394.5	57.3	129	1 KV3M HUMAN	P18136 homo sapien
13	393.5	57.1	129	1 KV3L HUMAN	P18135 homo sapien
14	392	56.9	121	1 KV40 HUMAN	P06312 homo sapien
15	390	56.6	236	2 Q6GMX9	Q6gmx9 homo sapien
16	389	56.5	236	2 Q6PIH7	Q6pih7 homo sapien
17	388	56.3	114	1 KV4A HUMAN	P01625 homo sapien
18	388	56.3	129	1 KV1W HUMAN	P04431 homo sapien
19	388	56.3	234	2 Q7Z473	Q7z473 homo sapien
20	385	55.9	132	1 KV3F MOUSE	P01658 mus musculus
21	384	55.7	238	2 Q66J57	Q66j57 mus musculus
22	382.5	55.5	129	1 KV3H HUMAN	P04207 homo sapien
23	382.5	55.5	235	2 Q6GMW0	Q6gmw0 homo sapien
24	381	55.3	236	2 Q6PIL8	Q6pil8 homo sapien
25	380.5	55.2	235	2 Q6GMV9	Q6gmv9 homo sapien
26	380	55.2	108	1 KV1M HUMAN	P01605 homo sapien
27	378.5	54.9	235	2 Q6PJ72	Q6pj72 homo sapien
28	378	54.9	99	2 Q5JL74	Q5jl74 mus musculus
29	378	54.9	236	2 Q6PIT5	Q6pit5 homo sapien
30	377	54.7	129	1 KV1X HUMAN	P04432 homo sapien
31	377	54.7	236	2 Q6P5S8	Q6p5s8 homo sapien

32	375.5	54.5	107	2	Q96SA9	Q96sa9 homo sapien
33	375	54.4	108	1	KV1Y HUMAN	P80162 homo sapien
34	375	54.4	237	2	Q7S236	P78236 xenopus lae
35	374	54.3	108	2	Q9UL77	Q9ul77 homo sapien
36	372	54.0	236	2	Q723Y4	Q723y4 homo sapien
37	371.5	53.9	109	2	Q9UL78	Q9ul78 homo sapien
38	371	53.8	244	2	Q85ZC8	Q85zc8 homo sapien
39	369	53.6	108	1	KV1O HUMAN	P01607 homo sapien
40	369	53.6	128	1	KV3K HUMAN	P06311 homo sapien
41	368.5	53.5	109	2	Q9UL85	Q9ul85 homo sapien
42	368	53.4	108	1	KV1V HUMAN	P04430 homo sapien
43	368	53.4	240	2	Q65ZC9	Q65zc9 homo sapien
44	366	53.1	236	2	Q7TS98	Q7ts98 mus musculu
45	364	52.8	108	1	KV1H HUMAN	P01600 homo sapien

#### ALIGNMENTS

##### RESULT 1

KV5B MOUSE  
ID KV5B MOUSE STANDARD; PRT; 136 AA.  
AC P01634;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, last sequence update)  
DT 25-OCT-2004 (Rel. 45, last annotation update)  
DE Ig kappa chain V-V region MOPC 21 precursor.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OK NCBI\_taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82059477; PubMed=6170937;  
RA Hanlynn P.H., Gait M.J., Milstein C.;  
RT "Complete sequence of an immunoglobulin mRNA using specific priming  
and the dideoxynucleotide method of RNA sequencing."  
RL Nucleic Acids Res. 9:4485-4494(1981).  
[2]  
RP SEQUENCE OF 30-136.  
RX MEDLINE=73053310; PubMed=4638343;  
RA Svasti J., Milstein C.;  
RT "The complete amino acid sequence of a mouse kappa light chain.";  
RL Biochem. J. 128:427-444(1972).  
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-----  
EMBL; V00810; CAA24192.1; ALT\_TERM.  
PIN; A93736; KVM521.  
PDB; 1IGC; X-ray; L=..  
InterPro; IPR007110; Ig-like.  
InterPro; IPR003596; Ig\_v.  
Pfam; PF00047; ig; 1.  
SMART; SM00406; IGV; 1.  
PROSITE; PS00835; IG\_LIKE; 1.  
3D-structure; Direct protein sequencing; Immunoglobulin V region;  
Signal.  
FT CHAIN 1 29  
FT DOMAIN 30 136  
FT DOMAIN 30 52  
FT DOMAIN 53 63  
FT DOMAIN 64 78  
FT DOMAIN 79 85  
FT DOMAIN 86 117  
FT DOMAIN 118 126  
FT DOMAIN 127 136  
FT STRAND 34 36  
Ig kappa chain V-V region MOPC 21.  
Framework-1.  
Complementarity-determining-1.  
Framework-2.  
Complementarity-determining-2.  
Framework-3.  
Complementarity-determining-3.  
Framework-4.

FT STRAND 41 43  
 FT TURN 44 45  
 FT STRAND 48 53  
 FT TURN 59 60  
 FT STRAND 62 67  
 FT TURN 69 70  
 FT STRAND 74 78  
 FT TURN 79 81  
 FT STRAND 82 83  
 FT TURN 85 86  
 FT TURN 89 90  
 FT STRAND 93 95  
 FT STRAND 99 104  
 FT TURN 110 111  
 FT STRAND 112 119  
 FT STRAND 126 127  
 FT STRAND 132 136  
 FT NON\_TER 136 136  
 SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;  
  
 Query Match 96.7%; Score 666; DB 1; Length 136;  
 Best Local Similarity 98.5%; Pred. No. 6.4e-60;  
 Matches 129; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
 QY 1 MGIKMESQTLVFIISILLWYLGADGNIVMTQSPKSMSSVGERVTLTKASENVVTVSWY 60  
 DB 6 MGIKMESHVLVFIISILLCLYLGADGNIVMTQSPKSMSSVGERVTLTKASENVVTVSWY 65  
  
 QY 61 QKQPEQSPKLLIYGASNRVYGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPY 120  
 DB 66 QKQPEQSPKLLIYGASNRVYGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGQGYSPY 125  
  
 QY 121 TFGGKTLEIK 131  
 DB 126 TFGGKTLEIK 136

RESULT 2  
 KV5A\_MOUSE STANDARD; PRT; 149 AA.  
 AC P01633;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Ig kappa chain V-V region MPC11 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE OF 1-71 FROM N.A.  
 RX MEDLINE=83001944; PubMed=6288267; DOI=10.1016/0092-8674(82)90184-2;  
 RA Kelley D.E., Coleclough C., Perry R.P.;  
 RT "Functional significance and evolutionary development of the 5'-  
 RT terminal regions of immunoglobulin variable-region genes.";  
 RL Cell 29:681-689(1982).  
 RN [2]  
 RP SEQUENCE OF 41-149 FROM N.A.  
 RX MEDLINE=80176554; PubMed=6245773;  
 RA Rabbitts T.H., Hamlyn P.H., Matthysens G., Roe B.A.;  
 RT "The variability, arrangement, and rearrangement of immunoglobulin  
 RT genes.";  
 RL Can. J. Biochem. 58:176-187(1980).  
 RN [3]  
 RP SEQUENCE OF 30-149.  
 RX MEDLINE=78186617; PubMed=418775;  
 RA Smith G.P.;  
 RT "Sequence of the full-length immunoglobulin kappa-chain of mouse  
 RT myeloma MPC 11.";  
 RL Biochem. J. 171:337-347(1978).  
 CC -!- MISCELLANEOUS: The mature chain has 12 additional residues at its  
 CC amino end, due to a tandem duplication of 36 nucleotides after the  
 CC codon for residue 36. Residue 42 corresponds to the amino-terminal

CC residue of typical kappa chains.  
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 CC -----  
 CC EMBL; J00561; AAA38776.1; -.  
 DR PIR; A90823; KVM511.  
 DR HSP; P01634; IIGC.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG LIKE; 1.  
 KW Direct protein sequencing; Immunoglobulin V region; Repeat; Signal.  
 FT SIGNAL 1 29  
 FT CHAIN 30 149  
 FT DOMAIN 42 64  
 FT DOMAIN 65 75  
 FT DOMAIN 76 90  
 FT DOMAIN 91 97  
 FT DOMAIN 98 129  
 FT DOMAIN 130 138  
 FT DOMAIN 139 148  
 FT REPEAT 26 35  
 FT REPEAT 38 47  
 FT NON\_TER 149 149  
 SQ SEQUENCE 149 AA; 16434 MW; B0480C87B682AC3E CRC64;  
  
 Query Match 72.0%; Score 496; DB 1; Length 149;  
 Best Local Similarity 70.1%; Pred. No. 1.6e-42;  
 Matches 101; Conservative 10; Mismatches 21; Indels 12; Gaps 1;  
  
 QY 1 MGIKMESQTLVFIISILLWYLGADGNIVMTQSPKSMSSVGERVTLTKCK 48  
 DB 6 MGIKMESQIQVFFVFWLWSGVGDIVMTQFAGVDGDIWMTQSHKPFMTSVGDRVSITCK 65  
  
 QY 49 ASENVTYVSVYQKPEQSPKLLIYGASNRVYGVDPDRFTGSGSATDFTLTISVQAEADLA 108  
 DB 66 ASQDVSTTVANVYQKPEQSPKLLIYASVRYTVGVDPDRFTGSGSGTDTFTTISVQAEADLA 125  
  
 QY 109 DYHCGQGYSPYTFGGKTLEIKR 132  
 DB 126 VYVYQGHYSTPTTFGGKTLEIKR 149  
  
 RESULT 3  
 KV4C\_HUMAN STANDARD; PRT; 134 AA.  
 AC P06314;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-IV region B17 precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86041854; PubMed=2997713;  
 RA Marsh P., Mills P., Gould H.;  
 RT "Detection of a unique human V kappa IV germline gene by a cloned cDNA  
 RT probe.";  
 RL Nucleic Acids Res. 13:6531-6544(1985).  
 RN [2]  
 RP REVISION TO 76.  
 RA Marsh P.;  
 RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.



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CC -----
DR EMBL; X02990; CAA26733.1; -.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 Ig kappa chain V-IV region B17.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 21 43 Complementarity-determining-1.
FT DOMAIN 44 60 Framework-2.
FT DOMAIN 61 75 Framework-3.
FT DOMAIN 76 82 Framework-4.
FT DOMAIN 83 114 Complementarity-determining-2.
FT DOMAIN 115 121 Complementarity-determining-3.
FT DOMAIN 122 133 Complementarity-determining-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 64.2%; Score 442; DB 1; Length 134;
Best Local Similarity 63.4%; Pred. No. 4.e-37;
Matches 85; Conservative 23; Mismatches 20; Indels 6; Gaps 1;

QY 5 MESQTLVFISILLWYAGDNIVMTQSPKSMVSGERVITLTKASENVV-----TVYS 58
Db 1 MVLQTVFISILLWYAGDNIVMTQSPKSMVSGERVITLTKASENVV-----TVYS 58
QY 59 WYQKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCQGYSY 118
Db 61 WYQKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCQGYSY 118
QY 119 PYTFGGGKLEIKR 132
Db 121 PWTFGGKLEIKR 134

RESULT 4
KV4B HUMAN STANDARD; PRT; 133 AA.
AC P0313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G.; Bornkamm G.W.; Combrato G.; Mocikat R.; Pohlenz H.D.;
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
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CC -----
DR EMBL; Z00022; CAA77317.1; -.
DR PIR; A01904; K4HUJ1.
DR HSSP; P01625; ILVE.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 Ig kappa chain V-IV region JI.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 60 Complementarity-determining-1.
FT DOMAIN 61 75 Framework-2.
FT DOMAIN 76 82 Complementarity-determining-2.
FT DOMAIN 83 114 Complementarity-determining-3.
FT DOMAIN 115 122 Complementarity-determining-4.
FT DOMAIN 123 132 Framework-4.
FT DISULFID 43 114 By similarity.
FT NON_TER 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 62.2%; Score 428.5; DB 1; Length 133;
Best Local Similarity 64.2%; Pred. No. 1e-35;
Matches 86; Conservative 21; Mismatches 20; Indels 7; Gaps 2;

QY 5 MESQTLVFISILLWYAGDNIVMTQSPKSMVSGERVITLTKASENVV-----TVYS 58
Db 1 MVLQTVFISILLWYAGDNIVMTQSPKSMVSGERVITLTKASENVV-----TVYS 58
QY 59 WYQKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCQGYSY 118
Db 61 WYQKPEQSPKLLIYGASNRVTGVPDRFTGSGSATDFTLTSSVQAEADLADYHCQGYSY 118
QY 119 PYTFGGGKLEIKR 132
Db 121 P-TFGGKLEIKR 133

RESULT 5
QSVIJO
ID QSVIJO PRELIMINARY; PRT; 108 AA.
AC QSVIJO;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN Name=Vk19;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ-lpr/lpr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K.; Alexander A.L.; Phippen A.M.; Pisetsky D.S.; Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis."
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59155; AAB02917.1; -.
DR PIR; A33933; A33933.
DR PIR; A37262; A37262.
DR PIR; PH1072; PH1072.

```

```
DR HSSP; P01634; 1IGC.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 108
FT SEQUENCE 108 AA; 11859 MW; 68506D75613DBFEE CRC64;
SQ
Query Match 59.7%; Score 411; DB 2; Length 108;
Best Local Similarity 75.0%; Pred. No. 5e-34;
Matches 81; Conservative 10; Mismatches 17; Indels 0; Gaps 0;
QY 25 NIWMTQSPKMSMSVGERVTLTKASENVVTVYSWYQQRPEQSPKLLIYGASNR 84
Db 1 DIVMTQSPFLAVTASKVTVISCTASESIYSSKHVHLAWYQKKPEQSPKLLIYGASNR 60
QY 85 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGTYKLEIKR 132
Db 61 RFTGSGSGTDFLTISVQVEDLTHYCAQFYSPYPLTFGAGTKLEIKR 108
RESULT 6
KVIA_MOUSE STANDARD; PRT; 114 AA.
ID Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region S107A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=81241357; PubMed=6788890;
RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
RT chains".
RL J. Exp. Med. 153:1366-1370(1981).
CC -|- FUNCTION: Anti-phosphocholine antibody.
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CC -----
DR EMBL; U29423; AAC00033.1; -.
DR FIR; A01915; KWS7A.
DR HSSP; Q9ERZ9; ZAP2.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 40
FT DOMAIN 41 55
FT DOMAIN 56 62
FT DOMAIN 63 94
FT DOMAIN 95 103
FT DOMAIN 104 113
FT DISULFID 23 94
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12717 MW; 32008ECBE9DBE67B CRC64;
Query Match 59.2%; Score 408; DB 1; Length 114;
Best Local Similarity 67.5%; Pred. No. 1.1e-33;
Matches 77; Conservative 16; Mismatches 15; Indels 6; Gaps 1;
QY 1 MGIKMESQTLVTFISILLWYAGDGNIVMTQSPKMSMSVGERVTLTKASENVTVYSWY 60
Db 1 MDMRVPQALLGL--LILLWLPGARCAITQMTQSPSSLSASVGDRTVITCRASQGISNDLGWY 58
```

```
QY 25 NIWMTQSPKMSMSVGERVTLTKASENV-----VTYVSWYQQRPEQSPKLLIYGASNR 78
Db 1 DIVMTQSPFLAVTASKVTVISCTASESIYSSKHVHLAWYQKKPEQSPKLLIYGASNR 60
QY 79 YTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGTYKLEIKR 132
Db 61 YTGVPDRFTGSGSGTDFLTISVQVEDLTHYCAQFYSPYPLTFGAGTKLEIKR 114
RESULT 7
Q6GMW1
ID Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.J., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL [2]
SEQUENCE FROM N.A.
RP
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;
Query Match 58.5%; Score 403; DB 2; Length 236;
Best Local Similarity 59.8%; Pred. No. 8.2e-33;
Matches 79; Conservative 22; Mismatches 29; Indels 2; Gaps 1;
QY 1 MGIKMESQTLVTFISILLWYAGDGNIVMTQSPKMSMSVGERVTLTKASENVTVYSWY 60
Db 1 MDMRVPQALLGL--LILLWLPGARCAITQMTQSPSSLSASVGDRTVITCRASQGISNDLGWY 58
```

[illegible]

RESULT 8	
KV31_MOUSE	STANDARD; PRT; 131 AA.
ID	
AC	P01661;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Ig kappa chain V-III region MOPC 63 precursor.
DE	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE OF 1-35.
RP	MEDLINE=78235887; PubMed=98179;
RX	Burstein Y., Schechter I.;
RA	"Primary structures of N-terminal extra peptide segments linked to the
RA	variable and constant regions of immunoglobulin light chain
RT	precursors: implications on the organization and controlled expression
RT	of immunoglobulin genes.;"
RL	Biochemistry 17:2392-2400(1978).
RN	[2]
RP	SEQUENCE OF 21-131.
RP	MEDLINE=73140225; PubMed=4691517;
RX	McKean D.J., Potter M., Hood L.E.;
RA	"Mouse immunoglobulin chains. Pattern of sequence variation among
RT	kappa chains with limited sequence differences.;"
RL	Biochemistry 12:760-771(1973).
RN	[3]
RP	REVISIONS.
RP	MEDLINE=79012520; PubMed=99744;
RX	McKean D.J., Bell M., Potter M.;
RA	"Mechanisms of antibody diversity: multiple genes encode structurally
RT	related mouse kappa variable regions.;"
RT	Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
RL	PIR; B90412; KQMSM6.
DR	HSSP; P01665; 1ONZ.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	PFam; PF00047; Ig; 1.
DR	SMART; SM00406; Igv; 1.
DR	PROSITE; PS50835; IG LIKE; 1.
KW	Direct protein sequencing; Immunoglobulin V region; Signal.
FT	SIGNAL 1 20
FT	CHAIN 21 131
FT	DOMAIN 21 43
FT	DOMAIN 44 58
FT	DOMAIN 59 73
FT	DOMAIN 74 80
FT	DOMAIN 81 112
FT	DOMAIN 113 121
FT	DOMAIN 122 131
FT	DISULFID 43 112
FT	NON TER 131 131
FT	SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

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Query Match      58.2%; Score 401; DB 1; Length 131;
Best Local Similarity 59.5%; Pred. No. 6.Se-33;
Matches         78; Conservative    23; Mismatches 26; Indels   4; Gaps   1;
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[illegible]

```

RESULT 9
Q6KB05
ID Q6KB05 PRELIMINARY; PRT; 255 AA.
AC Q6KB05; 2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE ScFv B8E5 protein (Fragment).
GN Name=scFv B8E5;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCEI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA Briand J.P., Hobeke J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ746180; CAG34081.1; -.
DR HSP; P01837; ILCR.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00409; IG_2.
DR SMART; SM00406; IGv; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON TER
SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF7138 CRC64;

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Query Match      58.2%; Score 401; DB 2; Length 255;  
Best Local Similarity 65.8%; Pred. No. 1.4e-32;  
Matches       77; Conservative    16; Mismatches   18; Indels     6; Gaps     1
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Qy 21 GAGDNIVMTQSPKSMNSVGERVTLTCKASENV-----TYSWYQQKPSKPLIYG 74  
| : | : | : | : | : | : | : | : | : | :  
Db 133 GGGSDIVMAQSPSSLVSACEKVIMSCKSQSLLNRSNRQNKLAWYQQKPSKPLIYG 192

Qy 75 ASNRYTGVPDRFTFGSSGATDFTLTISSVOAEDLDADHYCGGOYSYPYTFGGGTGLEIK 131  
| : | : | : | : | : | : | : | : | : | :  
Db 193 ASTRESGVPRFTFGSGSGETFLTISSVOAEDLVAVYCONDHSPLYFPGAGTKLEIK 249

RESULT	10
Q6GMX8	
ID	PRELIMINARY; PRT; 236 AA.
AC	Q6GMX8;
DT	05-JUL-2004 (T-EMBLrel. 27, Created)
DT	05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISUVE=Primary B-Cells;
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Ahtschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

```
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC073764; AH73764.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 58.1%; Score 400; DB 2; Length 236;
Best Local Similarity 56.8%; Pred. No. 1.7e-32;
Matches 75; Conservative 29; Mismatches 26; Indels 2; Gaps 1;

QY 1 MGIKMSQTLVFISILLWLYGADGNIVMTQSPKSMVSGERVTLTKASENVVTVSWY 60
Db 1 MDMRVPQALLGL--LLMLPFGSCDIQMTQSPSSVSASVGDRTVITCRASQGLSSWLAWY 58

QY 61 QKQPEQSKLLIYGASNRYTGVDPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGSYPY 120
Db 59 QKQPGKAPKLLIYAASSLQSGVPSRFSGSGTDFLTLTSSLPQEDFATYYCQQAHPFP 118

QY 121 TFGGGTKLEIKR 132
Db 119 TFGGGRKVDIKR 130

RESULT 11
Q6GMX0 PRELIMINARY; PRT; 236 AA.
ID Q6GMX0
AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC073775; AH73775.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 57.9%; Score 399; DB 2; Length 236;
Best Local Similarity 57.6%; Pred. No. 2.1e-32;
Matches 76; Conservative 25; Mismatches 29; Indels 2; Gaps 1;

QY 1 MGIKMSQTLVFISILLWLYGADGNIVMTQSPKSMVSGERVTLTKASENVVTVSWY 60
Db 1 MDMRVPQALLGL--LLMLRGRACDIQMTQSPSSVSASVGDRTVITCRASQINNYLWY 58

QY 61 QKQPEQSKLLIYGASNRYTGVDPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGSYPY 120
Db 59 QLKPGKAPKLLIYAASSLQSGVPSRFSGSGTDFLTLTSSLRPDDFATYYCQGSYNIP 118

QY 121 TFGGGTKLEIKR 132
Db 119 TFGGGRNVSEIKR 130

RESULT 12
QV3M_HUMAN STANDARD; PRT; 129 AA.
ID QV3M_HUMAN
AC P18136;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HIC precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
RT expressed in chronic lymphocytic leukemia with little or no somatic
```



DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:006955; P:immune response; NAS.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam: PF00047; IG; 1.  
 DR SMART: SM00406; IG; 1.  
 DR PROSITE: PS0835; IG LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 >121 Ig kappa chain V-IV region.  
 FT DOMAIN 21 43 Framework-1.  
 FT DOMAIN 44 60 Complementarity-determining-1.  
 FT DOMAIN 61 75 Framework-2.  
 FT DOMAIN 76 82 Complementarity-determining-2.  
 FT DOMAIN 83 114 Framework-3.  
 FT DOMAIN 115 121 Complementarity-determining-3.  
 FT DISULFID 43 114 By similarity.  
 FT NON\_TER 121 121  
 SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 56.9%; Score 392; DB 1; Length 121;  
 Best Local Similarity 63.8%; Pred. No. 4.9e-32;  
 Matches 77; Conservative 19; Mismatches 19; Indels 6; Gaps 1;

QY 5 MESQTLVFISILLWLYGADGNIVMTQSPKSMMSVGERVTLTCKASENVV-----TYVS 58  
 DB 1 MVLTQVFLSLWISGAYGDI VMTQSPSLAVSLGERATINCKSSQSVLYSSNNKNYLA 60  
 QY 59 WYQKPEQSPKLIYGASNRYTCVDPRTGSGSATDFTLTISVQAEADLADYHCGGYSY 118  
 DB 61 WYQKPEQSPKLIYWASTRESGVDPFRFGSGSGTDFTLTISLQAEADVAVYCCQYYSY 120  
 QY 119 P 119  
 DB 121 P 121

## RESULT 15

O6GMX9 PRELIMINARY; PRT; 236 AA.  
 ID Q6GMX9  
 AC O6GMX9; 27, Created  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyzinski M.I., Skalek U., Smaluk D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073763; AAH73763.1; -.  
 DR InterPro: IPR003599; IG.  
 DR InterPro: IPR007110; IG-like.  
 DR InterPro: IPR003597; IG c1.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR003596; IG\_v.  
 DR Pfam; PF07654; C1-set; 1.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS0835; IG LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;

Query Match 56.6%; Score 390; DB 2; Length 236;  
 Best Local Similarity 62.7%; Pred. No. 1.7e-31;  
 Matches 74; Conservative 20; Mismatches 24; Indels 0; Gaps 0;

QY 15 ILLWLYGADGNIVMTQSPKSMMSVGERVTLTCKASENVVYVSWYQKPEQSPKLIYG 74  
 DB 13 LLLCFPGARCDLQMTQSPSSLSASVGRVTITCRASQNVSRWLAWYQORPEKAPKSLIYA 72  
 QY 75 ASNRYTGVDPDRFTGSGSATDFTLTISVQAEADLADYHCGGYSYPYTFGGGKLEIKR 132  
 DB 73 TSSLHSGVPSRFGSGSGTDFTLTISLQPEDFATVYCCQYNTYPLTFGGGKVEIKR 130

Search completed: May 25, 2005, 15:56:07  
 Job time : 64.3423 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 65.8977 Seconds  
(without alignments)  
821.675 Million cell updates/sec

Title: US-10-006-773A-4

Perfect score: 739

Sequence: 1 MNFGSLFLVLKGVQCR.....DRGAWFFDVWGAGTTVTVSS 140

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	739	100.0	140	6	ABG74241 Mouse ant
2	605	81.9	462	6	AAO29869 Mouse ant
3	605	81.9	462	7	ADJ79787 TRA-8 ant
4	605	81.9	464	5	AU72801 TRA-8 hea
5	599	81.1	138	2	AAR20064 MRK16-H C
6	592	80.1	247	2	AAW11917 Murine MA
7	587	79.4	140	5	AAU76122 Mouse mon
8	585.5	79.2	139	1	AAU76132 Mouse mAb
9	582	78.8	140	5	AAU76132 Mouse mAb
10	581	78.6	138	2	AAW03722 Anti-huma
11	581	78.6	138	3	AAU32404 Mouse ant
12	581	78.6	139	2	AAU32404 Mouse ant
13	581	78.6	144	5	ABU79730 Anti-Stre
14	580	78.5	140	5	AAU76133 Mouse mAb
15	577	78.1	139	2	AAU27053 Anti-CEA
16	573.5	77.6	137	2	AAW57592 Chimeric
17	573.5	77.6	137	2	AAW89825 Mouse hum
18	573.5	77.6	137	3	AAU77513 Mouse ant
19	573.5	77.6	137	4	AAU77513 Amino aci
20	573.5	77.6	137	4	AAU77513 Amino aci
21	573.5	77.6	137	4	AAU77513 Amino aci
22	573.5	77.6	137	5	AAU77513 Amino aci
23	573.5	77.6	137	6	AAU77513 Amino aci
24	573.5	77.6	137	8	AAU77513 Amino aci
25	564.5	76.4	139	2	AAU77513 Amino aci

26	564.5	76.4	139	2	AAU77513 Amino aci
27	563	76.2	477	2	AAU77513 Amino aci
28	563	76.2	477	2	AAU77513 Amino aci
29	560	75.8	138	8	ADR88408 Murine 3D
30	559	75.6	138	8	ADR88408 Murine 3D
31	559	75.6	142	2	AAU30882 Antibody
32	558	75.5	138	4	AAU81977 Ganglioside
33	558	75.5	138	5	ABG76924 Mouse 3D6
34	558	75.5	138	6	ABU11002 Modified
35	554	75.0	136	2	AAU56962 MAb A33 h
36	553.5	74.9	139	2	AAU21656 Chimeric
37	553.5	74.9	139	6	ABG74247 Mouse ant
38	553	74.8	138	3	AAU32406 Mouse ant
39	553	74.8	158	8	ADL27491 Amino aci
40	552	74.7	138	2	AAU32246 BR55-2 mu
41	552	74.7	138	2	AAU32242 Chimeric
42	552	74.7	139	2	AAU31588 BR55-2 he
43	552	74.7	144	8	ADR47417 Heavy cha
44	551.5	74.6	141	8	ADO43555 Amino aci
45	551	74.6	136	2	AAU06251 Variable

#### ALIGNMENTS

##### RESULT 1

ABG74241

ID ABG74241 standard; protein; 140 AA.

AC ABG74241;

DT 22-APR-2003 (first entry)

DE Mouse antibody MB3.6 heavy chain variable region.

XX T-cell receptor; cytostatic; dermatological; neuroprotective;  
 KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;  
 KW CDalpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;  
 KW small cell lung cancer; heavy chain variable region; mouse.

OS Mus sp.

XX US2002132983-A1.

PN 19-SEP-2002.

PD 10-DEC-2001; 2001US-00006773.

PP 30-NOV-2000; 2000US-0250087P.

PR 30-NOV-2000; 2000US-0250089P.

XX (JUNG/) JUNGHANS R P.

XX Junghans RP;

XX WPI; 2003-208946/20.

XX N-PSDB; ABX16566.

XX New chimeric molecule useful in treating patients with disorders, such as  
 PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer  
 PT comprises GD3 and/or PSMA binding domains of antibody.

PS Disclosure; Page 9; 35pp; English.

XX The invention relates to a chimeric molecule comprising the GD3  
 CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3  
 CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)  
 CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene  
 CC sequences, the zeta signalling chain of the T cell receptor and an  
 CC intervening CD8alpha hinge in which cysteine residues have been mutated.  
 CC The chimeric molecules expressed in T cells or NK cells or other  
 CC effector cells are useful in treating patients with cancers expressing



CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),  
 CC and/or together with each other or with heterologous constructs to engage  
 CC additional stimulatory and functional properties of the effector cells to  
 CC enhance the antitumour therapeutic efficacy (claimed). They are  
 CC particularly useful in disorders including melanoma, neuroendocrine  
 CC tumours and prostate and small cell lung cancer. The present sequence  
 CC represents the mouse antibody MB3.6 heavy chain variable region  
 XX  
 XX

SQ Sequence 140 AA;

Query Match 100.0%; Score 739; DB 6; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-61;  
 Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFGSLIFLVVLKGVQCEVVVSGGFGFVKPGGSLKLSCAAAGTFPSRYAMSWRQTP 60  
 |||||  
 DB 1 MNFGSLIFLVVLKGVQCEVVVSGGFGFVKPGGSLKLSCAAAGTFPSRYAMSWRQTP 60  
 |||||  
 QY 61 EKRLWVATISSGSHYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARPGY 120  
 |||||  
 DB 61 EKRLWVATISSGSHYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARPGY 120  
 |||||  
 QY 121 DRGAWFFDVWGAGTTVTSS 140  
 |||||  
 DB 121 DRGAWFFDVWGAGTTVTSS 140  
 |||||

RESULT 2

AAO29869  
 ID AAO29869 standard; protein; 462 AA.

XX AAO29869;

XX 27-AUG-2003 (first entry)

XX Mouse anti-human DR5 antibody (TRA-8) heavy chain.

DE Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;  
 KW inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;  
 KW Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;  
 KW multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;  
 KW Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;  
 KW Crohn's disease; diabetes mellitus; antibody; mouse.

XX Mus sp.

XX WO2003037913-A2.

XX 08-MAY-2003.

XX 01-NOV-2002; 2002WO-US035333.

XX 01-NOV-2001; 2001US-0346402P.

XX (UABR-) UAB RES FOUND.

XX Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;

XX WPI; 2003-441350/41.

XX N-PSDB; AAL60477.

XX New purified antibody that specifically binds a TNF-related apoptosis-  
 PT inducing ligand receptor DR4 or DR5, useful for treating cancer,  
 PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or  
 PT rheumatoid arthritis.

XX Example 16; Page 224-225; 251pp; English.

XX The invention relates to an antibody that specifically binds a tumour  
 CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor  
 CC DR4 or DR5. Antibodies of the invention are useful for selectively  
 CC inducing apoptosis in target cells expressing DR4, for inhibiting  
 CC proliferation of target cells expressing DR4 or for treating cancer,

CC inflammatory disease or autoimmune disease in a subject e.g. systemic  
 CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-  
 CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple  
 CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or  
 CC glomerular nephritis. The present sequence is mouse anti-human DR5  
 CC antibody (TRA-8) heavy chain  
 XX  
 XX

SQ Sequence 462 AA;

Query Match 81.9%; Score 605; DB 6; Length 462;  
 Best Local Similarity 85.0%; Pred. No. 2.1e-48;  
 Matches 119; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVVLKGVQCEVVVSGGFGFVKPGGSLKLSCAAAGTFPSRYAMSWRQTP 60  
 |||||  
 DB 1 MNFGSLIFLVVLKGVQCEVVLVSGGGLVKPGGSLKLSCAASGTFPSRYAMSWRQTP 60  
 |||||  
 QY 61 EKRLWVATISSGSHYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARPGY 120  
 |||||  
 DB 61 EKRLWVATISSGSHYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARRG- 119  
 |||||  
 QY 121 DRGAWFFDVWGAGTTVTSS 140  
 |||||  
 DB 120 -DSMITDYWGOGTTITVSS 138  
 |||||

RESULT 3

ADJ79787

ID ADJ79787 standard; protein; 462 AA.

XX ADJ79787;

XX 06-MAY-2004 (first entry)

XX TRA-8 antibody heavy chain.

XX nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;  
 KW antiallergic; antiinflammatory; antidiabetic; haemostatic;  
 KW neuroprotective; antinfertility; immunosuppressive; dermatological;  
 KW antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;  
 KW proliferation;  
 KW tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;  
 KW TRAIL; synovial cell; lymphocyte; neutrophil;  
 KW systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;  
 KW graft-versus-host disease; Sjogren's syndrome; pernicious anemia;  
 KW Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;  
 KW autoimmune hemolytic anemia; sterility; myasthenia gravis;  
 KW multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;  
 KW thrombopenia purpura; insulin dependent diabetes mellitus; allergy;  
 KW asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; hypoplastic anemia.

XX Homo sapiens.

XX WO2003038043-A2.

XX 08-MAY-2003.

XX 25-OCT-2002; 2002WO-US034420.

XX 01-NOV-2001; 2001US-0346402P.

XX 24-JUN-2002; 2002US-0391478P.

XX (UABR-) UAB RES FOUND.

XX Zhou T, Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;

XX Lobuglio AF, Buchsbaum DJ;

XX WPI; 2003-421518/39.

XX Inducing apoptosis and inhibiting proliferation of target cells  
 PT expressing DR5, by contacting the target cell with an antibody that binds  
 PT TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic



PT agents.  
 PS Example 16; SEQ ID NO 23; 274pp; English.  
 XX  
 CC The invention relates to a method of selectively inducing apoptosis in  
 CC and inhibiting (M1) proliferation of target cells expressing DR5,  
 CC comprising contacting the cell with an antibody that specifically binds  
 CC tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)  
 CC receptor DR5, where the antibody, in its soluble form, has in vivo and in  
 CC vitro apoptosis-inducing activity in the cell expressing DR5, and  
 CC contacting the cell with one or more therapeutic agents. M1 is useful for  
 CC inducing apoptosis in target cell and inhibiting proliferation of target  
 CC cell expressing DR5, where the target cell is an abnormally proliferating  
 CC synovial cells (e.g. rheumatoid arthritis synovial cell), activated  
 CC immune cell (e.g. activated lymphocyte), neutrophil, or virally infected  
 CC cell. M2 is useful for treating a subject having inflammatory and  
 CC autoimmune diseases. The inflammatory or autoimmune disease are selected  
 CC from systemic lupus erythematosus, Hashimoto's disease, rheumatoid  
 CC arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious  
 CC anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,  
 CC thrombopenia purpura, insulin dependent diabetes mellitus, allergy,  
 CC asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerular nephritis, and hypoplastic anemia. This sequence represents a  
 CC protein used in the method of the invention.  
 XX  
 SQ Sequence 462 AA;

Query Match 81.9%; Score 605; DB 7; Length 462;  
 Best Local Similarity 85.0%; Pred. No. 2.1e-48;  
 Matches 119; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

OY 1 MNFGSLIFLVVLKGVQCEVVVSGGFKVPGGSLKSCAAAGFTFSRYAMSWRQTP 60  
 DB 1 MNFGSLIFLVVLKGVQCEVVVSGGFKVPGGSLKSCAAAGFTFSRYAMSWRQTP 60  
 OY 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQWSSLRSDTAIYYCARGP 120  
 DB 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQWSSLRSDTAIYYCARGP 119  
 OY 121 DRGAWFFDVWGAGTTVTVSS 140  
 DB 120 -DSMITTDYWGQGTTLTVSS 138

RESULT 4  
 AAU72801  
 ID AAU72801 standard; protein; 464 AA.  
 XX AAU72801;  
 AC  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE TRA-8 heavy chain.  
 XX  
 KW Tumor necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;  
 KW TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;  
 KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;  
 KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; sterility;  
 KW Addison disease; scleroderma; Goodpasture's syndrome; myasthenia gravis;  
 KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;  
 KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;  
 KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200183560-A1.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US014151.

PR 02-MAY-2000; 2000US-0201344P.  
 XX (UABR-) UAB RES FOUND.  
 PA  
 XX Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;  
 PI WPI; 2002-049338/06.  
 XX N-PSDB; AAS97062.  
 DR  
 XX Novel antibody specific for tumor necrosis factor-related apoptosis-  
 XX inducing ligand, useful for inhibiting cell proliferation in cancer.  
 PT  
 XX Claim 26; Page 198-199; 229pp; English.  
 PS  
 XX The invention describes a novel antibody which recognizes a tumour  
 XX necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor  
 XX DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing  
 XX activity to a cell expressing DR5 in vivo. It is also useful for  
 XX preparing a therapeutic for selective apoptosis of abnormal or  
 XX dysregulated cells, and for inhibiting cell proliferation in a cell,  
 XX preferably a human breast, ovary, colon, haematopoietic, prostate,  
 XX lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may  
 XX also be administered e.g. paclitaxel, taxol or cycloheximide. The  
 XX antibody is used to treat an autoimmune disease, systemic lupus  
 XX erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-  
 XX host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,  
 XX Addison disease, scleroderma, Goodpasture's syndrome, autoimmune  
 XX haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,  
 XX Basedow's disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular  
 XX disease, nephritis, hypoplastic anaemia, rejection after organ transplantation,  
 XX and numerous malignancies of lung, prostate, liver, ovary, lymphatic or  
 XX breast tissue. Peptides used to design primers for isolating heavy and  
 XX light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are  
 XX shown in AAU72799 and AAU72800  
 XX  
 SQ Sequence 464 AA;

Query Match 81.9%; Score 605; DB 5; Length 464;  
 Best Local Similarity 85.0%; Pred. No. 2.1e-48;  
 Matches 119; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

OY 1 MNFGSLIFLVVLKGVQCEVVVSGGFKVPGGSLKSCAAAGFTFSRYAMSWRQTP 60  
 DB 1 MNFGSLIFLVVLKGVQCEVVVSGGFKVPGGSLKSCAAAGFTFSRYAMSWRQTP 60  
 OY 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQWSSLRSDTAIYYCARGP 120  
 DB 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQWSSLRSDTAIYYCARGP 119  
 OY 121 DRGAWFFDVWGAGTTVTVSS 140  
 DB 120 -DSMITTDYWGQGTTLTVSS 138

RESULT 5  
 AAR20064  
 ID AAR20064 standard; protein; 138 AA.  
 XX AAR20064;  
 AC  
 XX 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 27-MAR-1992 (first entry)  
 XX  
 DE MRK16-H chain.  
 XX  
 KW Monoclonal antibody; light; heavy; chain; cancer; drug resistance.  
 XX  
 OS Homo sapiens.  
 OS Mus musculus.  
 OS Chimeric.  
 XX

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PN JP03254691-A.
XX
PD 13-NOV-1991.
XX
PF 02-MAR-1990; 90JP-00051563.
XX
PR 02-MAR-1990; 90JP-00051563.
XX
PA (GANK-) ZH GAN KENYUKAI.
PA (FUJI-) FUJITA GAKUEN GH.
PA (NICA-) JAPAN FOUND CANCER RES.
XX
DR WPI: 1992-002461/01.
DR N-PSDB; AAQ20070.
XX
PT Chimera antibody against drug resistant cancer - comprises variable
PT region homologous to region in mouse monoclonal antibody and constant
PT region homologous to region in human immunoglobulin.
XX
PS Disclosure; Fig 4; 20pp; Japanese.
XX
CC A chimeric antibody against drug-resistant cancer consists of (1) a
CC variable region having an amino acid sequence homologous to a variable
CC region in the mouse monoclonal antibody against drug- resistance and (2)
CC a constant region having an amino acid sequence homologous to the
CC constant region in human immunoglobulin. The chimeric antibody
CC selectively inhibits the growth of cancer cells showing drug resistance
CC or enhances the sensitivity to the drug. The antibody is very low in
CC immunogenicity. The MK16-L chain is shown in AAQ20071. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 138 AA;

Query Match 81.1%; Score 599; DB 2; Length 138;
Best Local Similarity 83.6%; Pred. No. 1.9e-48;
Matches 117; Conservative 7; Mismatches 14; Indels 2; Gaps 2;

QY 1 MNFGSLIFLVLVLKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFSGRYAMSWVRQTP 60
DB 1 MNFGSLIFLVLVLKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFSGRYAMSWVRQTP 60
QY 61 EKRLEWATISSGGSHYYPPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYCARPGY 120
DB 61 EKRLEWATISSGGSHYYPPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYCAR-YY 119

QY 121 DRGAWFFDVWGAGTTVTSS 140
DB 120 RYEAWFAS-WGQGLTLVTUSA 138

RESULT 6
AAW11917
ID AAW11917 standard; protein; 247 AA.
XX
AC AAW11917;
XX
XX 24-JUN-1997 (first entry)
XX
XX Murine MAb SK48-E26 heavy chain.
XX
KW Interleukin-1 beta; IL-1 beta; recombinant antibody; humanised antibody;
KW chimeric antibody; antibody engineering; monoclonal antibody; MAb;
KW SK48-E26; inflammation; therapy.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
PH Peptide 1..19
FT /label= Sig_peptide
FT 20..49
FT /label= FR1
FT /note= "framework region 1"
FT

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FT Region
FT 50..54
FT /label= CDR1
FT /note= "complementarity determining region 1 (Claim 10,
FT page 48)"
FT 55..68
FT /label= FR2
FT /note= "framework region 2"
FT 69..85
FT /label= CDR2
FT /note= "complementarity determining region 2 (Claim 10,
FT page 48)"
FT 86..117
FT /label= FR3
FT /note= "framework region 3"
FT 118..127
FT /label= CDR3
FT /note= "complementarity determining region 3 (Claim 10,
FT page 48)"
FT 128..138
FT /label= FR4
FT /note= "framework region 4"
FT 139..247
FT /label= Constant_region
FT
WO9501997-A1.
XX
PD 19-JAN-1995.
XX
PF 07-JUL-1994; 94WO-US007659.
XX
PR 09-JUL-1993; 93US-00090534.
XX
PR 04-MAR-1994; 94US-00206190.
XX
PA (SMIX ). SMITHKLINE BEECHAM CORP.
XX
XX Young PR, Gross MS, Jonak ZL, Theisen TW, Hurle MR, Jackson JR;
XX WPI: 1995-066968/09.
XX N-PSDB; AAT51436.
XX
PT Recombinant and humanised chimeric antibodies against human interleukin-1
PT -beta - for preventing and treating interleukin-mediated inflammatory
PT disorders.
XX
PS Claim 5; Page 36-37; 62pp; English.
XX
CC Amino acid sequences of the heavy chain (AAW11917) and light chain
CC (AAW11918) of anti-human interleukin-1 beta (IL-1 beta) murine monoclonal
CC antibody (MAb) SK48-E26 were deduced from nucleic acids (AAT51436-37)
CC derived from hybridoma SK48-E26. The heavy and light chains, esp. the
CC complementarity determining region sequences, can be utilised in novel
CC recombinant chimeric and humanised antibodies (see also AAW11919-20)
CC useful for the treatment and prevention of IL-1 mediated inflammatory
CC disorders
XX
SQ Sequence 247 AA;

Query Match 80.1%; Score 592; DB 2; Length 247;
Best Local Similarity 82.1%; Pred. No. 1.7e-47;
Matches 115; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVLVLKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFSGRYAMSWVRQTP 60
DB 1 MNFGSLIFLVLVLKGVQCEVVVSGGGFVKPGGSLKLSCAAAGTFSGRYAMSWVRQTP 60
QY 61 EKRLEWATISSGGSHYYPPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYCARPGY 120
DB 61 EKRLEWATISSGGSHYYPPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYCARGGV 120
QY 121 DRGAWFFDVWGAGTTVTSS 140
DB 121 RRG--YFDVWGAGTTVTSS 138

```

[illegible]

PI Hardman N, Gill LL, Dewinter RFJ, Wagner K, Heusser C;  
 XX WPI; 1989-200701/28.  
 DR N-PSDB; AAN90301.  
 XX  
 PT Chimeric monoclonal antibody to human carcinoembryonic antigen -  
 PT comprises variable regions of mouse origin and human constant regions,  
 PT for cancer diagnosis and therapy.  
 XX  
 PS Claim 30; Page 37; 53pp; English.  
 XX  
 CC The peptide is expressed by the sequence of AAN90301. The heavy chain  
 CC variable region is specific for human carcinoembryonic antigen. (Updated  
 CC on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to  
 CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated  
 CC on 25-MAR-2003 to correct PI field.)  
 XX  
 SQ Sequence 139 AA;  
 Query Match 79.2%; Score 585.5; DB 1; Length 139;  
 Best Local Similarity 81.4%; Pred. No. 3.6e-47;  
 Matches 114; Conservative 10; Mismatches 15; Indels 1; Gaps 1;  
 QY 1 MNFGSLIFLVLKGVQCEVWVVGSGGFVKPGGSLKLSCAAAGTFRYAMSWVRQTP 60  
 DB 1 MNFGSLIFLVLKGVQCEVWVVGSGGFVKPGGSLKLSCAAAGTFRYAMSWVRQTP 60  
 QY 61 EKRLWVATISSGGSHYYPDSVKGRFTISRDNKNTLYQMSSLSRSEDATYYCARGPY 120  
 DB 61 EKRLWVATISSGGT-TYYPDSVKGRFTISRDNKNTLYQMSSLSRSEDATYYCARGFY 119  
 QY 121 DRGAWFFDVGAGTTVTSS 140  
 DB 120 DGYLYVDYWGQGTSLTVSS 139  
 RESULT 9  
 AAU76132  
 ID AAU76132 standard; protein; 140 AA.  
 XX  
 AC AAU76132;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Mouse mAb 26-2F heavy chain variable region mutant M100Y.  
 XX  
 KW Mouse; angiogenesis; tumour; cancer; retinopathy;  
 KW ocular neovascular disease; vitamin A deficiency; syphilis;  
 KW Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;  
 KW sickle cell anaemia; Paget's disease; mycobacterial infection;  
 KW osteoarthritis; graft versus host disease; autoimmune disease;  
 KW type I diabetes; multiple sclerosis; systemic lupus erythematosus;  
 KW myasthenia gravis; mutant; mutein; monoclonal antibody; 26-2F;  
 KW heavy chain variable region; M100Y.  
 XX  
 OS Mus sp.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19 /label= Signal\_peptide  
 FT Protein 20..140 /label= Mature\_VH  
 FT Misc-difference 100 /note= "Wild-type Met substituted by Tyr"  
 FT  
 XX  
 PN US2002010320-A1.  
 XX  
 PD 24-JAN-2002.  
 XX  
 PF 05-APR-1999; 99US-00286240.  
 XX  
 PR 05-APR-1999; 99US-00286240.

XX (FETT/) FETT J W.  
 PA FETT JW;  
 PI  
 XX WPI; 2002-187790/24.  
 DR  
 XX New antibody immunologically reactive to angiogenin useful for inhibiting  
 PT angiogenesis and for treating conditions associated with abnormal  
 PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid  
 PT arthritis.  
 XX  
 PS Claim 10; Page; 20pp; English.  
 XX  
 CC The invention relates to an antibody immunologically reactive to  
 CC angiogenin or a fragment of angiogenin comprising light and heavy chain  
 CC nonhuman-derived complementarity determining regions having a binding  
 CC affinity to the angiogenin or its fragment in combination with human  
 CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also  
 CC included are an expression vector comprising a nucleic acid encoding the  
 CC antibody and a host cell transformed with the vector. The antibody or its  
 CC fragment is useful for inhibiting the angiogenic activity of angiogenin.  
 CC The antibody is useful for treating a tumour in humans, by inhibiting the  
 CC ability of circulating tumour cell to form a vascularised tumour mass.  
 CC The antibody is useful for treating a mammal with abnormal or unwanted  
 CC angiogenesis, including cancer, and other diseases mediated by  
 CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,  
 CC retinopathy of prematurity, corneal graft rejection, neovascular glaucoma  
 CC and retrolental fibroplasia, and other diseases associated with corneal  
 CC neovascularisation including epidemic keratoconjunctivitis, vitamin A  
 CC deficiency, contact lens overwear, atopic keratitis, superior limbic  
 CC keratitis, syphilis, mycobacteria infections, lipid degeneration,  
 CC chemical burns, bacterial ulcers, fungal ulcers, herpes simplex  
 CC infections, herpes zoster infections, protozoan infections, Kaposi's  
 CC sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma,  
 CC Wegener's sarcoidosis, scleritis, Steven Johnson's disease, and corneal  
 CC graft rejection. Diseases associated with retinal/choroidal  
 CC neovascularisation include macular degeneration, sickle cell anaemia,  
 CC sarcoid, Paget's disease, mycobacterial infections, Behcet's disease,  
 CC trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host  
 CC disease, transplant rejection, autoimmune diseases such as type I  
 CC diabetes, multiple sclerosis, systemic lupus erythematosus, and  
 CC myasthenia gravis. The present sequence represents the M100Y mutant of  
 CC the mouse monoclonal antibody 26-2F light chain variable region. Note:  
 CC The present sequence is not shown in the specification but was created by  
 CC the indexer using the sequence appearing as AAU76122 and the information  
 CC in the claims  
 XX  
 SQ Sequence 140 AA;  
 Query Match 78.8%; Score 582; DB 5; Length 140;  
 Best Local Similarity 80.0%; Pred. No. 7.7e-47;  
 Matches 112; Conservative 10; Mismatches 18; Indels 0; Gaps 0;  
 QY 1 MNFGSLIFLVLKGVQCEVWVVGSGGFVKPGGSLKLSCAAAGTFRYAMSWVRQTP 60  
 DB 1 MDGFLSWFLVLKGVQCEVWVVGSGGFVKPGGSLKLSCAAAGTFRYAMSWVRQTP 60  
 QY 61 EKRLWVATISSGGSHYYPDSVKGRFTISRDNKNTLYQMSSLSRSEDATYYCARGPY 120  
 DB 61 EKRLWVATISSGGNTYYPDSVKGRFTISRDNKNTLYQMSSLSRSEDATYYCARGPY 120  
 QY 121 DRGAWFFDVGAGTTVTSS 140  
 DB 121 YGVAYTMDYWGQGTSLTVSS 140  
 RESULT 10  
 AAU03722  
 ID AAU03722 standard; protein; 138 AA.  
 XX  
 AC AAU03722;

XX 02-APR-1997 (first entry)  
 DE Anti-human gp39 Mab 39-1.106 heavy chain variable region.  
 DE Heavy chain; variable region; murine; mouse; anti-human; disease;  
 KW glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;  
 KW diagnosis; inhibition; B-cell; activation; treatment; disorder; immune;  
 KW autoimmune; allergic response; organ rejection; drug; graft versus host;  
 KW cell imaging; tumour; targeted; delivery; targeted.  
 OS Mus musculus.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1. .19  
 FT /label= sig\_peptide  
 FT Peptide 20. .138  
 FT /label= mat\_peptide  
 FT Region 50. .54  
 FT /note= "complementarity determining region 1"  
 FT Region 69. .84  
 FT /note= "complementarity determining region 2"  
 FT Region 117. .126  
 FT /note= "complementarity determining region 3"  
 XX  
 XX WO9623071-A2.  
 XX  
 XX 01-AUG-1996.  
 XX  
 XX 26-JAN-1996; 96WO-US001119.  
 XX  
 XX 26-JAN-1995; 95US-00379057.  
 XX  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 XX  
 XX Siedak A, Hollenbaugh D, Gilliland LK, Gordon ML, Bajorath J;  
 PI Aruffo AA, Harris LJ;  
 DR WPI; 1996-362694/36.  
 DR N-PSDB; AAT35974.  
 XX  
 XX Monoclonal antibodies specific for different epitope(s) on human gp39 -  
 PT used for inhibiting B cell activation and for the diagnosis of various  
 PT disorders, e.g. cancer, psoriasis etc..  
 XX  
 XX Claim 91; Fig 6B; 167pp; English.  
 XX  
 XX The present sequence is the heavy chain variable region of the murine  
 CC anti-human glycoprotein (gp) 39 monoclonal antibody (MAB) 39-1.106 (a  
 CC member of the murine III(D) subgroup). The MAB was prepd. by immunising a  
 CC 6-8 week old BALB/c mouse with a gp39-CD8 fusion protein, and 3 days  
 CC later harvesting and fusing spleen and lymph cells to mouse melanoma  
 CC cells, to produce an anti-human gp39 MAB producing hybridoma. The MAB may  
 CC be useful for diagnosing disease states, inhibiting B-cell activation and  
 CC for treating immunological disorders, e.g. autoimmune disorders, allergic  
 CC responses, organ rejection and graft versus host disease. It may also be  
 CC used for imaging cells which express gp39 on their surface, e.g. tumour  
 CC cells, and to target therapeutic agents to such cells. The MAB inhibits  
 CC the CD40/gp39 interaction, therefore limiting both prim. and sec.  
 CC responses to T-cell dependent antigens and Ab prodn. specific to these  
 CC antigens. A typical compsn. for intramuscular injection pref. contains 50  
 CC mg of MAB in 1 ml of sterile buffered water  
 XX  
 XX Sequence 138 AA;  
 SQ  
 Query Match 78.6%; Score 581; DB 2; Length 138;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-47;  
 Matches 114; Conservative 10; Mismatches 14; Indels 2; Gaps 2;  
 QY 1 MNFGSLFLVLVLKGVQCEVSVESGGGVKPGGSLKLSCAAAGFTFSRVMASWVRQTP 60  
 DB 1 MNFGSLFLVLVLKGVQCEVSVESGGGVKPGGSLKLSCTTSGFTFNVMASWVRQTP 60

QY 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLOWSSLSRSDTAIYYCARGY 120  
 DB 61 EKRLWVASISSGDS-TYTPDSVGRGFTISRDNARNILYLOWSSLSRSDTAIYYCAR-HY 118  
 QY 121 DRGAFFPDVWGAGTTVTVSS 140  
 DB 119 DYDSYAMDYWCQGSVTVSS 138  
 RESULT 11  
 AAY32404  
 ID AAY32404 standard; protein; 138 AA.  
 XX  
 XX AAY32404;  
 AC AAY32404 (first entry)  
 DT 13-MAR-2000  
 XX Mouse anti-verotoxin II antibody VTml-1 heavy chain variable region.  
 DE  
 XX Verotoxin II; VT2; shiga-like toxin; VTml-1; MuVTml-1;  
 KW monoclonal antibody; heavy chain; mouse; humanised antibody;  
 KW Escherichia coli; VTEC; infection; haemolytic uraemic syndrome; HUS;  
 KW therapy.  
 XX  
 XX Mus musculus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1. .19  
 FT /note= "signal peptide"  
 FT Protein 20. .138  
 FT /note= "mature protein"  
 FT Region 50. .54  
 FT /note= "complementarity determining region 1"  
 FT Region 69. .85  
 FT /note= "complementarity determining region 2"  
 FT Region 118. .127  
 FT /note= "complementarity determining region 3"  
 XX  
 XX WO9959629-A1.  
 XX  
 XX 25-NOV-1999.  
 XX  
 XX 19-MAY-1999; 99WO-US011179.  
 XX  
 XX 20-MAY-1998; 98US-0086570P.  
 XX  
 XX (TEIJ ) TEIJIN LTD.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasesques M;  
 PI  
 XX WPI; 2000-086580/07.  
 DR N-PSDB; AAZ35241.  
 XX  
 XX Humanized antibody binding to verotoxin II used for treating Verotoxin  
 PT producing E. coli.  
 XX  
 XX Claim 5; Fig 1a; 59pp; English.  
 XX  
 XX This sequence represents the heavy chain variable region of murine  
 CC monoclonal antibody VTml-1 (MuVTml-1), an antibody that specifically  
 CC binds to the B subunit of verotoxin II (VT2). The invention relates to  
 CC humanised antibodies against VT2 that are capable of neutralizing VT2  
 CC and/or VT2 variants. The humanised antibody is a humanized form of MuVTml  
 CC -1 comprising the complementarity determining regions of MuVTml-1 and the  
 CC heavy and light chain variable region frameworks from the human GF4  
 CC antibody heavy and light chain frameworks, provided that at least 1  
 CC position selected from L49, H29, H30, H49 and H98 is occupied by the  
 CC amino acid at the equivalent position of the MuVTml-1 antibody heavy or  
 CC light chain variable region framework. Such humanized antibodies (see  
 CC AAY32406-07) have an affinity for VT2 that is 3-, 5 or 10-times that of  
 CC MuVTml-1. They are used for treating a patient suffering from, or at risk  
 CC of, the toxic effects from VT2 (claimed), especially for treating

CC verotoxin producing Escherichia coli (VTEC) infection, and haemolytic  
 CC uraemic syndrome (HUS)

SQ Sequence 138 AA;

Query Match 78.6%; Score 581; DB 3; Length 138;  
 Best Local Similarity 81.6%; Pred. No. 9.4e-47;  
 Matches 115; Conservative 6; Mismatches 16; Indels 4; Gaps 2;  
 QY 1 MNFGSLIFLVLKGVCEVVVSGGGFVKPGGSLKLSCAAAGTFPSRYAMSWRQTP 60  
 DB 1 MNFVLSIFLALILKGVCEVQVSGGGFVKPGGSLKLSCAAAGTFPSRYAMSWRQTP 60  
 QY 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARPG- 120  
 DB 61 EKRLWVATISGGSHTYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARPG- 119

QY 121 DRGAW-FFDVWAGTIVTVSS 140  
 DB 120 --DAWGNLDYWGQGTSTVTVSS 138

#### RESULT 12

AAR30480  
 ID AAR30480 standard; protein; 139 AA.

AC AAR30480;

XX 06-MAY-1993 (first entry)

DT 06-MAY-1993 (first entry)

DE hCEA specific mouse heavy chain variable chain region.

DE Chimeric antibody; human cancer embryonal antigen; treatment; diagnosis;

KW cancer.

XX Mus musculus.

OS Key

XX Location/Qualifiers

FT Peptide

FT 1..19

FT /note= "signal peptide"

FT Protein

FT 20..139

FT /note= "mature peptide"

XX JP04330295-A.

XX 18-NOV-1992.

XX 28-DEC-1990; 90JP-00408811.

XX 28-DEC-1990; 90JP-00408811.

XX (MITU ) MITSUBISHI KASEI CORP.

XX WPI; 1993-003502/01.

XX N-PSDB; AAQ33052.

XX Mouse-human chimeric antibody for diagnosis and treatment of cancer -

PT obtd. by combining variable region of mouse antibody specifically

PT combining to human cancer embryonic antigen with constant region of human

PT antibody.

XX Disclosure; Page 6; 10pp; Japanese.

XX The sequence is that of the heavy chain variable region of a mouse

CC antibody specific to human cancer embryonal antigen (hCEA). The region is

CC used, with the corresponding mouse light chain variable region and the

CC constant region of a human antibody, to prepare a mouse-human chimeric

CC antibody which can be used for the diagnosis and treatment of cancer

XX Sequence 139 AA;

SQ Query Match 78.6%; Score 581; DB 2; Length 139;

Best Local Similarity 83.7%; Pred. No. 9.5e-47;

Matches 118; Conservative 7; Mismatches 12; Indels 4; Gaps 3;  
 QY 1 MNFGSLIFLVLKGVCEVVVSGGGFVKPGGSLKLSCAAAGTFPSRYAMSWRQTP 60  
 DB 1 MNFGSLIFLVLKGVCEVQVSGGGFVKPGGSLKLSCAAAGTFPSRYAMSWRQTP 60  
 QY 61 EKRLWVATISSGGSHYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARPG- 119  
 DB 61 EKRLWVATISDGS-TYTPDSVKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCARVHY 119  
 QY 120 YDRGAWFFDVWAGTIVTVSS 140  
 DB 120 YDSPA--MDYWGQGTSTVTVSS 138

#### RESULT 13

ABB79730

ID ABB79730 standard; protein; 144 AA.

XX ABB79730;

XX 29-OCT-2002 (first entry)

DT 29-OCT-2002 (first entry)

DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VH.

DE Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;

KW antibody; anticaries; transgenic plant; transgenic animal; caries;

KW immunotherapy; therapy.

XX Mus musculus.

XX US2002068066-A1.

XX 06-JUN-2002.

XX 15-JUN-2001; 2001US-00881823.

XX 20-AUG-1999; 99US-00378577.

XX (SHIW/) SHI W.

XX (MORR/) MORRISON S L.

XX (TRIN/) TRINH K.

XX (WIMS/) WIMS L.

XX (CHEN/) CHEN L.

XX (ANDE/) ANDERSON M H.

XX Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;

XX WPI; 2002-565838/60.

XX N-PSDB; ABN84611.

XX Treatment and prevention of dental caries in mammals, in particular

PT humans by orally administering genetically engineered or purified

PT antibodies that bind to surface antigens of carcinogenic organisms.

XX Claim 14; Fig 3B; 30pp; English.

XX The present sequence is the protein sequence of the heavy chain variable

CC region (VH) of the murine monoclonal antibody SWLA3 (IgG), which binds

CC specifically to the surface antigens of cariogenic type c Streptococcus

CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC

CC HB 12558) hybridoma cells. In an example from the invention, chimeric

CC monoclonal antibody TEFE was produced comprising SWLA3 variable regions

CC and human antibody constant regions. Such chimeric monoclonal antibodies

CC can be used to prevent or treat dental caries in humans. The antibodies

CC engage the effector apparatus of the human immune system when they bind

CC cariogenic organisms, resulting in their destruction. The chimeric

CC antibodies may be produced in edible plants, in transgenic animals, or in

CC chicken eggs for oral ingestion

XX Sequence 144 AA;

SQ Query Match 78.6%; Score 581; DB 5; Length 144;

Best Local Similarity 76.8%; Pred. No. 9.9e-47;  
Matches 109; Conservative 17; Mismatches 14; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVVLKVGOCCEVVVVEGGGFVKGSLKLSKSCAAAGTFSRYAMSWRQTP 60  
Db 1 MDFGLSWFLVVLKVGOCCEVVVVEGGGFVKGSLKLSKSCAAAGTFSRYAMSWRQTP 60  
QY 61 EKRLVAVATISSGGSHYTPDSVKGRFTISRDNANKNTLYLQWSLSRSEDTALYYCARPCY 120  
Db 61 EKRLVAVATISSGGSHYTPDSVKGRFTISRDNANKNTLYLQWSLSRSEDTALYYCARPCY 120  
QY 121 DRGAMFF--DVGAGTTVTVSS 140  
Db 121 SYGYYAYMDYWGQGTSTVTVSS 142

RESULT 14  
AAU76133  
ID AAU76133 standard; protein; 140 AA.

AC AAU76133;

DT 08-MAY-2002 (first entry)

DE Mouse mAb 26-2F heavy chain variable region mutant E59Y.

XX Mouse; angiogenesis; tumour; cancer; retinopathy;  
XX ocular neovascular disease; vitamin A deficiency; syphilis;  
XX Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;  
XX sickle cell anaemia; Paget's disease; mycobacterial infection;  
XX osteoarthritis; graft versus host disease; autoimmune disease;  
XX type I diabetes; multiple sclerosis; systemic lupus erythematosus;  
XX myaechenia gravis; mutant; monoclonal antibody; 26-2F;  
XX heavy chain variable region; E59Y.

OS Mus sp.  
OS Synthetic.

XX key Location/Qualifiers

FT Peptide 1..19  
FT /label= Signal\_peptide  
FT Protein 20..140  
FT /label= Mature\_VH

FT Misc-difference 59  
FT /note= "Wild-type Glu substituted by Tyr"

PN US2002010320-A1.

PD 24-JAN-2002.

PF 05-APR-1999; 99US-00286240.

PR 05-APR-1999; 99US-00286240.

XX (FETT/) FETT J W.

XX Fect JW;

XX WPI; 2002-187790/24.

PT New antibody immunologically reactive to angiogenin useful for inhibiting  
PT angiogenesis and for treating conditions associated with abnormal  
PT angiogenesis e.g. cancer, ocular neovascular disease, rheumatoid  
PT arthritis.

PS Claim 11; Page; 20pp; English.

CC The invention relates to an antibody immunologically reactive to  
CC angiogenin or a fragment of angiogenin comprising light and heavy chain  
CC nonhuman-derived complementarity determining regions having a binding  
CC affinity to the angiogenin or its fragment in combination with human  
CC derived polypeptide regions (e.g. mouse monoclonal antibody 26-2F). Also  
CC included are an expression vector comprising a nucleic acid encoding the

CC antibody and a host cell transformed with the vector. The antibody or its  
CC fragment is useful for inhibiting the angiogenic activity of angiogenin.  
CC The antibody is useful for treating a tumour in humans, by inhibiting  
CC prohibiting, reducing or eliminating a tumour growth, or inhibiting the  
CC ability of circulating tumour cell to form a vascularised tumour mass.  
CC The antibody is useful for treating a mammal with abnormal or unwanted  
CC angiogenesis, including cancer, and other diseases mediated by  
CC angiogenesis, including ocular neovascular disease, diabetic retinopathy,  
CC retinopathy of prematurity, corneal graft rejection, neovascular glaucoma  
CC and retrolental fibroplasia, and other diseases associated with corneal  
CC neovascularisation including epidemic keratoconjunctivitis, vitamin A  
CC deficiency, contact lens overwear, atopic keratitis, superior limbic  
CC keratitis, syphilis, mycobacteria infections, lipid degeneration,  
CC chemical burns, bacterial ulcers, fungal ulcers, herpes simplex  
CC infections, herpes zoster ulcers, protozoan infections, Kaposi's  
CC sarcoma, Mooren ulcer, rheumatoid arthritis, polyarteritis, trauma,  
CC Wegener's sarcoidosis, Scleritis, Steven Johnson's disease, and corneal  
CC graft rejection. Diseases associated with retinal/choroidal  
CC neovascularisation include macular degeneration, sickle cell anaemia,  
CC sarcoid, Paget's disease, mycobacterial infections, Bechets disease,  
CC trauma, osteoarthritis, Osler-Weber-Rendu disease, graft versus host  
CC disease, transplant rejection, autoimmune diseases such as type I  
CC diabetes, multiple sclerosis, systemic lupus erythematosus, and  
CC myaechenia gravis. The present sequence represents the E59Y mutant of the  
CC mouse monoclonal antibody 26-2F light chain variable region. Note: The  
CC present sequence is not shown in the specification but was created by the  
CC index using the sequence appearing as AAU76122 and the information in  
CC the claims

SQ Sequence 140 AA;

Query Match 78.5%; Score 580; DB 5; Length 140;

Best Local Similarity 80.0%; Pred. No. 1.2e-46;  
Matches 112; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 MNFGSLIFLVVLKVGOCCEVVVVEGGGFVKGSLKLSKSCAAAGTFSRYAMSWRQTP 60  
Db 1 MDFGLSWFLVVLKVGOCCEVVVVEGGGFVKGSLKLSKSCAAAGTFSRYAMSWRQTP 60

QY 61 EKRLVAVATISSGGSHYTPDSVKGRFTISRDNANKNTLYLQWSLSRSEDTALYYCARPCY 120  
Db 61 EKRLVAVATISSGGSHYTPDSVKGRFTISRDNANKNTLYLQWSLSRSEDTALYYCARPCY 120

QY 121 DRGAMFFDVGAGTTVTVSS 140  
Db 121 YGYAYTMDYWGQGTSTVTVSS 140

RESULT 15

AAU7053  
ID AAU7053 standard; protein; 139 AA.

AC AAU7053;

DT 01-MAR-1993 (first entry)

XX Anti-CEA specific heavy chain variable region.

XX Human; carcinoembryonic antigen; heavy chain; light chain; variable;  
XX region; diagnostic; tumour; markers; targeting.

XX Mus musculus.

OS Mus

XX key Location/Qualifiers

FT Peptide 1..19  
FT /note= "signal peptide"  
FT Protein 20..139  
FT /note= "mature peptide"

PN JP04234987-A.

PD 24-AUG-1992.

PF 28-DEC-1990; 90JP-00408810.  
 XX  
 PR 28-DEC-1990; 90JP-00408810.  
 XX  
 PA (MITU ) MITSUBISHI KASEI CORP.  
 XX  
 DR WPI; 1992-327631/40.  
 DR N-PSDB; AAQ28746.  
 XX  
 PT New DNA fragments encoding variable regions of ABS specific for human CEA  
 PT - for diagnosing and monitoring tumours, as tumour markers and for  
 PT treatment of tumours.  
 XX  
 PS Disclosure; Fig 1; 7pp; Japanese.  
 XX  
 CC The anti-CEA murine monoclonal antibody heavy chain variable region was  
 CC obt'd. by screening a cDNA library prep'd. from mRNA obt'd. from hybridomas  
 CC producing anti-CEA-specific antibodies with a probe based on the constant  
 CC region of the H-chain. The antibodies reacts specifically with human CEA  
 CC and are useful as a diagnostic agents, as tumour markers for digestive  
 CC organs, for diagnosis of malignant tumours, for monitoring after cancer  
 CC operations, to follow up bloodless therapy or as therapeutic agents in  
 CC passive immune therapy and targetting therapy. See also AAR27054  
 XX  
 SQ Sequence 139 AA;

Query Match 78.1%; Score 577; DB 2; Length 139;  
 Best Local Similarity 83.0%; Pred. No. 2.3e-46;  
 Matches 117; Conservative 8; Mismatches 12; Indels 4; Gaps 3;

QY 1 MNRGFSILFLVLYKGVQCEVVVSGGFGFVKGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 DB 1 MNRGFSILFLVLYKGVQCEVVVSGGFGFVKGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 QY 61 EKRLWVATISSGSHYYPDSVKGRTISRDNAXNTLYLQMSLRSEDTAIYYCARPG- 119  
 DB 61 EKRLWVATISDGS-TYPPDSVKGRTISRDNARNLTYLQMSLRSEDTAMTYCARVHY 119  
 QY 120 YDRGAMFFDVWCAGTIVTVSS 140  
 DB 120 YDSPA--MDYMGQGTSTVTVSS 138

Search completed: May 25, 2005, 15:47:13  
 Job time : 67.8977 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 17.4512 Seconds  
(without alignments)  
598.864 Million cell updates/sec

Title: US-10-006-773A-4

Perfect score: 739  
Sequence: 1 MNFSPSLFLVLKGVCE.....DRGAFPDVWGAGTTVTSS 140

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	592	80.1	247	5	PCT-US94-07659-2
2	586.5	79.4	135	3	US-08-579-378A-16
3	581	78.6	138	2	US-08-579-057-14
4	566	76.6	135	3	US-08-579-183A-32
5	565.5	76.5	135	3	US-08-579-378A-20
6	565	76.5	136	3	US-08-579-183A-34
7	560	75.8	136	3	US-08-579-183A-33
8	559	75.6	136	3	US-08-579-183A-31
9	554	75.0	136	1	US-08-253-877C-57
10	554	75.0	136	1	US-08-452-164A-57
11	552	74.7	138	1	US-08-053-171-7
12	552	74.7	138	1	US-08-053-171-11
13	545.5	73.8	139	1	US-08-129-930B-96
14	545.5	73.8	139	3	US-08-134-346A-51
15	545.5	73.8	139	3	US-08-976-288A-96
16	538	72.8	140	3	US-08-836-561-23
17	538	72.8	140	3	US-08-434-122-23
18	538	72.8	158	2	US-08-653-402B-6
19	531	71.9	130	4	US-09-225-322B-8
20	531	71.9	130	4	US-09-225-322B-18
21	531	71.9	130	4	US-09-764-304-8
22	531	71.9	130	4	US-09-764-304-18
23	528.5	71.5	159	2	US-08-653-402B-2
24	527	71.3	119	4	US-08-875-674A-1
25	522	69.3	158	2	US-08-653-402B-10
26	512	69.3	119	4	US-08-875-674A-3
27	508	68.7	121	1	US-08-339-582-2

28	505.5	68.4	255	2	US-07-690-192-4	Sequence 4, Appl
29	504.5	68.3	123	1	US-08-356-272-3	Sequence 3, Appl
30	501	67.8	170	2	US-08-652-558-40	Sequence 40, Appl
31	496.5	67.2	135	5	PCT-US95-07302-8	Sequence 8, Appl
32	494	66.8	119	2	US-08-475-000-16	Sequence 16, Appl
33	494	66.8	119	2	US-08-483-199-16	Sequence 16, Appl
34	494	66.8	119	2	US-08-484-508-16	Sequence 16, Appl
35	491.5	66.5	135	3	US-08-619-491-8	Sequence 8, Appl
36	488	66.0	119	4	US-09-232-290-55	Sequence 55, Appl
37	487.5	66.0	463	4	US-09-472-087-4	Sequence 4, Appl
38	487.5	66.0	463	4	US-09-472-087-68	Sequence 68, Appl
39	486	65.8	123	3	US-09-344-587-13	Sequence 13, Appl
40	485.5	65.7	144	1	US-08-026-320A-2	Sequence 2, Appl
41	484.5	65.6	120	4	US-08-435-516-3	Sequence 3, Appl
42	484	65.5	142	1	US-08-305-683A-2	Sequence 2, Appl
43	483	65.4	239	2	US-08-553-497A-18	Sequence 18, Appl
44	483	65.4	464	4	US-09-472-087-2	Sequence 2, Appl
45	483	65.4	464	4	US-09-472-087-66	Sequence 66, Appl

## ALIGNMENTS

RESULT 1  
PCT-US94-07659-2  
Sequence 2, Application PC/TUS9407659  
GENERAL INFORMATION:  
APPLICANT: Young, Peter  
APPLICANT: Gross, Mitchell  
APPLICANT: Jonak, Zdenka L.  
APPLICANT: Theisen, Timothy  
APPLICANT: Harle, Mark  
APPLICANT: Jackson, Jeffrey R.  
TITLE OF INVENTION: Recombinant and Humanized IL-1 beta  
TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory  
NUMBER OF INVENTIONS: 21  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation - Corp.  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07659  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/090,534  
FILING DATE: 09-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sulton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50171-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5024  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-07659-2  
Query Match 80.1%; Score 592; DB 5; Length 247;

Best Local Similarity 82.1%; Pred. No. 4.1e-54;  
Matches 115; Conservative 9; Mismatches 14; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVLYLVKGVQCEVVVSGGFFVKPGSLKLSGCAAGFTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIFLVLYLVKGVQCEVVVSGGFFVKPGSLKLSGCAAGFTFSRYAMSWVRQTP 60  
QY 61 EKRLVAVATISSGSHHTYPPDSVKGRFTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120  
DB 61 EKRLVAVATISSGSHHTYPPDSVKGRFTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120  
QY 121 DRGAMFEDVWAGCTTVTVSS 140  
DB 121 DRGAMFEDVWAGCTTVTVSS 140

## RESULT 2

US-08-579-378A-16  
Sequence 16, Application US/08579378A  
Patent No. 6210671  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew  
STREET: One Market Plaza, Steuart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/579,378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,074  
FILING DATE: 30-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschutz, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-579-378A-16

Query Match 79.4%; Score 586.5; DB 3; Length 135;  
Best Local Similarity 83.6%; Pred. No. 7.3e-54;  
Matches 117; Conservative 9; Mismatches 9; Indels 5; Gaps 3;

QY 1 MNFGSLIFLVLYLVKGVQCEVVVSGGFFVKPGSLKLSGCAAGFTFSRYAMSWVRQTP 60

DB 1 MNFGSLIFLVLYLVKGVQCEVVVSGGFFVKPGSLKLSGCAAGFTFSRYAMSWVRQTP 60

QY 61 EKRLVAVATISSGSHHTYPPDSVKGRFTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120  
DB 61 EKRLVAVATISSGSHHTYPPDSVKGRFTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120  
QY 121 DRGAMFEDVWAGCTTVTVSS 140  
DB 121 DRGAMFEDVWAGCTTVTVSS 140

## RESULT 3

US-08-379-057-14  
Sequence 14, Application US/08379057  
Patent No. 5876950  
GENERAL INFORMATION:  
APPLICANT: Siadak, Anthony W.  
APPLICANT: Hollenbaugh, Diane L.  
APPLICANT: Gilliland, Lisa K.  
APPLICANT: Gordon, Marcia L.  
APPLICANT: Bajorath, Jürgen  
APPLICANT: Aruffo, Alejandro A.  
TITLE OF INVENTION: Monoclonal Antibodies Specific for  
TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods for Their Use  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: 3005 First Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,057  
FILING DATE: 26-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Poor, Brian W.  
REGISTRATION NUMBER: 32,928  
REFERENCE/DOCKET NUMBER: ONO133-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 727-3670  
TELEFAX: (206) 727-3601  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
US-08-379-057-14

Query Match 78.6%; Score 581; DB 2; Length 138;  
Best Local Similarity 81.4%; Pred. No. 2.8e-53;  
Matches 114; Conservative 10; Mismatches 14; Indels 2; Gaps 2;

QY 1 MNFGSLIFLVLYLVKGVQCEVVVSGGFFVKPGSLKLSGCAAGFTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIFLVLYLVKGVQCEVVVSGGFFVKPGSLKLSGCAAGFTFSRYAMSWVRQTP 60

QY 61 EKRLVAVATISSGSHHTYPPDSVKGRFTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120  
DB 61 EKRLVAVATISSGSHHTYPPDSVKGRFTISRDNAKNTLYLQMSLSRSEDTAIYYCARPGY 120

QY 121 DRGAMFEDVWAGCTTVTVSS 140

DB 119 DYDSYAMDYMGQTSVTWSS 138

RESULT 4

US-08-976-183A-32  
 ; Sequence 32, Application US/08976183A  
 ; Patent No. 6307026  
 ; GENERAL INFORMATION:  
 ; APPLICANT: King, David J.  
 ; APPLICANT: Adair, John R.  
 ; APPLICANT: Owens, Raymond J.  
 ; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33  
 ; TITLE OF INVENTION: ANTIGEN  
 ; NUMBER OF SEQUENCES: 55  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FOLEY & LARDNER  
 ; STREET: 3000 K. Street, N.W., Suite 500  
 ; CITY: Washington, D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/976,183A  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/595,848  
 ; FILING DATE: 02-FEB-1996  
 ; APPLICATION NUMBER: PCT/GB93/02529  
 ; FILING DATE: 10-DEC-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: GB 9225853.2  
 ; FILING DATE: 10-DEC-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 9315249.4  
 ; FILING DATE: 22-JUL-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Bernhard D. Saxe  
 ; REGISTRATION NUMBER: 28,665  
 ; REFERENCE/DOCKET NUMBER: 40283/151/CARA  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 672-5300  
 ; TELEFAX: (202) 672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 32:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 136 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-976-183A-32

Query Match 76.6%; Score 566; DB 3; Length 136;

Best Local Similarity 78.5%; Pred. No. 1e-51;  
 Matches 113; Conservative 8; Mismatches 11; Indels 12; Gaps 2;

QY 1 MNFGSLFLVLYLVKGVCEVVVSGGPFVKPGSLKSLSCAAAGTFPSRYMSWVRQRP 60  
 DB 1 MNFGSLFLVLYLVKGVCEVVVSGGPFVKPGSLKSLSCAAAGTFPSRYMSWVRQRP 60  
 QY 61 EKRLKLVATISSGSGHTYYPDSVKGKFTISRDNKNTLYLQMSLSRSEDTAIYYCAR--- 117  
 DB 61 EKRLKLVATISSGSGHTYYPDSVKGKFTISRDNKNTLYLQMSLSRSEDTAIYYCAR--- 117  
 QY 118 -PGYDRGAMFPDVMGAGTIVTVSS 140  
 DB 121 VP-----PAYMGQGLTVTVSA 136

RESULT 5

US-08-579-378A-20  
 ; Sequence 20, Application US/08579378A  
 ; Patent No. 6210671  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Co, Man Sung  
 ; TITLE OF INVENTION: Humanized Antibodies Reactive with  
 ; TITLE OF INVENTION: L-Selectin  
 ; NUMBER OF SEQUENCES: 20  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew  
 ; STREET: One Market Plaza, Stewart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/579,378A  
 ; FILING DATE: 27-DEC-1995  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/160,074  
 ; FILING DATE: 30-NOV-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/983,946  
 ; FILING DATE: 01-DEC-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 95112895.8  
 ; FILING DATE: 17-AUG-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 95114696.8  
 ; FILING DATE: 19-SEP-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Liebscheut, Joe O.  
 ; REGISTRATION NUMBER: 37,505  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-326-2400  
 ; TELEFAX: 415-326-2422  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 135 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-579-378A-20

Query Match 76.5%; Score 565.5; DB 3; Length 135;

Best Local Similarity 80.7%; Pred. No. 1.2e-51;  
 Matches 113; Conservative 10; Mismatches 12; Indels 5; Gaps 3;

QY 1 MNFGSLFLVLYLVKGVCEVVVSGGPFVKPGSLKSLSCAAAGTFPSRYMSWVRQRP 60  
 DB 1 MNFGSLFLVLYLVKGVCEVVVSGGPFVKPGSLKSLSCAAAGTFPSRYMSWVRQRP 60  
 QY 61 EKRLKLVATISSGSGHTYYPDSVKGKFTISRDNKNTLYLQMSLSRSEDTAIYYCARPGY 120  
 DB 61 GKGLKLVATISSGSGHTYYPDSVKGKFTISRDNKNTLYLQMSLSRSEDTAIYYCAR-DY 118  
 QY 121 DRGAMFPDVMGAGTIVTVSS 140  
 DB 119 D---GYFDYMGQGLTVTVSS 135

RESULT 6

US-08-976-183A-34  
 ; Sequence 34, Application US/08976183A  
 ; Patent No. 6307026

```

; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; City: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183a-34

Query Match          76.5%; Score 565; DB 3; Length 136;
Best Local Similarity 77.8%; Pred. No. 1,3e-51;
Matches 112; Conservative 9; Mismatches 11; Indels 12; Gaps 2;

QY 1 MNFGSLIFLVYLKGVQCEVVVSSGGGFVXPGSLKLSCAAGFTFSRYAMSWVRQTP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MNFGSLIFLVYLKGVQCEVVVSSGGGFVXPGSLKLSCAAGFTFSRYAMSWVRQTP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 EKRLWVAITSSGGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSDTAIYYCAR--- 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EKRLWVAITSSGGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSDTAIYYCAPTTV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 -PGYDRGAMFEDVWGAGTTVTVSS 140
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 VP-----FAYWGQGLTVTVSA 136
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
US-08-976-183a-33
; Sequence 33, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
```

```

; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K. Street, N.W., Suite 500
; City: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,183A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,848
; FILING DATE: 02-FEB-1996
; APPLICATION NUMBER: PCT/GB93/02529
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9225853.2
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9315249.4
; FILING DATE: 22-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Bernhard D. Saxe
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 40283/151/CARA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-976-183a-33

Query Match          75.8%; Score 560; DB 3; Length 136;
Best Local Similarity 77.8%; Pred. No. 4.4e-51;
Matches 112; Conservative 8; Mismatches 12; Indels 12; Gaps 2;

QY 1 MNFGSLIFLVYLKGVQCEVVVSSGGGFVXPGSLKLSCAAGFTFSRYAMSWVRQTP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MNFGSLIFLVYLKGVQCEVVVSSGGGFVXPGSLKLSCAAGFTFSRYAMSWVRQTP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 EKRLWVAITSSGGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSDTAIYYCAR--- 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EKRLWVAITSSGGSHYTPDSYKGRFTISRDNKNTLYLQMSLSRSDTAIYYCAPTTV 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 118 -PGYDRGAMFEDVWGAGTTVTVSS 140
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 VP-----FAYWGQGLTVTVSA 136
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
US-08-976-183a-31
; Sequence 31, Application US/08976183A
; Patent No. 6307026
; GENERAL INFORMATION:
; APPLICANT: King, David J.
; APPLICANT: Adair, John R.
; APPLICANT: Owens, Raymond J.
; TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33
```

```

NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLLEY & LARDNER
STREET: 3000 K. Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976, 183A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/595, 848
FILING DATE: 02-FEB-1996
APPLICATION NUMBER: PCT/GB93/02529
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9225853.2
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9315249.4
FILING DATE: 22-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bernhard D. Saxe
REGISTRATION NUMBER: 28, 665
REFERENCE/DOCKET NUMBER: 40283/151/CARA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ. ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 136 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-976-183A-31

Query Match      75.6%; Score 559; DB 3; Length 136;
Best Local Similarity 77.1%; Pred. No. 5, 6e-51;
Matches 111; Conservative 9; Mismatches 12; Indels 12; Gaps 2

Qy      1 MNFGSLFLVLVLRKGVCEVVWSSGGFFYKPPGSLKSCAAAGTFESRYAMSWRRQP 60
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 MNFGSLFLVLILRGVCEVLVSBSGGGLVRPGSLKSCAASGAFESTYMSWRQP 60
Qy      61 EKRLFWVTISSGSHTYVPDSVKRFTISRDNANKTVLLOMSLRSEPTAIYYCAR--- 117
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 EKRLFWVTISSGSYTYLLDYSVKGRFTISRDSARNTLYLONSLRSEDPAIYYCAPTTV 120
Qy      118 -PGYDRGAMFPDVWGAGTIVYSS 140
        |-----|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      121 VP-----FAVWGQGLTLVTYSA 136
        |-----|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 9
US-08-253-877C-57
Sequence 57, Application US/08253877C
Patent No. 5773001
GENERAL INFORMATION:
APPLICANT: Hamann, Philip R.
APPLICANT: Hinman, Lois
APPLICANT: Hollander, Irwin
APPLICANT: Holcomb, Ryan
APPLICANT: Halleck, William
APPLICANT: Tseou, Hwei-Ru
APPLICANT: Weiss, Martin J.
TITLE OF INVENTION: Conjugates of Methylylritibio Antitumor

```

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1  TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
2
3  NUMBER OF SEQUENCES: 73
4
5  CORRESPONDENCE ADDRESS:
6
7  ADDRESSEE: American Cyanamid Company
8
9  STREET: One Cyanamid Plaza
10
11 CITY: Wayne
12
13 STATE: New Jersey
14
15 COUNTRY: U.S.A.
16
17 ZIP: 07470-8426
18
19 COMPUTER READABLE FORM:
20
21 MEDIUM TYPE: Floppy disk
22
23 COMPUTER: IBM PC compatible
24
25 OPERATING SYSTEM: PC-DOS/MS-DOS
26
27 SOFTWARE: Patentin Release #1.0, Version #1.30
28
29 CURRENT APPLICATION DATA:
30
31 APPLICATION NUMBER: US/08/253,877C
32
33 FILING DATE: 03-JUN-1994
34
35 CLASSIFICATION: 424
36
37 ATTORNEY/AGENT INFORMATION:
38
39 NAME: Barnhard, Elizabeth M.
40
41 REGISTRATION NUMBER: 31,088
42
43 REFERENCE/DOCKET NUMBER: 32,368
44
45 TELECOMMUNICATION INFORMATION:
46
47 TELEPHONE: 201-831-3246
48
49 TELEFAX: 201-831-3305
50
51 INFORMATION FOR SEQ ID NO: 57:
52
53 SEQUENCE CHARACTERISTICS:
54
55 LENGTH: 136 amino acids
56
57 TYPE: amino acid
58
59 TOPOLOGY: linear
60
61 MOLECULE TYPE: protein
62
63 US-08-253-877C-57

```

```

Query March 75.0%: Score 554; DB 1; Length 136;
Best Local Similarity 76.4%: Pred. No. 1.9e-50;
Matches 110; Conservative 9; Mismatches 13; Indels 12; Gaps 2

Cy 1 MNFGSLFLVLVYKGVCEVWVSSGGFVYKPGSLKLSCAAAGFTSRVMSWYRQT 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MNFGSLFLVLILKGVCEVWVSSGGGLVYKPGSLKLSCAAASFAPSTYMSWYRQT 60

Cy 61 EKRLWVATISSGSHYYPDSVKGRFTISRDNANNTLYLQSSLRSEDTAIYCAR--- 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 EKRLWVATISSGSHYTYLDSVKGRFTISRDSRNTLYLQSSLRSEDTAIYCAPTV 120

Db 118 -PGYDRGAMFPDWGAGCTTVYSS 140
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:
121 VP-----FAYWQGGTLVTVA 136

RESULT 10
US-08-452-164A-57
: Sequence 57, Application US/08452164A
: Patent No. 5877296
: GENERAL INFORMATION:
: APPLICANT: Hamann, Philip R.
: APPLICANT: Hinman, Lois
: APPLICANT: Hollander, Irwin
: APPLICANT: Holcomb, Ryan
: APPLICANT: Halleck, William
: APPLICANT: Tsou, Hwei-Ru
: APPLICANT: Weiss, Martin J.
: TITLE OF INVENTION: Conjugates of Methylcrithio Antitumor
: TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
: NUMBER OF SEQUENCES: 73
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: American Home Products Corporation
: STREET: One Campus Drive
: CITY: Parsippany
: STATE: New Jersey
: COUNTRY: U.S.A.
: ZIP: 07054
: COMPUTER READABLE FORM:

```

MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,164A  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2158  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-452-164A-57

Query Match 75.0%; Score 554; DB 2; Length 136;  
Best Local Similarity 76.4%; Pred. No. 1,9e-50;  
Matches 110; Conservative 9; Mismatches 13; Indels 12; Gaps 2;

QY 1 MNFGSLIPVLVILKGVCEVVVVGSGGFVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIPVLVILKGVCEVVLKVGCEVKLVESGGGLVQPGSLKLSCTSGFTFSRYAMSWVRQTP 60  
QY 61 EKLEWVATISSGSHYTPDSVKGRTISRDNKNTLYLQMSLSRSEDTAIYYCAR-- 117  
DB 61 EKLEWVATISSGSHYTPDSVKGRTISRDNKNTLYLQMSLSRSEDTAIYYCARPTTV 120  
QY 118 -PGYDNGAMFFDVWGAATTVTSS 140  
DB 121 VP-----FAYWGGTLVTVSA 136

RESULT 11  
US-08-053-171-7  
Sequence 7, Application US/08053171  
Patent No. 5562903  
GENERAL INFORMATION:  
APPLICANT: Co. Loibner  
TITLE OF INVENTION: Antibody Derivatives  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,171  
FILING DATE: 22-APR-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-54-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:

LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-053-171-7

Query Match 74.7%; Score 552; DB 1; Length 138;  
Best Local Similarity 78.6%; Pred. No. 3.1e-50;  
Matches 110; Conservative 9; Mismatches 19; Indels 2; Gaps 2;

QY 1 MNFGSLIPVLVILKGVCEVVVVGSGGFVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIPVLVILKGVCEVVLKVGCEVKLVESGGGLVQPGSLKLSCTSGFTFSRYAMSWVRQTP 60  
QY 61 EKLEWVATISSGSHYTPDSVKGRTISRDNKNTLYLQMSLSRSEDTAIYYCARPGY 120  
DB 61 EKLEWVATISSGSHYTPDSVKGRTISRDNKNTLYLQMSLSRSEDTAIYYHCAH-CM 119  
QY 121 DRGAMFFDVWGAATTVTSS 140  
DB 120 DYGAW-FAYWGGTLVTVSA 138

RESULT 12  
US-08-053-171-11  
Sequence 11, Application US/08053171  
Patent No. 5562903

GENERAL INFORMATION:  
APPLICANT: Co. Loibner  
TITLE OF INVENTION: Antibody Derivatives  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,171  
FILING DATE: 22-APR-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-54-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-053-171-11

Query Match 74.7%; Score 552; DB 1; Length 138;  
Best Local Similarity 78.6%; Pred. No. 3.1e-50;  
Matches 110; Conservative 9; Mismatches 19; Indels 2; Gaps 2;

QY 1 MNFGSLIPVLVILKGVCEVVVVGSGGFVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIPVLVILKGVCEVVLKVGCEVKLVESGGGLVQPGSLKLSCTSGFTFSRYAMSWVRQTP 60  
QY 61 EKLEWVATISSGSHYTPDSVKGRTISRDNKNTLYLQMSLSRSEDTAIYYCARPGY 120  
DB 61 EKLEWVATISSGSHYTPDSVKGRTISRDNKNTLYLQMSLSRSEDTAIYYHCAH-CM 119

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Qy      121 DRGAEFFDVWGACTVTSS 140
          |||| | ||| ||||:
Db      120 DYGAW-FAVWGQGLTVSA 138
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RESULT 13  
US-08-129-930B-96  
; Sequence 96, Application US/08129930B  
; Date: 08-12-2008 10:50:18

1 GENERAL INFORMATION:  
2 APPLICANT: do Couto Dr., Fernando J.R.  
3 APPLICANT: Ceriani Dr., Roberto L.  
4 APPLICANT: Peterson Dr., Jerry A.  
5 APPLICANT: Padian Dr., Eduardo A.  
6 TITLE OF INVENTION: Analogue Peptides With Broad  
7 TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
8 TITLE OF INVENTION: diagnostic Vaccination and  
9 TITLE OF INVENTION: therapeutic Methods  
10 NUMBER OF SEQUENCES: 96  
11 CORRESPONDENCE ADDRESS: 96

Query Match	73.8%	Score 545.5	DB 1	Length 139
Best Local Similarity	74.3%	Pred. No. 1.5e-49		
Matches 104	Conservative 14	Mismatches 21	Indels 1	Gaps 1

RESULT 14  
US-08-134-346A-51  
; Sequence 51, Application US/08134346A  
; Patent No. 6281335

```

? GENERAL INFORMATION:
? APPLICANT: do Couto, F.J.R.
? APPLICANT: Ceriani, R.L.C.
? APPLICANT: Petersen, O.A.
? TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED
? TITLE OF INVENTION: MONOCLONAL ANTIBODY AND DNA AND RNA ENCODING IT, KIT AND
? TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
? NUMBER OF SEQUENCES: 51
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Oestrager, Chong & Flaherty
? STREET: 300 Park Avenue
? CITY: New York
? STATE: NY
? COUNTRY: US
? ZIP: 10022-7499
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette-3.50 inch, 1.44 Mb storage
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/134,346A
? FILING DATE: 08-OCT-1993
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Onofrio, Dara L.
? REGISTRATION NUMBER: 34,889
? REFERENCE/DOCKET NUMBER: CIT 149,608
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 212-826-5909
? TELEFAX: 212-826-5909
? INFORMATION FOR SEQ ID NO: 51:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 139 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-134-346A-51

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Query Match	73.8%;	Score 545.5;	DB 3;	Length 139;
Best Local Similarity	74.3%;	Pred. No. 1.5e-49;		
Matches 104;	Conservative 14;	Mismatches 21;	Indels 1;	Gaps 1

RESULT 15  
 US-08-976-288A-96  
 , Sequence 96, Application US/08976288A  
 , Patent No. 631597  
 , GENERAL INFORMATION:  
 , APPLICANT: do Couto Dr., Fernando J.R.  
 , APPLICANT: Certani Dr., Roberto L.  
 , APPLICANT: Peterson Dr., Jerry A.  
 , APPLICANT: Padlan Dr., Eduardo A.  
 , TITLE OF INVENTION: Analogue Peptides With Broad  
 , TITLE OF INVENTION: Carcinoma Specificity, and Kit and  
 , TITLE OF INVENTION: Diagnostic Vaccination and  
 , TITLE OF INVENTION: Therapeutic Methods  
 , NUMBER OF SEQUENCES: 96  
 , CORRESPONDENCE ADDRESS:  
 , ADDRESSEE: Pretty, Schroeder & Poplawski





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## OM protein - protein search, using bw model

Run on: May 25, 2005, 15:37:58 ; Search time 64.5954 Seconds  
(without alignments)  
724.991 Million cell updates/sec

Title: US-10-006-773a-4

Perfect score: 739  
Sequence: 1 MNFGSLFLVLVLAGVQCE.....DRGAMFDVWGAGTTVTSS 140

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09C\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	739	100.0	140	13	US-10-006-773-4
2	605	81.9	462	14	US-10-281-479A-23
3	605	81.9	462	14	US-10-286-132A-23
4	605	81.9	464	14	US-10-275-180A-23
5	587	79.4	140	9	US-09-286-240-4
6	581	78.6	144	9	US-09-881-823-12
7	573.5	77.6	137	9	US-09-423-800-76
8	573.5	77.6	137	14	US-10-337-981-76
9	559	75.6	138	14	US-10-010-942B-4
10	559	75.6	138	15	US-10-388-389-4
11	559	75.6	138	16	US-10-703-713-4
12	559	75.6	138	16	US-10-704-070-4
13	559	75.6	138	17	US-10-233-030-4

14	553.5	74.9	139	13	US-10-006-773-17	Sequence 17, Appl
15	553	74.8	158	15	US-10-226-795-32	Sequence 32, Appl
16	550.5	74.5	133	13	US-10-006-773-9	Sequence 9, Appl
17	545.5	73.8	139	10	US-09-947-839-96	Sequence 96, Appl
18	545	73.7	138	14	US-10-010-942B-12	Sequence 12, Appl
19	545	73.7	138	15	US-10-388-389-12	Sequence 12, Appl
20	545	73.7	138	16	US-10-703-713-12	Sequence 12, Appl
21	545	73.7	138	16	US-10-704-070-12	Sequence 12, Appl
22	545	73.7	138	17	US-10-233-030-12	Sequence 12, Appl
23	543	73.5	138	14	US-10-010-942B-8	Sequence 8, Appl
24	543	73.5	138	15	US-10-388-389-8	Sequence 8, Appl
25	543	73.5	138	16	US-10-703-713-8	Sequence 8, Appl
26	543	73.5	138	16	US-10-704-070-8	Sequence 8, Appl
27	543	73.5	138	17	US-10-233-030-8	Sequence 8, Appl
28	540	73.1	470	15	US-10-038-591-46	Sequence 46, Appl
29	539	72.9	468	17	US-10-476-265-20	Sequence 20, Appl
30	538	72.8	140	14	US-10-283-349-23	Sequence 23, Appl
31	534.5	72.3	177	16	US-10-693-629-64	Sequence 64, Appl
32	534	72.3	121	15	US-10-276-939-3	Sequence 3, Appl
33	532	72.0	138	9	US-09-796-744-15	Sequence 15, Appl
34	532	72.0	138	14	US-10-231-452-62	Sequence 62, Appl
35	532	72.0	133	15	US-10-291-265-427	Sequence 427, App
36	531	71.9	130	9	US-09-764-304-8	Sequence 8, Appl
37	531	71.9	130	9	US-09-764-304-18	Sequence 18, Appl
38	531	71.9	130	14	US-10-265-713-8	Sequence 8, Appl
39	531	71.9	130	14	US-10-265-713-18	Sequence 18, Appl
40	531	71.9	130	14	US-10-166-626-8	Sequence 8, Appl
41	531	71.9	130	14	US-10-166-626-18	Sequence 18, Appl
42	530.5	71.8	137	9	US-09-423-800-77	Sequence 77, Appl
43	530.5	71.8	137	14	US-10-337-981-77	Sequence 77, Appl
44	530	71.7	143	15	US-10-469-304-17	Sequence 17, Appl
45	530	71.7	159	15	US-10-291-265-333	Sequence 333, App

## ALIGNMENTS

RESULT 1  
US-10-006-773-4  
Sequence 4, Application US/10006773  
Publication No. US20020132983A1  
GENERAL INFORMATION:  
APPLICANT: Junghans, Richard P.  
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Ant.  
FILE REFERENCE: 003  
CURRENT APPLICATION NUMBER: US/10/006,773  
PRIOR FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: 60/250,089  
PRIOR FILING DATE: 2000-11-30  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 140  
TYPE: PRT  
ORGANISM: Mus sp.  
US-10-006-773-4

Query Match	100.0%	Score 739,	DB 13,	Length 140,
Best Local Similarity	100.0%	Pred. No. 2.3e-61,		
Matches 140,	Conservative 0,	Mismatches 0,	Indels 0,	Gaps 0,
QY	1	MNFGSLFLVLVLAGVQCEVVVSSGGGFFKPGGSLKSCAAAGTFSRYMSWRQRP	60	
DB	1	MNFGSLFLVLVLAGVQCEVVVSSGGGFFKPGGSLKSCAAAGTFSRYMSWRQRP	60	
QY	61	ERLEWVATISSGSHHTYPPDSVKGRFTTSDNNAKTYLYLQWSSLRSEDTAIYCARPGY	120	
DB	61	ERLEWVATISSGSHHTYPPDSVKGRFTTSDNNAKTYLYLQWSSLRSEDTAIYCARPGY	120	
QY	121	DRGAMFDVWGAGTTVTSS 140		
DB	121	DRGAMFDVWGAGTTVTSS 140		

RESULT 2  
US-10-281-479A-23  
; Sequence 23, Application US/10281479A  
; Publication No. US2003013932A1  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Ichikawa, Kimihisa  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; APPLICANT: Oshumi, Jun  
; APPLICANT: Lobuglio, Albert S.  
; APPLICANT: Buchsbaum, Donald J.  
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS  
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER  
; TITLE OF INVENTION: AGENTS  
; FILE REFERENCE: 21085.002906  
; CURRENT APPLICATION NUMBER: US/10/281,479A  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: 60/391,478  
; PRIOR FILING DATE: 2002-06-24  
; PRIOR APPLICATION NUMBER: 60/346,402  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/14151  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,344  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 462  
; TYPE: PR  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US2003013932A1e = Synthe  
US-10-281-479A-23

Query Match 81.9%; Score 605; DB 14; Length 462;  
Best Local Similarity 85.0%; Pred. No. 2,8e-48;  
Matches 119; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVLVKGVQCEVVVVESSGGFVKPGSLKLSCAAAGTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIFLVLVKGVQCEVMLVESGGGLVKPGSLKLSCAAAGTFSRYAMSWVRQTP 60  
QY 61 EKRLWVATISSGSGSHYYPDYSVKGRTISRDNAAKNTLYLQMSLSRSEDTAIYYCARPGY 120  
DB 61 EKRLWVATISSGSGSHYYPDYSVKGRTISRDNAAKNTLYLQMSLSRSEDTAIYYCARPGY 119  
QY 121 DRGAMFDDVWAGCTTVTVSS 140  
DB 120 -DSMITTDYWGQGTTLTVSS 138

RESULT 3  
US-10-286-132A-23  
; Sequence 23, Application US/10286132A  
; Publication No. US20030198637A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhou, Tong  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; APPLICANT: Lobuglio, Albert S.  
; APPLICANT: Buchsbaum, Donald J.  
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED  
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF  
; FILE REFERENCE: 21085.002907  
; CURRENT APPLICATION NUMBER: US/10/286,132A  
; CURRENT FILING DATE: 2003-01-22  
; PRIOR APPLICATION NUMBER: US 60/346,402  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: PCT/US01/14151

; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: US 60/201,344  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 462  
; TYPE: PR  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synth.  
US-10-286-132A-23

Query Match 81.9%; Score 605; DB 14; Length 462;  
Best Local Similarity 85.0%; Pred. No. 2,8e-48;  
Matches 119; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVLVKGVQCEVVVVESSGGFVKPGSLKLSCAAAGTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIFLVLVKGVQCEVMLVESGGGLVKPGSLKLSCAAAGTFSRYAMSWVRQTP 60  
QY 61 EKRLWVATISSGSGSHYYPDYSVKGRTISRDNAAKNTLYLQMSLSRSEDTAIYYCARPGY 120  
DB 61 EKRLWVATISSGSGSHYYPDYSVKGRTISRDNAAKNTLYLQMSLSRSEDTAIYYCARPGY 119  
QY 121 DRGAMFDDVWAGCTTVTVSS 140  
DB 120 -DSMITTDYWGQGTTLTVSS 138

RESULT 4  
US-10-275-180A-23  
; Sequence 23, Application US/10275180A  
; Publication No. US20030190687A1  
; GENERAL INFORMATION:  
; APPLICANT: The UAB Research Foundation  
; APPLICANT: Zhou, Tong  
; APPLICANT: Ichikawa, Kimihisa  
; APPLICANT: Kimberly, Robert P.  
; APPLICANT: Koopman, William J.  
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTO  
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF  
; FILE REFERENCE: 21085.002905  
; CURRENT APPLICATION NUMBER: US/10/275,180A  
; CURRENT FILING DATE: 2002-10-31  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 23  
; LENGTH: 464  
; TYPE: PR  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =  
US-10-275-180A-23

Query Match 81.9%; Score 605; DB 14; Length 464;  
Best Local Similarity 85.0%; Pred. No. 2,8e-48;  
Matches 119; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVLVKGVQCEVVVVESSGGFVKPGSLKLSCAAAGTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIFLVLVKGVQCEVMLVESGGGLVKPGSLKLSCAAAGTFSRYAMSWVRQTP 60  
QY 61 EKRLWVATISSGSGSHYYPDYSVKGRTISRDNAAKNTLYLQMSLSRSEDTAIYYCARPGY 120  
DB 61 EKRLWVATISSGSGSHYYPDYSVKGRTISRDNAAKNTLYLQMSLSRSEDTAIYYCARPGY 119  
QY 121 DRGAMFDDVWAGCTTVTVSS 140  
DB 120 -DSMITTDYWGQGTTLTVSS 138



Query Match 77.6%; Score 573.5; DB 14; Length 137;  
Best Local Similarity 78.6%; Pred. No. 6.6e-46;  
Matches 110; Conservative 11; Mismatches 16; Indels 3; Gaps 1;

QY 1 MNFGSLIFLVYLKGVQCEVVVVESSGGGFVFKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIFLVYLKGVQCEVVVVESSGGGLVKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60

QY 61 EKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSASEDTAIYYCARPGY 120  
DB 61 DKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSASEDTAIYYCARPGY 117

QY 121 DRGAMFPDVWAGATTVTSS 140  
DB 118 QTTMTYFAYWGGTTLVTSSA 137

RESULT 9  
US-10-010-942B-4  
; Sequence 4, Application US/10010942B  
; Publication No. US20030165496A1  
; GENERAL INFORMATION:  
; APPLICANT: Baai, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE  
; FILE REFERENCE: ELN-002  
; CURRENT APPLICATION NUMBER: US/10/010,942B  
; CURRENT FILING DATE: 2002-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(19)  
US-10-010-942B-4

Query Match 75.6%; Score 559; DB 14; Length 138;  
Best Local Similarity 77.9%; Pred. No. 1.5e-44;  
Matches 109; Conservative 9; Mismatches 20; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVYLKGVQCEVVVVESSGGGFVFKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIFLVYLKGVQCEVVVVESSGGGLVKPGSLKLSCAAAGFTFSRYAMSWVRQNS 60

QY 61 EKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSASEDTAIYYCARPGY 120  
DB 61 DKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSASEDTAIYYCARPGY 118

QY 121 DRGAMFPDVWAGATTVTSS 140  
DB 119 DHYSGSSDYWGGTTLVTSS 138

RESULT 10  
US-10-388-389-4  
; Sequence 4, Application US/10388389  
; Publication No. US2004008777A1  
; GENERAL INFORMATION:  
; APPLICANT: Baai, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE  
; FILE REFERENCE: ELN-002CD  
; CURRENT APPLICATION NUMBER: US/10/388,389  
; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(19)  
US-10-388-389-4

Query Match 75.6%; Score 559; DB 15; Length 138;  
Best Local Similarity 77.9%; Pred. No. 1.5e-44;  
Matches 109; Conservative 9; Mismatches 20; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVYLKGVQCEVVVVESSGGGFVFKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIFLVYLKGVQCEVVVVESSGGGLVKPGSLKLSCAAAGFTFSRYAMSWVRQNS 60

QY 61 EKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSASEDTAIYYCARPGY 120  
DB 61 DKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSASEDTAIYYCARPGY 118

QY 121 DRGAMFPDVWAGATTVTSS 140  
DB 119 DHYSGSSDYWGGTTLVTSS 138

RESULT 11  
US-10-703-713-4  
; Sequence 4, Application US/10703713  
; Publication No. US20040171815A1  
; GENERAL INFORMATION:  
; APPLICANT: Baai, Gurig  
; APPLICANT: Saldanha, Jose  
; APPLICANT: Vednock, Ted  
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE  
; FILE REFERENCE: ELN-002CD  
; CURRENT APPLICATION NUMBER: US/10/703,713  
; CURRENT FILING DATE: 2003-11-07  
; PRIOR APPLICATION NUMBER: US/10/388,389  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 10/010,942  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: US 60/251,892  
; PRIOR FILING DATE: 2000-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: (1)...(19)  
US-10-703-713-4

Query Match 75.6%; Score 559; DB 16; Length 138;  
Best Local Similarity 77.9%; Pred. No. 1.5e-44;  
Matches 109; Conservative 9; Mismatches 20; Indels 2; Gaps 1;

QY 1 MNFGSLIFLVYLKGVQCEVVVVESSGGGFVFKPGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
DB 1 MNFGSLIFLVYLKGVQCEVVVVESSGGGLVKPGSLKLSCAAAGFTFSRYAMSWVRQNS 60

QY 61 EKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSASEDTAIYYCARPGY 120  
DB 61 DKRLWVATISSGSGSHYTPDSYKGRFTISRDNKNTLYLQMSLSASEDTAIYYCARPGY 118

RESULT 15  
US-10-226-795-32  
; Sequence 32, Application US/10226795  
; Publication No. US20040053865A1  
; GENERAL INFORMATION:  
; APPLICANT: HART, MARY KATE  
; APPLICANT: WILSON, JULIE

```

1 TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
2   TITLE OF INVENTION: REGIONS BINDING TO EBOLA GLYCOPROTEIN
3   FILE REFERENCE: ARMY 166
4   CURRENT APPLICATION NUMBER: US/10/226,795
5   CURRENT FILING DATE: 2002-11-18
6   NUMBER OF SEQ ID NOS: 40
7   SOFTWARE: PatentIn Ver. 2.1
8   SEQ ID NO 32
9   LENGTH: 158
10  TYPE: PRT
11  ORGANISM: Artificial Sequence
12  FEATURE:
13  OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
14  OTHER INFORMATION: chain of Mab Egp13p6-1-2 amino acid sequence
15  US-10-226-795-32

```

Query Match	74.8%	Score 553	DB 15	Length 158
Best Local Similarity	76.1%	Pred. No. 6.4e-44		
Match 108	Conservative 11	Mismatches 21	Indels 2	Gaps 1

  

QY	1	MNFGSLILFLVILKGVQCEVNVVSSGGGFKYKPGSKLKLSCAAAGFTFSRYAMSVWRQTP	60
	:		
DB	1	MELGSMWIFVLVLTLKGVKCEVNVVSSGGGLVKPGSKLKLSCAASFAFVSSVDMVWRQTP	60
	:		
QY	61	EKLELWVATLISGSHHTYPPDSVYKGRFTISRDNANKTLYLQMSLRSDTALYYCARPGY	120
	:		
DB	61	EKRLWVAVYISRGGGYTYPPDVKGRFTISRDNANKTLYLQMSLRSDTALYYCSRAIY	120
	:		
QY	121	DRGAMFF--DVMGAGTIVTSS	140
	:		
DB	121	YGSSHTYAMDYWGQGTIVTSS	142

Search completed: May 25, 2005, 16:06:49  
Job time : 68.7204 secs



A/Note: the authors translated the codon GAG for residue 117 as Lys  
 A/Note: the sequence of residues 134-139 and the corresponding nucleotide sequence are  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 F/34-116/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 583.5; DB 2; Length 139;  
 Best Local Similarity 82.1%; Pred. No. 7.2e-45;  
 Matches 115; Conservative 8; Mismatches 14; Indels 3; Gaps 2;  
 QY 1 MNFGSLIFLVLYLVKVGQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 DB 1 MNFGSLIFLVLYLVKVGQCEVKGESGGLVKGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 QY 61 EKRLWVATISSGSGSHYTPDSYKGRFTISRDNAAKNTLYLQMSLSRSEDTAIYYCARP- 119  
 DB 61 EKRLWVASISRGST-TYYPDSYKGRFTISRDNAAKNTLYLQMSLSRSEDTAIYYCARP- 119  
 QY 120 -YDRGAMFPDVGAGTTVTV 138  
 DB 120 YYGVALYGMDDYMGQGTSTVT 139

## RESULT 3

Ig heavy chain precursor V region (5-27) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 16-Aug-1996  
 C/Accession: C34903  
 R/Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
 J. Biol. Chem. 265, 133-138, 1990  
 A/Title: Active site structure and antigen binding properties of idiotypically cross-re-  
 A/Reference number: A34903; MUID:90094387; PMID:2104617  
 A/Accession: C34903  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-142 <BED>  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/34-119/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 578; DB 2; Length 142;  
 Best Local Similarity 79.6%; Pred. No. 2.3e-44;  
 Matches 113; Conservative 8; Mismatches 19; Indels 2; Gaps 1;  
 QY 1 MNFGSLIFLVLYLVKVGQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 DB 1 MNFGSLIFLVLYLVKVGQCEVKGESGGLVKGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 QY 61 EKRLWVATISS-GSGSHYTPDSYKGRFTISRDNAAKNTLYLQMSLSRSEDTAIYYCARP 118  
 DB 61 EKRLWVASFGNKPRTYGRFTYTPDSYKGRFTISRDNAAKNTLYLQMSLSRSEDTAIYYCARP 120  
 QY 119 GYDRGAMFPDVGAGTTVTVSS 140  
 DB 121 GYYGGYGFAYMGQGLTVTVSA 142

## RESULT 4

Ig heavy chain precursor V region (MAK3) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 23-Jul-1999  
 C/Accession: B26471; S70410  
 R/Buckel, P.; Hubner-Parajcz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.  
 Gene 51, 13-19, 1987  
 A/Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine  
 A/Reference number: A91572; MUID:87248058; PMID:3110009  
 A/Accession: B26471  
 A/Molecule type: mRNA  
 A/Residues: 1-152 <BUC>  
 A/Cross-references: GB:M16163; NID:g195405; PIDN:AAA38292.1; PID:g195406  
 J./Lebecque, S.G.; Gearhart, P.J.  
 J. Exp. Med. 172, 1717-1727, 1990

A/Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary  
 A/Reference number: S70410; MUID:91079775; PMID:2258702

A/Accession: S70410  
 A/Status: translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-119 <LEB>  
 A/Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476  
 C/Genetics: 16/1  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/1-19/Domain: signal sequence #status predicted <Sig>  
 F/20-152/Product: Ig heavy chain V region MAK3 #status predicted <Mat>  
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 77.9%; Score 576; DB 2; Length 152;  
 Best Local Similarity 81.0%; Pred. No. 3.7e-44;  
 Matches 115; Conservative 5; Mismatches 20; Indels 2; Gaps 1;  
 QY 1 MNFGSLIFLVLYLVKVGQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 DB 1 MNFGSLIFLVLYLVKVGQCEVKGESGGLVKGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 QY 61 EKRLWVATISSGSGSHYTPDSYKGRFTISRDNAAKNTLYLQMSLSRSEDTAIYYCARP- 119  
 DB 61 EKRLWVATISDGSSTYTPDSYKGRFTISRDNAAKNTLYLQMSLSRSEDTAIYYCARP- 120  
 QY 120 -YDRGAMFPDVGAGTTVTVSS 140  
 DB 121 YGNYGDAMDYMGQGTSTVT 142

## RESULT 5

Ig heavy chain V region - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C/Accession: S31666  
 R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.  
 submitted to the EMBL Data Library, June 1992  
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A/Reference number: S31585  
 A/Accession: S31666  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-138 <CUI>  
 A/Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.3%; Score 542; DB 2; Length 136;  
 Best Local Similarity 72.5%; Pred. No. 3.5e-41;  
 Matches 103; Conservative 14; Mismatches 19; Indels 6; Gaps 2;  
 QY 1 MNFGSLIFLVLYLVKVGQCEVVVSGGFGVFKPGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 DB 1 MERGLWLFVLYLVKVGQCEVQLBSGGGLVKGSGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 QY 61 EKRLWVATISSGSGSHYTPDSYKGRFTISRDNAAKNTLYLQMSLSRSEDTAIYYCARP- 118  
 DB 61 GKRLWVASISGSGSTYVADSVKGRFTISRDNAAKNTLYLQMSLSRSEDTAIYYCARP- 120  
 QY 119 GYDRGAMFPDVGAGTTVTVSS 140  
 DB 121 GY---WYFDLMGRGTLTVTVSS 138

## RESULT 6

Ig heavy chain precursor V region (5-76) - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004







## RESULT 14

PL0249

Ig heavy chain V region (anti-DNA, J#12VR) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 16-Aug-1996

C:Accession: PL0249

R:Shlomchik, M.; Maecelli, M.; Shan, H.; Radic, M.Z.; Piatecky, D.; Marshak-Rothstein, A.

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231, PMID:9011618; PMID:2104919

A:Accession: PL0249

A:Molecule type: mRNA

A:Residues: 1-117 &lt;SHL&gt;

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-30/Region: framework 1

F:15-98/Domain: immunoglobulin homology &lt;IMM&gt;

F:31-35/Region: complementarity-determining 1

F:36-49/Region: framework 2

F:50-66/Region: complementarity-determining 2

F:67-98/Region: framework 3

F:99-108/Region: complementarity-determining 3

F:109-117/Region: framework 4

Query Match

Best Local Similarity 70.1%; Score 518; DB 2; Length 117;

Matches 99; Conservative 4; Mismatches 14; Indels 2; Gaps 1;

QY 20 EYVYVESGGGFLYKPGGSLKSCAAAGFTSRVAMSVWROTPERKLEWATISSGSHYY 79

DB 1 EYKLVESGGGLVYKPGGSLKSCAAAGFTSRVAMSVWROTPERKLEWATISSGSHYY 60

QY 80 PDSVKGRTISRDNANKNTLYLQMSLSRSDTAIYCARPGYDRGAMFPDVGAGTTVY 138

DB 61 PDSVKGRTISRDNANKNTLYLQMSLSRSDTAIYCARPGYDRGAMFPDVGAGTTVY 117

RESULT 15

S5537

Ig heavy chain V region pe21 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S5537

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A:Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using

A:Reference number: S5528; PMID:95239763; PMID:7536850

A:Accession: S5537

A:Molecule type: mRNA

A:Residues: 1-120 &lt;BOE&gt;

A:Cross-references: EMBL:X82590; NID:g854306; PIDN:CAA57926.1; PID:g854307

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:14-97/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match

Best Local Similarity 70.0%; Score 517; DB 2; Length 120;

Matches 100; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY 21 VVVVSGGGFLYKPGGSLKSCAAAGFTSRVAMSVWROTPERKLEWATISSGSHYY 80

DB 1 VOLOSGGGLVYKPGGSLKSCAAAGFTSRVAMSVWROTPERKLEWATISSGSHYY 60

QY 81 DSVKGRFTISRDNANKNTLYLQMSLSRSDTAIYCARPGYDRGAMFPDVGAGTTVY 140

DB 61 DSVKGRFTISRDNANKNTLYLQMSLSRSDTAIYCARPGYDRGAMFPDVGAGTTVY 120

Search completed: May 25, 2005, 16:48:37

Job time: 25.7953 secs

**BEST AVAILABLE COPY**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 68.2419 Seconds  
(without alignments)  
1050.544 Million cell updates/sec

Title: US-10-006-773a-4

Perfect score: 739  
Sequence: 1 KMFGSLIFLVILKGVCE.....DRGAFEDVWGAGTTVSS 140

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602.5	81.5	487	2 Q99KA4	Q99KA4 mus musculus
2	573	77.5	479	2 Q91WP5	Q91WP5 mus musculus
3	570.5	77.2	196	2 Q65ZL8	Q65ZL8 mus musculus
4	557	75.4	480	2 Q91XE1	Q91XE1 mus musculus
5	549	74.3	486	2 Q91Z07	Q91Z07 mus musculus
6	532	72.0	117	1 HV58_MOUSE	P18529 mus musculus
7	525	71.0	117	1 HV54_MOUSE	P18525 mus musculus
8	524	70.9	117	1 HV55_MOUSE	P18530 mus musculus
9	523	70.8	117	1 HV59_MOUSE	P18530 mus musculus
10	517.5	70.0	606	2 Q6GWT2	Q6GWT2 homo sapien
11	510	69.0	478	2 Q6P181	Q6P181 homo sapien
12	509.5	68.9	473	2 Q91Z05	Q91Z05 mus musculus
13	507.5	68.7	613	2 Q8WUK1	Q8WUK1 homo sapien
14	507	68.6	470	2 Q6P2A4	Q6P2A4 homo sapien
15	506	68.5	119	2 Q920E7	Q920E7 mus musculus
16	506	68.5	485	2 Q6PDB8	Q6PDB8 mus musculus
17	505.5	68.4	475	2 Q6M2Q6	Q6M2Q6 homo sapien
18	504	68.2	464	2 Q6M2U6	Q6M2U6 homo sapien
19	499	67.5	597	2 Q6GBB9	Q6GBB9 homo sapien
20	498	67.4	117	1 HV53_MOUSE	P01783 mus musculus
21	491.5	66.5	136	1 HV16_MOUSE	P01783 mus musculus
22	490	66.3	255	2 Q6KB05	Q6KB05 mus musculus
23	489	66.2	493	2 Q6GKX2	Q6GKX2 homo sapien
24	488.5	66.1	465	2 Q6P6C4	Q6P6C4 homo sapien
25	488	66.0	487	2 Q80Z17	Q80Z17 mus musculus
26	487	65.9	492	2 Q8N5K4	Q8N5K4 homo sapien
27	477.5	64.6	494	2 Q96K68	Q96K68 homo sapien
28	476.5	64.5	573	2 Q8W338	Q8W338 homo sapien
29	475.5	64.3	473	2 Q6M2V7	Q6M2V7 homo sapien
30	475	64.3	117	1 HV3C_HUMAN	P01764 homo sapien
31	470.5	63.7	487	2 Q6ZVX0	Q6ZVX0 homo sapien

32	468	63.3	472	2 Q6N089	Q6N089 homo sapien
33	466.5	63.1	544	2 Q6P095	Q6P095 homo sapien
34	464.5	62.9	483	2 Q6M2X9	Q6M2X9 homo sapien
35	464	62.8	493	2 Q8NCL6	Q8NCL6 homo sapien
36	461.5	62.4	475	2 Q6GKX7	Q6GKX7 homo sapien
37	460	62.2	466	2 Q6N096	Q6N096 homo sapien
38	458	62.0	466	2 Q6IN78	Q6IN78 homo sapien
39	458	62.0	480	2 Q6N094	Q6N094 homo sapien
40	453	61.3	98	1 HV57_MOUSE	P18528 mus musculus
41	452.5	61.2	97	1 HV56_MOUSE	P18527 mus musculus
42	449.5	60.8	116	1 HV05_CARAU	P19181 carassius a
43	446.5	60.4	519	2 Q6N092	Q6N092 homo sapien
44	444.5	60.1	479	2 Q6M2V6	Q6M2V6 homo sapien
45	443	59.9	493	2 Q68CN4	Q68CN4 homo sapien

## ALIGNMENTS

RESULT 1  
Q99KA4 PRELIMINARY; PRT; 487 AA.  
AC Q99KA4;  
DT 01-JUN-2001 (TREMBLrel, 17, Created)  
DT 01-JUN-2001 (TREMBLrel, 17, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel, 26, Last annotation update)  
DE Igh-VJ558 protein.  
GN Name=Igh-VJ558;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II; TISSUE=Mammary tumor;  
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., Mewhan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Maier M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II; TISSUE=Mammary tumor;  
RA Director MGC Project;  
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC004786; AA04786.1; -.  
DR HSPF, P01810; ZFBD.  
DR MGD, MGI:96486; Igh-VJ558.  
DR InterPro, IPR007110; I9-1like.  
DR InterPro, IPR003597; I9-1c.  
DR InterPro, IPR003006; I9\_MHC.  
DR InterPro, IPR003596; I9\_v.  
DR Pfam, PF07654; C1-sec; 2.  
DR SMART, SM00406; IGV; 1.  
DR PROSITE, PS00835; IGV\_LIKE; 4.  
DR PROSITE, PS00290; IGV\_MHC; UNKNOWN 2.  
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;



```

RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC010798; AAH10798.1; -.
DR HSSP; P01789; IMCP.
DR Pfam; PF07654; Cl-sec; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ
SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;
FT
NON TER 1
Query Match 75.4%; Score 557; DB 2; Length 480;
Best Local Similarity 76.3%; Pred. No. 3.5e-48;
Matches 106; Conservative 13; Mismatches 16; Indels 4; Gaps 1;
QY 2 NFGFSILFLVVLKGVCEVVVSGGFGVPGSKLKSCAAAGFTFSRYAMSWVRQP 61
DB 1 NFGFSILFLVVLKGVCEVVVSGGFGVPGSKLKSCAAAGFTFSRYAMSWVRQP 60
QY 62 KLELVVATISGSGSHYTPDVSVKGRFTISRDNANKTLVQLQMSLRSEDTAIYCARPGYD 121
DB 61 KLELVVATISGSGSHYTPDVSVKGRFTISRDNANKTLVQLQMSLRSEDTAIYCARPGYD 119
QY 122 RCAMPFDVWAGATTVTYSS 140
DB 120 ---WYFDVWAGATTVTYSS 135

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RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RC Director MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010324; AAH10324.1; -.
DR HSSP; P01789; IMCP.
DR Pfam; PF07654; Cl-sec; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ
SEQUENCE 486 AA; 52681 MW; 4FEF835125DA870B CRC64;

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Query Match 74.3%; Score 549; DB 2; Length 486;
Best Local Similarity 74.1%; Pred. No. 2.3e-47;
Matches 106; Conservative 13; Mismatches 20; Indels 4; Gaps 2;
QY 1 NMFGRILFLVVLKGVCEVVVSGGFGVPGSKLKSCAAAGFTFSRYAMSWVRQP 60
DB 1 NMFGRILFLVVLKGVCEVVVSGGFGVPGSKLKSCAAAGFTFSRYAMSWVRQP 60
QY 61 EKRLVAVATISGSGSHYTPDVSVKGRFTISRDNANKTLVQLQMSLRSEDTAIYCARPG- 119
DB 61 EKRLVAVATISGSGSHYTPDVSVKGRFTISRDNANKTLVQLQMSLRSEDTAIYCARPG- 119
QY 120 --YDRGAMPDVWAGATTVTYSS 140
DB 120 PLYYSGSYFDSMGCGTTITVSS 142

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RESULT 6

HV58 MOUSE STANDARD; PRT; 117 AA.

AC P18529;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Ig heavy chain V region 5-76 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALE/cj;

RX MEDLINE=89279149; PubMed=2499654;

RA Levy N.S., Malipiero U.V., Lebeckue S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during the

RT primary immune response."

RL J. Exp. Med. 169:2007-2019(1989).

CC -1- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.

DR PIR; J70506; HVM557.

DR PDB; 1I8I; X-ray; B=20-117.

DR PDB; 1I8K; X-ray; B=20-117.

DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM 3D-structure; Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 Ig heavy chain V region 5-76.  
 FT DOMAIN 20 49 Framework-1.  
 FT DOMAIN 50 54 Complementarity-determining-1.  
 FT DOMAIN 55 68 Framework-2.  
 FT DOMAIN 69 85 Complementarity-determining-2.  
 FT DOMAIN 86 117 Framework-3.  
 FT DISULFID 41 115 By similarity.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78BFA0 CRC64;  
 Query Match 72.0%; Score 532; DB 1; Length 117;  
 Best Local Similarity 86.3%; Pred. No. 2.6e-45;  
 Matches 101; Conservative 7; Mismatches 9; Indels 0; Gaps 0;  
 QY 1 MNFGSLIFLVLTAKVQCEVNVVSGSGGFVKGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 DB 1 MNFVLSLIFLALIKGVQCEVHLVSGGGLVKEGSLKSCVSGFTFNKTAAMSWVRQTP 60  
 QY 61 EKRLWVATISSGGSTTYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117  
 DB 61 EKRLWVATISSGGLTYYPDSYVGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117  
 RESULT 7  
 HV54\_MOUSE  
 ID HV54\_MOUSE STANDARD; PRT; 117 AA.  
 AC P18525;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 5-84 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/cj;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.:  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the  
 primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.  
 DR HSSP: JTO502; HVMS34.  
 DR HSSP: P01810; PFBJ  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 Ig heavy chain V region 5-84.  
 FT DOMAIN 20 49 Framework-1.  
 FT DOMAIN 50 54 Complementarity-determining-1.  
 FT DOMAIN 55 68 Framework-2.  
 FT DOMAIN 69 85 Complementarity-determining-2.  
 FT DOMAIN 86 117 Framework-3.  
 FT DISULFID 41 115 By similarity.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12872 MW; 23A055CB6A469861 CRC64;  
 Query Match 71.0%; Score 525; DB 1; Length 117;  
 Best Local Similarity 85.5%; Pred. No. 1.4e-45;  
 Matches 100; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 MNFGSLIFLVLTAKVQCEVNVVSGSGGFVKGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 DB 1 MNFGLSLIFLVLTAKVCEVNLVSGGGLVKEGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 QY 61 EKRLWVATISSGGSTTYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117  
 DB 61 EKRLWVATISSGGSTTYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117  
 RESULT 8  
 HV55\_MOUSE  
 ID HV55\_MOUSE STANDARD; PRT; 117 AA.  
 AC P18526;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 345 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/cj;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.:  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the  
 primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -I- MISCELLANEOUS: This sequence belongs to the VH7183 subfamily.  
 DR HSSP: JTO502; HVMS34.  
 DR HSSP: P01783; IIGC.  
 DR InterPro: IPR007110; Ig-like.  
 DR InterPro: IPR003596; Ig\_v.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS50835; IG\_LIKE; 1.  
 KM Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 Ig heavy chain V region 345.  
 FT DOMAIN 20 49 Framework-1.  
 FT DOMAIN 50 54 Complementarity-determining-1.  
 FT DOMAIN 55 68 Framework-2.  
 FT DOMAIN 69 85 Complementarity-determining-2.  
 FT DOMAIN 86 117 Framework-3.  
 FT DISULFID 41 115 By similarity.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12902 MW; 49380E4627AC99A CRC64;  
 Query Match 70.9%; Score 524; DB 1; Length 117;  
 Best Local Similarity 85.5%; Pred. No. 1.7e-45;  
 Matches 100; Conservative 6; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 MNFGSLIFLVLTAKVQCEVNVVSGSGGFVKGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 DB 1 MNFGLSLIFLVLTAKVCEVNLVSGGGLVKEGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 QY 61 EKRLWVATISSGGSTTYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117  
 DB 61 EKRLWVATISSGGSTTYPDSYKGRFTISRDNKNTLYLQMSLSRSEDTAIYYCAR 117  
 RESULT 9  
 HV59\_MOUSE  
 ID HV59\_MOUSE STANDARD; PRT; 117 AA.  
 AC P18530;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 7-39 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/cJ;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malpiero U.V., Lebecqz S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the  
 primary immune response";  
 RL J. Exp. Med. 169:2007-2019 (1989).  
 CC -1- MISCELLANEOUS: This sequence belongs to the VH183 subfamily.  
 DR PIR; J0507; HWS39.  
 DR HSSP; P18529; 118K.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 DR Immunoglobulin V region; Signal.  
 FT CHAIN 1 19  
 FT DOMAIN 20 117 Ig heavy chain V region 7-39.  
 FT DOMAIN 20 49 Framework-1.  
 FT DOMAIN 50 54 Complementarity-determining-1.  
 FT DOMAIN 55 68 Framework-2.  
 FT DOMAIN 69 85 Complementarity-determining-2.  
 FT DOMAIN 86 117 Framework-3.  
 FT DISULFID 41 115 By similarity.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;  
 Query Match 70.8%; Score 523; DB 1; Length 117;  
 Best Local Similarity 85.5%; Pred. No. 2, 2e-45;  
 Matches 100; Conservative 6; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 NMFPSLFLVVLKVGCEVNVVSGGFFVKGSLKLSCAAGFTFRYAMSWVRQP 60  
 DB 1 NMFPSLFLVVLKVGCEVNVVSGGFFVKGSLKLSCEASGFTFRYAMSWVRQP 60  
 QY 61 EKRLVNAVATISSGSGSHYTPDVKGRFTISRDNAKNTLYLQMSLRSEPTAIYCAR 117  
 DB 61 EKRLVNAVATISSGSGSHYTPDVKGRFTISRDNAKNTLYLQMSLRSEPTAIYCAR 117  
 DB 61 EKRLVNAVATISSGSGSHYTPDVKGRFTISRDNAKNTLYLQMSLRSEPTAIYCAR 117  
 RESULT 10  
 O6GMV2 PRELIMINARY; PRT; 606 AA.  
 ID O6GMV2  
 AC O6GMV2; 05-JUL-2004 (TREMblrel. 27, Created)  
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carinci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073758; AAH73758.1; -  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF07654; C1-sec; 4.  
 DR Pfam; PF00047; Ig; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; ICG1; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 5.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_3.  
 KW Hypothetical protein.  
 SQ SEQUENCE 606 AA; 66184 MW; B6B38B51114E4C55 CRC64;  
 Query Match 70.0%; Score 517.5; DB 2; Length 606;  
 Best Local Similarity 66.0%; Pred. No. 4, 8e-44;  
 Matches 101; Conservative 17; Mismatches 22; Indels 13; Gaps 2;  
 QY 1 NMFPSLFLVVLKVGCEVNVVSGGFFVKGSLKLSCAAGFTFRYAMSWVRQP 60  
 DB 1 NMFPSLFLVVLKVGCEVNVVSGGFFVKGSLKLSCEASGFTFRYAMSWVRQP 60  
 QY 61 EKRLVNAVATISSGSGSHYTPDVKGRFTISRDNAKNTLYLQMSLRSEPTAIYCAR 119  
 DB 61 EKRLVNAVATISSGSGSHYTPDVKGRFTISRDNAKNTLYLQMSLRSEPTAIYCAR 120  
 DB 61 EKRLVNAVATISSGSGSHYTPDVKGRFTISRDNAKNTLYLQMSLRSEPTAIYCAR 120  
 QY 120 -----YDRGAMF---DVGAGTIVTVSS 140  
 DB 121 GAAAGRVVYADYYGYGMDVGGGTIVTVSS 153  
 RESULT 11  
 O6PI81 PRELIMINARY; PRT; 478 AA.  
 ID O6PI81  
 AC O6PI81; 05-JUL-2004 (TREMblrel. 27, Created)  
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carinci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smallus D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Primary B-Cells;

RA Strausberg R.,  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC041037; AAH41037.1; -.

DR HSSP; P01861; IADQ.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003596; IG-v.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGL; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG-LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.

DR Hypothetical protein.

SO SEQUENCE 478 AA; 52666 MW; 17BED3BD917970D6 CRC64;

Query Match 69.0%; Score 510; DB 2; Length 478;

Best Local Similarity 67.6%; Pred. No. 2.2e-43;

Matches 100; Conservative 13; Mismatches 27; Indels 8; Gaps 1;

QY 1 MNFGSLIFLVYLVKVGQCEVYVVGSGGFGYKPGSGSLKSCAAAGTFPSRYMSWVRQP 60

DB 1 MELGSLVFLVVAIEGQCEVQVYVSGGGLVPGSGSLRLSCAAGTFPSRYMSWVRQP 60

QY 61 EKLEWVAITSSGSHYTPDSYKGRFTISRDAKNTLYLQMSLSRSEDPAIYYCARP 118

DB 61 GKLEWVAITSSGSHYTPDSYKGRFTISRDAKNTLYLQMSLSRSEDPAIYYCARP 120

QY 119 -----GYDRGAMFEDVWGAGTTTVSS 140

DB 121 STMTTNAVADYYFYMDVWKGKTTTVSS 148

RESULT 12

Q91Z05 PRELIMINARY; PRT; 473 AA.

AC Q91Z05;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Expressed sequence AU044919.

GN Name=AU044919;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=C2ECH II; TISSUE=Mammary tumor;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,

RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skaleka U., Smallus D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]  
RP SEQUENCE FROM N.A.

RC STRAIN=C2ECH II; TISSUE=Mammary tumor;

RA Strausberg R.,

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC010327; AAH10327.1; -.

DR PIR; S68213; S68213.

DR HSSP; P01783; IIGC.

DR MCD; MGI2144667; AU044919.

DR Pfam; PF07654; CL-se; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN\_1.

DR PROSITE; PS00835; IG-LIKE; 4.

DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.

SO SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 68.9%; Score 509.5; DB 2; Length 473;

Best Local Similarity 70.4%; Pred. No. 2.4e-43;

Matches 100; Conservative 13; Mismatches 22; Indels 7; Gaps 2;

QY 1 MNFGSLIFLVYLVKVGQCEVYVVGSGGFGYKPGSGSLKSCAAAGTFPSRYMSWVRQP 60

DB 1 MDSRLNVLFLVLLKVGQCEVQVYVSGGGLVPGSGSLRLSCAAGTFPSRYMSWVRQP 60

QY 61 EKLEWVAITSSGSHYTPDSYKGRFTISRDAKNTLYLQMSLSRSEDPAIYYCARP 120

DB 61 EKLEWVAITSSGSHYTPDSYKGRFTISRDAKNTLYLQMSLSRSEDPAIYYCARP 118

QY 121 DRGAMF--FDVWGAGTTTVSS 140

DB 119 ---LMLRRIDYWGQGTITVSS 137

RESULT 13

Q98WUK1 PRELIMINARY; PRT; 613 AA.

AC Q98WUK1;

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE IGHM protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helin F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uudin T.B., Tohiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC020240; AAH20240.1; -.  
 DR PIR; F36005; F36005.  
 DR PIR; G36005; G36005.  
 DR PIR; PH1642; PH1642.  
 DR PIR; PH1643; PH1643.  
 DR PIR; PH1645; PH1645.  
 DR PIR; PH1646; PH1646.  
 DR PIR; PL0098; PL0098.  
 DR PIR; PL0120; PL0120.  
 DR PIR; S15590; S15590.  
 DR PIR; S31116; S31116.  
 DR PIR; S31119; S31119.  
 DR PIR; S70442; S70442.  
 DR HSSP; P01861; IADQ.  
 DR Pfam; PF07654; C1-secl; 4.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; P550835; IG\_LIKE; 5.  
 DR PROSITE; P500290; IG\_MHC; UNKNOWN 3.  
 SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 68.7%; Score 507.5; DB 2; Length 613;  
 Best Local Similarity 69.3%; Pred. No. 5.1e-43;

Matches 97; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 MNFGSLIFLVLYLVKVGCEVVVBSGGFVPGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 DB 1 MEGGLSWVFLVALLRGVCQGLVESGGVVGPRSLRLSCAASGFTFSYGMHWYRQAP 60  
 QY 61 EKRLVNAVITSSGGSHYTPDSYKGRFTISRDNAAKNTLYLQNSLSASEDTAITYCARPGY 120  
 DB 61 GKGLEWNAVIAISYDGSNKKYVADSVKGRFTISRDNASKNTLYLQNSLSRAEDTAVYCAK-DW 119  
 QY 121 DRGAMPDPWAGCTTVTVSS 140  
 DB 120 SEGVETFDWGGCTWTVSS 139

## RESULT 14

Q6PJA4 PRELIMINARY; PRT; 470 AA.

AC Q6PJA4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
 RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.W., Hong L.,  
 RA Stapleton W., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schwartz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018747; AAH18747.1; -.  
 DR HSSP; P01861; IADQ.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; C1-secl; 3.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGcl; 3.  
 DR PROSITE; P550835; IG\_LIKE; 4.  
 DR PROSITE; P500290; IG\_MHC; UNKNOWN 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 68.6%; Score 507; DB 2; Length 470;  
 Best Local Similarity 68.5%; Pred. No. 4.3e-43;

Matches 98; Conservative 13; Mismatches 26; Indels 6; Gaps 2;

QY 1 MNFGSLIFLVLYLVKVGCEVVVBSGGFVPGSLKLSCAAAGFTFSRYAMSWVRQTP 60  
 DB 1 MEGGLSWVFLVALLRGVCQGLVESGGVVGPRSLRLSCAASGFTFSYGMHWYRQAP 60  
 QY 61 EKRLVNAVITSSGGSHYTPDSYKGRFTISRDNAAKNTLYLQNSLSASEDTAITYCARPGY 120  
 DB 61 GKGLEWNAVIAISYDGSNKKYVADSVKGRFTISRDNAAKNTLYLQNSLSRAEDTAVYCAK-DG 119  
 QY 121 DRGAMPDPWAGCTTVTVSS 140  
 DB 120 --SWYRDFDPWGGCTWTVSS 140

## RESULT 15

Q920E7 PRELIMINARY; PRT; 119 AA.

AC Q920E7;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Pterin-mimicking anti-idiotope heavy chain variable region  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
 RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF307937; AAL09421.1; -.  
 DR PIR; C25913; C25913.  
 DR HSSP; P01783; IIGC.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; P550835; IG\_LIKE; 1.  
 FT NON TER 1 119  
 SQ SEQUENCE 119 AA; 13025 MW; F6B90404381CA7C CRC64;

Query Match 68.5%; Score 506; DB 2; Length 119;  
Best Local Similarity 82.0%; Pred. No. 1.2e-43;  
Matches 100; Conservative 7; Mismatches 11; Indels 4; Gaps 2;

```
QY 20 EVVVVESGGGFVVRPGSLKLSCAAAGFTFSRIYAMSWRQTPPEKRLKLEWVATISSGGSHTTY 79
   | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLVESGGDLVKRPGSLKLSCAAAGFTFSYGMWVWROTPEKRLKLEWVATISSGGSHTTY 60
   | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 80 PDSVKGKFTISRDNKNTLYLQMSLSRSEDTAIYYCARPG-YDRGAWFDDWGAGTTVTY 138
   | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 PDSVKGKFTISRDNKNTLYLQMSLSRSEDTAIYYCARHGDYDVG---FAYWGCTLVTV 117
   | : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 139 SS 140
   | :
Db 118 SA 119
```

Search completed: May 25, 2005, 15:56:02  
Job time : 69.2419 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 60.2493 Seconds  
(without alignments)  
821.675 Million cell updates/sec

Title: US-10-006-773a-6

Perfect score: 661

Sequence: 1 MFTPTQILGLMLFWISASRG.....QOSNMPPLFGSGTKLEIKR 128

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16dec04:\*

1: geneseqp19808:\*\n2: geneseqp19908:\*\n3: geneseqp20008:\*\n4: geneseqp20018:\*\n5: geneseqp20028:\*\n6: geneseqp20038:\*\n7: geneseqp2003bs:\*\n8: geneseqp20048:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	661	100.0	128	6	ABG74242 Mouse ant
2	634	95.9	127	4	ABG69687 Murine CM
3	634	95.9	127	8	AD047787 Mouse CMV
4	622	94.1	127	2	AARS4093 Sequence
5	619	93.6	127	3	AAY32405 Mouse ant
6	614	92.9	127	8	ADF73169 Anti-REL
7	551	83.4	127	3	AAY32407 Mouse ant
8	534	80.8	108	2	AAR15438 light cha
9	534	80.8	109	2	AAR52033 light cha
10	534	80.8	240	7	AAR15443 Single ch
11	533	80.6	107	7	ADJ80363 Murine an
12	531	80.3	107	4	ABG69677 Murine CM
13	531	80.3	107	8	AD047724 Murine CMV
14	529	80.0	107	8	ADG55713 Human Eph
15	526	79.6	107	2	AAR38601 HYH light
16	526	79.6	107	2	AAR38601 HYH light
17	526	79.6	107	8	AD101144 Murine HY
18	525	79.6	109	2	AAY06380 Murine mo
19	524.5	79.3	114	4	ABG86655 Murine pr
20	520	78.7	108	6	ABG27275 Murine 1A
21	518	78.4	108	2	AAR84094 Murine 1A
22	517	78.2	103	7	ADM33440 Naide0 VL
23	511	77.3	107	2	AAR76004 LM609 ant
24	511	77.3	107	4	ABG61362 Antibody
25	511	77.3	107	4	ABG63590 A light c

26	511	77.3	107	6	ABO19800 LM609 1lg
27	511	77.3	107	7	ADG71782 Mab LM609
28	511	77.3	107	8	ADJ57963 Murine LM
29	507	76.7	108	2	AAW00241 EGF recep
30	507	76.7	159	8	ADL15638 Murine an
31	507	76.7	214	8	ADL15723 Murine an
32	506	76.6	127	2	AAW08945 Kappla 1lg
33	505	76.4	128	2	AAW30199 light cha
34	505	76.4	128	5	ABG47724 light cha
35	503	76.1	123	8	ADL73175 Anti-idio
36	503	76.1	127	2	AAW44176 Monoclonal
37	494.5	74.8	126	1	AAW90479 Chimeric
38	494	74.7	159	8	ADL15664 Partial m
39	493	74.6	127	2	AAW08941 Kappla 1lg
40	493	74.6	109	2	AAW08943 Kappla 1lg
41	492.5	74.5	109	2	AAW89176 Anti-p53
42	492	74.4	259	3	AAW09775 TWV 30K m
43	492	74.4	264	7	ADD25839 Binding d
44	492	74.4	548	7	ADD25711 Binding d
45	487	73.7	127	7	ADD25703 Binding d

## ALIGNMENTS

RESULT 1	ABG74242	standard, protein, 128 AA.
AC	ABG74242	
XX	ABG74242	
XX	ABG74242	
DT	22-APR-2003	(first entry)
DE	Mouse antibody MB3.6 light chain variable region.	
KW	T-cell receptor; cytostatic; dermatological; neuroprotective;	
KW	immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;	
KW	3E11; prostate-specific membrane antigen; zeta signalling chain;	
KW	CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;	
KW	small cell lung cancer; light chain variable region; mouse.	
OS	Mus sp.	
PN	US200232983-A1.	
PD	19-SEP-2002.	
PR	30-NOV-2000; 2000US-0250087P.	
PR	30-NOV-2000; 2000US-0250089P.	
PA	(JUNG/) JUNGHANS R P.	
PI	Junghans RP;	
DR	WPI; 2003-208946/20.	
DR	N-PSDB; ABX16567.	
PT	New chimeric molecule useful in treating patients with disorders, such as	
PT	melanoma, neuroendocrine disorders, prostate and small cell lung cancer	
PT	comprises GD3 and/or PSMA binding domains of antibody.	
PS	Disclosure; Page 10-11; 35pp; English.	
CC	The invention relates to a chimeric molecule comprising the GD3	
CC	(ganglioside antigen) binding domain of antibody MB3.6, with any of 3	
CC	variable gene sequences, or the PSMA (prostate-specific membrane antigen)	
CC	binding domain of antibody 3D8, 4D4 and 3E11, with variable gene	
CC	sequences, the zeta signalling chain of the T cell receptor and an	
CC	intervening CD8alpha hinge in which cysteine residues have been mutated.	
CC	The chimeric molecules expressed in T cells or NK cells or other	
CC	effector cells are useful in treating patients with cancers expressing	

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),  
CC and/or together with each other or with heterologous constructs to engage  
CC additional stimulatory and functional properties of the effector cells to  
CC enhance the antitumour therapeutic efficacy (claimed). They are  
CC particularly useful in disorders including melanoma, neuroendocrine  
CC tumours and prostate and small cell lung cancer. The present sequence  
CC represents the mouse antibody MB3.6 light chain variable region  
XX  
SQ Sequence 128 AA;  
Query Match 100.0%; Score 661; DB 6; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.6e-40;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MVEPTQILGIMLFWISASRGDIVLTQSPATLSVTPGDVSVLSGRASQIISNNLHWYQOKS 60  
DB 1 MVEPTQILGIMLFWISASRGDIVLTQSPATLSVTPGDVSVLSGRASQIISNNLHWYQOKS 60  
QY 61 HESPRLLIKYASGISGIPSRFGSGSGTDFTLISINSEVEDFGMVFCCQSNWPPLTFGS 120  
DB 61 HESPRLLIKYASGISGIPSRFGSGSGTDFTLISINSEVEDFGMVFCCQSNWPPLTFGS 120  
QY 121 GTKLEIRK 128  
DB 121 GTKLEIRK 128  
RESULT 2  
AAB69687  
ID AAB69687 standard; protein; 127 AA.  
XX  
AC AAB69687;  
XX  
DT 30-APR-2001 (first entry)  
XX  
DE Murine CMV5 antibody light chain SEQ ID NO: 83.  
XX  
KM Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes;  
KM light chain; graft versus host disease; transplant; autoimmune disease;  
KM multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;  
KM myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.  
XX  
OS Mus sp.  
XX  
PN US6180370-B1.  
XX  
PD 30-JAN-2001.  
XX  
PF 07-JUN-1995; 95US-00484537.  
XX  
PR 28-DEC-1988; 88US-00290975.  
PR 13-FEB-1989; 89US-00310252.  
PR 28-SEP-1990; 90US-00590274.  
PR 19-DEC-1990; 90US-00634278.  
XX  
PA (PROT-) PROTEIN DESIGN LABS INC.  
XX  
PI Queen CL, Selick HE;  
XX  
DR WPI, 2001-190856/19.  
DR N-PSDB; AAF58747.  
XX  
PT Producing humanized immunoglobulin, involves producing a cell containing  
PT DNA segments encoding humanized heavy and light chain variable regions,  
PT and expressing the DNA segments in the cell.  
XX  
PS Example 8; Fig 39; 145pp; English.  
XX  
CC The present invention describes a method of producing humanised  
CC immunoglobulins involving expressing in a cell a nucleic acid encoding a  
CC humanised version of an immunoglobulin. This is obtained by comparing a  
CC donor and human immunoglobulin and producing a combined antibody which  
CC contains part of each. These are useful in the treatment of graft-versus-

CC host disease, transplant rejection, autoimmune diseases such as diabetes,  
CC rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic  
CC lupus erythematosus, herpes infections, CMV virus infections and myeloid  
CC leukemia. The present sequence is an antibody used to demonstrate the  
CC method of the invention  
XX  
SQ Sequence 127 AA;  
Query Match 95.9%; Score 634; DB 4; Length 127;  
Best Local Similarity 96.1%; Pred. No. 6.3e-38;  
Matches 122; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MVEPTQILGIMLFWISASRGDIVLTQSPATLSVTPGDVSVLSGRASQIISNNLHWYQOKS 60  
DB 1 MVEPTQILGIMLFWISASRGDIVLTQSPATLSVTPGDVSVLSGRASQIISNNLHWYQOKS 60  
QY 61 HESPRLLIKYASGISGIPSRFGSGSGTDFTLISINSEVEDFGMVFCCQSNWPPLTFGS 120  
DB 61 HESPRLLIKYASGISGIPSRFGSGSGTDFTLISINSEVEDFGMVFCCQSNWPPLTFGS 120  
QY 121 GTKLEIRK 127  
DB 121 GTKLEIRK 127  
RESULT 3  
ADO47787  
ID ADO47787 standard; protein; 127 AA.  
XX  
AC ADO47787;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Mouse CMV5 antibody light chain variable region #2.  
XX  
KM humanised immunoglobulin; Ig; immunoglobulin; framework; acceptor Ig;  
KM donor Ig; CDR; complementarity determining region; interleukin-2; IL-2;  
KM IL-2 receptor; T-cell mediated disorder; mouse; CMV5 antibody;  
KM light chain variable region.  
XX  
OS Mus sp.  
XX  
PN US2004058414-A1.  
XX  
PD 25-MAR-2004.  
XX  
PF 30-MAY-2003; 2003US-00452357.  
XX  
PR 28-DEC-1988; 88US-00290975.  
PR 13-FEB-1989; 89US-00310252.  
PR 28-SEP-1990; 90US-00590274.  
PR 07-JUN-1995; 95US-00484537.  
PR 22-NOV-2000; 2000US-00718993.  
XX  
PA (QUEB/) QUEEN C L.  
PA (COMS/) CO M S.  
PA (SCHN/) SCHNEIDER W P.  
PA (LAND/) LANDOLFI N F.  
PA (COEL/) COELINGH K L.  
PA (SELI/) SELICK H E.  
XX  
PI Queen CL, Co MS, Schneider WP, Landolfi NF, Coelinhg KL;  
PI Selick HE;  
XX  
DR WPI, 2004-304235/28.  
DR N-PSDB; ADO47786.  
XX  
PT Designing humanized immunoglobulin chain comprises substituting human  
PT framework amino acids of acceptor immunoglobulin with corresponding amino  
PT acid from donor immunoglobulin at position in immunoglobulin.  
XX  
PS Disclosure; Fig 48; 130pp; English.  
XX



FT /note= "signal peptide"  
FT Protein 21..127  
FT /note= "mature protein"  
FT Region 44..54  
FT /note= "complementarity determining region 1"  
FT Misc-difference 62  
FT /note= "encoded by GAG"  
FT Region 70..76  
FT /note= "complementarity determining region 2"  
FT Region 109..117  
FT /note= "complementarity determining region 3"  
XX  
XX WO9595629-A1.  
XX  
XX 25-NOV-1999.  
XX  
XX 19-MAY-1999; 99MO-US011179.  
XX  
XX 20-MAY-1998; 98US-0086570P.  
XX  
XX (TEIJ ) TEIJIN LTD.  
XX (PROT-) PROTEIN DESIGN LABS INC.  
XX  
XX Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M,  
XX WPI; 2000-086580/07.  
XX N-PSDB; AAY35242.  
XX  
XX Humanized antibody binding to verotoxin II used for treating Verotoxin  
XX producing E. coli.  
XX  
XX Claim 5; Fig 1b; 59pp; English.  
XX  
XX This sequence represents the light chain variable region of murine  
XX monoclonal antibody Vtm1-1 (Muvtm1-1), an antibody that specifically  
XX binds to the B subunit of verotoxin II (VT2). The invention relates to  
XX humanised antibodies against VT2 that are capable of neutralizing VT2  
XX and/or VT2 variants. The humanised antibody is a humanized form of Muvtm1  
XX -1 comprising the complementarity determining regions of Muvtm1-1 and the  
XX heavy and light chain variable region frameworks from the human GP4  
XX antibody heavy and light chain frameworks, provided that at least 1  
XX position selected from L49, H29, H30, H49 and H98 is occupied by the  
XX amino acid at the equivalent position of the Muvtm1-1 antibody heavy or  
XX light chain variable region framework. Such humanized antibodies (see  
XX AAY32406-07) have an affinity for VT2 that is 3-, 5 or 10-times that of  
XX Muvtm1-1. They are used for treating a patient suffering from, or at risk  
XX of, the toxic effects from VT2 (claimed), especially for treating  
XX verotoxin producing Escherichia coli (VTEC) infection, and haemolytic  
XX uraemic syndrome (HUS)  
XX  
XX Sequence 127 AA;  
SQ  
Query Match 93.6%; Score 619; DB 3; Length 127;  
Best Local Similarity 93.7%; Pred. No. 7,4e-37;  
Matches 119; Conservative 4; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MVFTPOLIGLMLFWISASRGDIVLTOSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKS 60  
DB 1 MVFTPOLIGLMLFWISASRGDIVLTOSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKS 60  
DB 1 MVFTPOLIGLMLFWISASRGDIVLTOSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKS 60  
QY 61 HESPRLLIKXASOSISGIPRFGSGSGTDFTLISNVEETDFGMYFCQOQSNWPLTFGS 120  
DB 61 HESPRLLIKXASOSISGIPRFGSGSGTDFTLISNVEETDFGMYFCQOQSNWPLTFGA 120  
QY 121 GTKLEIK 127  
DB 121 GTKLEIK 127  
RESULT 6  
ADP73169  
ID ADP73169 standard; protein; 127 AA.  
XX

AC ADF73169;  
XX  
XX 26-FEB-2004 (first entry)  
XX  
XX Anti-RELp fusion antibody CMO 338 LC variable region SEQ ID NO:28.  
XX  
XX anti-RELp fusion antibody; RELp fusion antibody; cytotatic;  
XX cardiovascular; immunomodulator; neuroprotective; nootropic;  
XX gene therapy; cancer; immune disorder; cardiovascular disorder;  
XX neurological disorder; human.  
XX  
XX Synthetic.  
XX OS  
XX Homo sapiens.  
XX  
XX WO2003102017-A2.  
XX  
XX 11-DEC-2003.  
XX  
XX 02-JUN-2003; 2003MO-US017357.  
XX  
XX 03-JUN-2002; 2002US-0385305P.  
XX  
XX (CENZ ) CENTOCOR INC.  
XX  
XX Carton J, Giles-Komar J, Scallion B, Straquet K,  
XX WPI; 2004-053426/05.  
XX N-PSDB; ADF73179.  
XX  
XX New mammalian Reg like protein (RELp) fusion antibody, useful for  
XX preparing a composition for diagnosing or treating a RELp protein-related  
XX condition in a cell, tissue, organ or animal, e.g., cancer.  
XX  
XX Claim 4; SEQ ID NO 28; 78pp; English.  
XX  
XX The present invention describes a mammalian anti-RELp fusion antibody (1)  
XX which comprises: (a) at least one heavy chain variable region comprising  
XX ADF73148 or ADF73168 and at least one light chain variable region  
XX comprising ADF73149, ADF73169 or ADF73180; or (b) all of the  
XX complementarity determining regions (CDRs) of ADF73142 to ADF73147 or  
XX ADF73162 to ADF73167. Also described: (1) a pharmaceutical composition  
XX comprising the mammalian RELp fusion antibody and at a carrier or diluent  
XX; (2) an isolated nucleic acid encoding the mammalian RELp fusion  
XX antibody; (3) an isolated nucleic acid vector comprising the isolated  
XX nucleic acid; (4) a prokaryotic or eukaryotic host cell comprising the  
XX isolated nucleic acid; (5) a method for producing at least one RELp  
XX fusion antibody; (6) a method for diagnosing or treating a RELp protein-  
XX related condition in a cell, tissue, organ or animal; (7) an article of  
XX manufacture for human pharmaceutical or diagnostic use, comprising  
XX packaging material and a container comprising a solution or a lyophilised  
XX form of the mammalian RELp fusion antibody; and (8) a medical device,  
XX comprising the isolated mammalian RELp fusion antibody, where the device  
XX is suitable to contacting or administering the at least one RELp fusion  
XX antibody. (1) has cytostatic, cardiovascular, immunomodulator,  
XX neuroprotective and nootropic activities, and can be used in gene  
XX therapy. The mammalian RELp fusion antibody is useful for preparing a  
XX composition for diagnosing or treating a RELp protein-related condition  
XX in a cell, tissue, organ or animal, e.g., cancer, immune disorders,  
XX cardiovascular and neurological disorders. The present sequence is used  
XX in the exemplification of the present invention.  
XX  
XX Sequence 127 AA;  
SQ  
Query Match 92.9%; Score 614; DB 8; Length 127;  
Best Local Similarity 91.3%; Pred. No. 1.7e-36;  
Matches 116; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MVFTPOLIGLMLFWISASRGDIVLTOSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKS 60  
DB 1 MVFTPOLIGLMLFWISASRGDIVLTOSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKS 60  
QY 61 HESPRLLIKXASOSISGIPRFGSGSGTDFTLISNVEETDFGMYFCQOQSNWPLTFGS 120  
DB 61 HESPRLLIKXASOSISGIPRFGSGSGTDFTLISNVEETDFGMYFCQOQSNWPLTFGS 120



DB 61 HSPRLIKYASQSIGIPRFGSGSGTDFLLTINNVEDFGLYFCOQNSWPLTFGA 120  
 QY 121 GTKLEIK 127  
 DB 121 GTKLEIK 127

RESULT 7  
 AAY32407  
 ID AAY32407 standard; protein; 127 AA.  
 XX  
 AC AAY32407;  
 XX  
 DT 13-MAR-2000 (first entry)  
 DE Mouse anti-verotoxin II antibody VTm1-1 humanised VL region.  
 XX  
 KW Verotoxin II; VT2; shiga-like toxin; VTm1-1; MuVTm1-1;  
 KW monoclonal antibody; light chain; mouse; humanised antibody; human;  
 KW Escherichia coli; VTBC; infection; haemolytic uraemic syndrome; HUS;  
 KW therapy.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FH Peptide 1..20 "signal peptide"  
 FT /note= "signal peptide"  
 FT Protein 21..127  
 FT /note= "mature protein"  
 FT Region 44..54  
 FT /note= "complementarity determining region 1"  
 FT Region 70..76  
 FT /note= "complementarity determining region 2"  
 FT Region 109..117  
 FT /note= "complementarity determining region 3"  
 XX  
 PN WO959629-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 19-MAY-1999; 99WO-US011179.  
 XX  
 PR 20-MAY-1998; 98US-0086570P.  
 XX  
 PA (TEJU ) TEJUIN LTD.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 PI Matsumoto Y, Imaizumi A, Kimura T, Takedo T, Co MS, Vasques M;  
 XX WPI; 2000-086580/07.  
 DR N-PSDB; AA235244.  
 XX  
 PT Humanized antibody binding to verotoxin II used for treating Verotoxin  
 PT producing E. coli.  
 XX  
 PS Claim 12; Fig 2b; 59pp; English.  
 XX  
 CC This sequence represents a humanised light chain variable region of  
 CC murine monoclonal antibody VTm1-1 (MuVTm1-1), an antibody that  
 CC specifically binds to the B subunit of verotoxin II (VT2). The invention  
 CC relates to humanised antibodies against VT2 that are capable of  
 CC neutralizing VT2 and/or VT2 variants. The humanised antibody is a  
 CC humanized form of MuVTm1-1 comprising the complementarity determining  
 CC regions of MuVTm1-1 and the heavy and light chain variable region  
 CC frameworks from the human Gf4 antibody heavy and light chain frameworks,  
 CC provided that at least 1 position selected from 149, H29, H30, H49 and  
 CC H98 is occupied by the amino acid at the equivalent position of the  
 CC MuVTm1-1 antibody heavy or light chain variable region framework. Such  
 CC humanized antibodies have an affinity for VT2 that is 3-, 5 or 10-times  
 CC that of MuVTm1-1. They are used for treating a patient suffering from, or  
 CC at risk of, the toxic effects from VT2 (claimed), especially for treating  
 CC verotoxin producing Escherichia coli (VTBC) infection, and haemolytic

CC uraemic syndrome (HUS)  
 XX  
 SQ Sequence 127 AA;  
 QY Query Match 83.4%; Score 534; DB 3; Length 127;  
 Best Local Similarity 95.4%; Pred. No. 7.3e-31;  
 Matches 103; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 1 MFTPOIIGLMFWISASRGDVLVQSPATLSVTPGDSVSLSCRASQITSNLHWYQOKS 60  
 DB 1 MFTPOIIGLMFWISASRGDVLVQSPATLSVTPGDSVSLSCRASQITSNLHWYQOKP 60  
 QY 61 HSPRLIKYASQSIGIPRFGSGSGTDFLLTINNVEDFGLYFCOQNSWPLTFGS 120  
 DB 61 GQAPRLIKSASQSIGIPARFSGSGSGTDFLLTISLESSEDFAYYCCQSYWPLTFQ 120  
 QY 121 GTKLEIK 127  
 DB 121 GTKLEIK 127

RESULT 8  
 AAR15438  
 ID AAR15438 standard; protein; 108 AA.  
 XX  
 AC AAR15438;  
 XX  
 DT 25-FEB-1992 (first entry)  
 DE Light chain variable region of Mab 1A6.  
 XX  
 KW HRV; ICAW-1; antigen-binding fragment; inflammation; auto-immune disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP459577-A.  
 XX  
 PD 04-DEC-1991.  
 XX  
 PF 25-MAY-1991; 91EP-00201243.  
 XX  
 PR 01-JUN-1990; 90US-00532001.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Colunno RJ, Condra JH, Tomassini JE, Sardana VV;  
 XX WPI; 1991-355850/49.  
 DR  
 XX  
 PT Microbially expressed portions of monoclonal antibody - can block  
 PT attachment of rhinovirus ligands to inter-cellular adhesion molecule  
 PT (ICAM-1).  
 XX  
 PS Claim 1; Page 19; 28pp; English.  
 XX  
 CC This is one of six antibody fragments from Mab's specific for domain 1 of  
 CC ICAM-1. Mab 1A6 also specifically blocks the major group of human  
 CC rhinovirus from binding to and infecting HeLa cells. The peptide  
 CC fragments can be used to treat or prevent rhinovirus infection. See  
 CC AAR15437-R15443  
 CC  
 SQ Sequence 108 AA;  
 QY Query Match 80.8%; Score 534; DB 2; Length 108;  
 Best Local Similarity 95.4%; Pred. No. 7.3e-31;  
 Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLQSPATLSVTPGDSVSLSCRASQITSNLHWYQOKSHSPRLIKYASQSIGIPS 80  
 DB 1 DIVLQSPATLSVTPGDSVSLSCRASQITSNLHWYQOKSHSPRLIKYASQSIGIPS 60  
 QY 81 RFGSGSGTDFLLTINNVEDFGLYFCOQNSWPLTFSGGTKLEIKR 128  
 |||||||

Db 61 RFGSGSGTDFTLINSVETEDFGMFCCQSNWPLYFGGTYLTIKR 108

# RESULT 9

AAAR52033 standard; protein; 109 AA.

AC AAR52033;

DT 26-SEP-1996 (first entry)

XX Light chain variable region of murine antibody 3Hm.

XX antibody; humanised; murine; human; heavy chain; light; variable;  
KW framework region; complementarity determining region; reshaping;  
XX modelling; surface residue; modify.

OS Mus sp.

XX Key Location/Qualifiers

FT 1.23 /label=framework\_region\_1

FT /note="FR 1"

FT 24.34 /label=complementarity\_determining\_region\_1

FT /note="CDR 1"

FT 35.49 /label=FR\_2

FT 50.56 /label=CDR\_2

FT 57.88 /label=FR\_3

FT 89.97 /label=CDR\_3

FT 98.109 /label=FR\_4

XX EP592106-A1.

XX 13-APR-1994.

PF 07-SEP-1993; 93EP-00307051.

PR 09-SEP-1992; 92US-00942245.

XX (IMMUNO-) IMMUNOGEN INC.

XX Pedersen JT, Searle SMJ, Rees AR, Roguoka MA, Guild BC,

XX WPI; 1994-120230/15.

PT Method of resurfacing of rodent antibodies to produce humanised antibody

XX PT forms - for producing non human antibodies with improved therapeutic

XX PT efficiency by presenting human surface on V-region.

XX Example 1; Fig 3A; 230pp; English.

XX The present sequence is that of the light chain variable (LC VR) region  
CC of murine antibody 3Hm. This sequence was aligned with 11 other known  
CC antibody LC VRs and a set of framework positions of surface exposed amino  
CC acid residues was determined. This information can be used in a method to  
CC determine how to modify a rodent antibody or fragment by resurfacing in  
CC order to produce a humanised rodent antibody. Residues (determined from  
CC alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,  
CC 87, 111, 115, 116 and 117 are accessible residues. None of the entire  
CC combinations of surface residues in the murine sequences were found in  
CC the human sequences and vice versa. However the residues in individual  
CC positions appear to be conserved

XX Sequence 109 AA;

Query Match 80.8%; Score 534; DB 2; Length 109;  
Best Local Similarity 95.4%; Pred. No. 7,4e-31;

Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPEDSVSLSCRASQIISNNLHWYQOKSHESPRLLIKXASQISGIPS 80  
DB 1 DIVLTQSPATLSVTPEDSVSLSCRASQIISNNLHWYQOKSHESPRLLIKXASQISGIPS 60

QY 81 RFGSGSGTDFTLINSVETEDFGMFCCQSNWPLYFGGTYLTIKR 128

DB 61 RFGSGSGTDFTLINSVETEDFGMFCCQSNWPLYFGGTYLTIKR 108

# RESULT 10

AAAR15443 standard; protein; 240 AA.

AC AAR15443;

DT 25-FEB-1992 (first entry)

XX Single chain Fv from pSCV1 for blocking HRV binding to ICAM-1.

XX antigen-binding fragment; inflammation; auto-immune disease.

XX Homo. sapiens.

XX EP459577-A.

PD 04-DEC-1991.

PF 25-MAY-1991; 91EP-00201243.

PR 01-JUN-1990; 90US-00532001.

XX (MERI ) MERCK & CO INC.

PI Colomo RJ, Condra JH, Tomassini JE, Sardana VV;

XX WPI; 1991-355850/49.

PT Microbially expressed portions of monoclonal antibody - can block

PT attachment of rhinovirus ligands to inter-cellular adhesion molecule

XX (ICAM-1).

PS Claim 5; Page 21; 28pp; English.

XX The Fv fragment encoded by pSCV1 was able to protect cells against

XX infection by HRV-14. It was less active than modified Fv fragments which

XX included a Gly-Gly-Gly-ser flexible linker between the L and H chains

XX as either a monomer or a dimer. See also AAR15437-R15442

XX Sequence 240 AA;

Query Match 80.8%; Score 534; DB 2; Length 240;

XX Best Local Similarity 95.4%; Pred. No. 1.5e-30;

XX Matches 103; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPEDSVSLSCRASQIISNNLHWYQOKSHESPRLLIKXASQISGIPS 80

DB 1 DIVLTQSPATLSVTPEDSVSLSCRASQIISNNLHWYQOKSHESPRLLIKXASQISGIPS 60

QY 81 RFGSGSGTDFTLINSVETEDFGMFCCQSNWPLYFGGTYLTIKR 128

DB 61 RFGSGSGTDFTLINSVETEDFGMFCCQSNWPLYFGGTYLTIKR 108

RESULT 11

ID ADJ80363 standard; protein; 107 AA.

AC ADJ80363;

DT 06-MAY-2004 (first entry)





CC disease or chronic obstructive pulmonary disease. They may also be used  
CC for monitoring the efficacy of therapy for cancer in a patient known to  
CC or suspected to have cancer, and in screening for anti-cancer drugs. The  
CC present sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 107 AA;

Query Match 80.0%; Score 529; DB 8; Length 107;  
Best Local Similarity 94.4%; Pred. No. 1.7e-30;  
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPGDVSVLSCRASQIISNNLHWYQOKSHSPRLIKYASQISGIPS 80  
DB 1 DIVLTQSPATLSVTPGDVSVLSCRASQIISNNLHWYQOKSHSPRLIKYVFGSISGIPS 60  
QY 81 RFGSGSGGTFDTLINSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 127  
DB 61 RFGSGSGGTFDTLINSVETEDFGMYFCQOQNSWPLTFGAGTKLEIK 107

# RESULT 15

ID AAR38601 standard; peptide; 107 AA.

AC AAR38601;

DT 25-MAR-2003 (revised)  
DT 28-OCT-1993 (first entry)

DE HYH light chain.

KM Antibody; variable domain; light; L; heavy; H; consensus; affinity;  
KM antigen; immunogenicity; humanisation; framework.

OS Homo sapiens.

PN WO9311794-A1.

PD 24-JUN-1993.

PF 14-DEC-1992; 92WO-US010906.

PR 13-DEC-1991; 91US-00808464.

PA (XOMA ) XOMA CORP.

PI Studnicka GM, Little RG, Fishwild DM, Kohn FR;

DR WPI; 1993-213827/26.

PT Antibodies prepn. used for treatment of auto-immune diseases - by  
PT replacement of critical residues to reduce immunogenicity but retain  
PT binding affinity, etc.

PS Disclosure; Page 84; 160pp; English.

CC The amino acid sequences of the light and heavy chains of the variable  
CC domains from antibodies HYH [HYHEL-10 Fab-lysosyme complex] (AAR38601 and  
CC AAR38608, respectively), MCPC [IGA Fab MCP603-phosphocholine complex]  
CC (AAR38602-03 and AAR38609-10, respectively), NEMW [Ig Fab' NEM] (AAR38604  
CC -05 and AAR38611, respectively) and KOL [IgG1 KOL] (AAR38606-07 and  
CC AAR38612, respectively) may be used to determine an alignment from which  
CC appropriate changes may be made. Unlike other methods of humanisation,  
CC which advocate the replacement of entire antibody framework regions with  
CC those of human antibodies, this method involves only the introduction of  
CC human residues into those positions not critical for antigen binding.  
CC This ensures that the binding properties of the modified antibody are not  
CC diminished. (Updated on 25-MAR-2003 to correct FN field.)  
XX  
SQ Sequence 107 AA;

Query Match 79.6%; Score 526; DB 2; Length 107;  
Best Local Similarity 94.4%; Pred. No. 2.7e-30;

Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPGDVSVLSCRASQIISNNLHWYQOKSHSPRLIKYASQISGIPS 80  
DB 1 DIVLTQSPATLSVTPGDVSVLSCRASQIISNNLHWYQOKSHSPRLIKYVFGSISGIPS 60  
QY 81 RFGSGSGGTFDTLINSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 127  
DB 61 RFGSGSGGTFDTLINSVETEDFGMYFCQOQNSWPLTFGAGTKLEIK 107

Search completed: May 25, 2005, 15:47:16  
Job time : 63.2493 secs

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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:02 ; Search time 15.9553 Seconds  
(without alignments)  
598.864 Million cell updates/sec

Title: US-10-006-773a-6

Perfect score: 661  
Sequence: 1 MVEFPOILGLMFMISASRG.....QQSNMWPLTFSGSTLEIKR 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCUTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfillseq1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	96.4	127	1	US-08-436-463-18 Sequence 18, Appl
2	634	95.9	127	1	US-07-634-278-83 Sequence 83, Appl
3	634	95.9	127	1	US-08-477-728-83 Sequence 83, Appl
4	634	95.9	127	1	US-08-474-040-83 Sequence 83, Appl
5	634	95.9	127	1	US-08-487-200-83 Sequence 83, Appl
6	634	95.9	127	3	US-08-484-537-83 Sequence 83, Appl
7	622	94.1	127	1	US-08-436-463-4 Sequence 4, Appl
8	534	80.8	108	4	US-09-232-290-27 Sequence 27, Appl
9	534	80.8	109	1	US-07-642-245-4 Sequence 4, Appl
10	531	80.3	107	1	US-07-634-278-62 Sequence 62, Appl
11	531	80.3	107	1	US-08-477-728-62 Sequence 62, Appl
12	531	80.3	107	1	US-08-474-040-62 Sequence 62, Appl
13	531	80.3	107	1	US-08-487-200-62 Sequence 62, Appl
14	531	80.3	107	3	US-08-484-537-62 Sequence 62, Appl
15	529	80.0	107	1	US-08-436-463-20 Sequence 20, Appl
16	526	79.6	107	1	US-08-107-669D-1 Sequence 1, Appl
17	526	79.6	107	1	US-08-172-788A-1 Sequence 1, Appl
18	526	79.6	107	2	US-08-477-531B-1 Sequence 1, Appl
19	526	79.6	107	2	US-08-487-200-62 Sequence 62, Appl
20	511	77.3	107	4	US-09-339-922A-8 Sequence 8, Appl
21	511	77.3	107	4	US-09-339-922A-8 Sequence 8, Appl
22	511	77.3	107	4	US-09-791-391A-8 Sequence 8, Appl
23	506	76.6	100	1	US-09-016-061-8 Sequence 8, Appl
24	492	74.4	103	4	US-08-436-463-19 Sequence 19, Appl
25	480	72.6	103	4	US-09-419-788-29 Sequence 29, Appl
26	471	71.3	108	3	US-08-436-463-21 Sequence 21, Appl
27	471	71.3	108	4	US-09-247-352-1 Sequence 1, Appl

28	471	71.3	214	3	US-09-247-352-4 Sequence 4, Appl
29	471	71.3	214	4	US-09-466-635-4 Sequence 4, Appl
30	468.5	70.9	127	2	US-08-476-176B-6 Sequence 6, Appl
31	468.5	70.9	127	3	US-08-127-721A-6 Sequence 6, Appl
32	468.5	70.9	127	3	US-08-485-246A-6 Sequence 6, Appl
33	468	70.8	108	2	US-08-737-560A-11 Sequence 11, Appl
34	467.5	70.7	127	2	US-08-476-176B-10 Sequence 10, Appl
35	467.5	70.7	127	3	US-08-127-721A-10 Sequence 10, Appl
36	467.5	70.7	127	3	US-08-485-246A-10 Sequence 10, Appl
37	467	70.7	143	2	US-08-653-402B-8 Sequence 8, Appl
38	464.5	70.3	127	2	US-08-476-176B-8 Sequence 8, Appl
39	464.5	70.3	127	3	US-08-127-721A-8 Sequence 8, Appl
40	464.5	70.3	127	3	US-08-485-246A-8 Sequence 8, Appl
41	455	68.8	107	4	US-09-438-954-38 Sequence 38, Appl
42	442	66.9	107	1	US-07-634-278-63 Sequence 63, Appl
43	442	66.9	107	1	US-07-634-278-87 Sequence 87, Appl
44	442	66.9	107	1	US-08-477-728-63 Sequence 63, Appl
45	442	66.9	107	1	US-08-477-728-87 Sequence 87, Appl

# ALIGNMENTS

RESULT 1  
US-08-436-463-18  
Sequence 18, Application US/08436463  
Patent No. 5760185  
GENERAL INFORMATION:  
APPLICANT: KIMACHI, Kazuhiko  
APPLICANT: MAEDA, Hiroaki  
APPLICANT: NISHIYAMA, Kiyoko  
APPLICANT: TOKIYOSHI, Sachio  
TITLE OF INVENTION: ANTI-PELVINE HERPES VIRUS-1 RECOMBINANT  
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT CODING FOR SAID ANTIBODY  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
STREET: 419 Seventh Street, N.W., Suite 400  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436,463  
FILING DATE: 26-JUN-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 341255/1992  
FILING DATE: 28-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: KIMACHI=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 127 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-463-18  
Query Match 96.4%; Score 637; DB 1; Length 127;  
Best Local Similarity 96.9%; Pred. No. 2.7e-53;  
Matches 123; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Oy      MVEFPPQLGMLFMWISASRGDIVLTQSPATLSVTPGDSVYSICRASQIISNNLHWYQOKS 60
Db      MWFPFQLGMLFMWISASRGDIVLTQSPATLSVTPGDSVYSICRASQIISNNLHWYQOKS 60
Oy      1 MWFPFQLGMLFMWISASRGDIVLTQSPATLSVTPGDSVYSICRASQIISNNLHWYQOKS 60
Oy      HESPRRLIKKASQSIGIPERFSGSGGDTFTLSINSVETEDFGMYFCQOQNSMPLTFGS 120
Db      HESPRRLIKKASQSIGIPERFSGSGGDTFTLSINSVETEDFGMYFCQOQNSMPLTFGA 120
Oy      |||||:|||||
Oy      61 HESPRRLIKKASQSIGIPERFSGSGGDTFTLSINSVETEDFGMYFCQOQNSMPLTFGS 120
Db      61 HESPRRLIKKASQSIGIPERFSGSGGDTFTLSINSVETEDFGMYFCQOQNSMPLTFGA 120
Oy      |||||:|||||
Oy      121 GTKLEIK 127
Db      121 GTKLEIK 127

```

```

1      RESULT 2
2      US-07-634-278-83
3      Sequence 83, Application US/07634278
4      Patent No. 5530101
5      GENERAL INFORMATION:
6      APPLICANT: QUEEN, Cary L.
7      APPLICANT: CO, Man Sung
8      APPLICANT: SCHNEIDER, William P.
9      APPLICANT: LANDOLFI, Nicholas F.
10     APPLICANT: COELINGH, Kathleen L.
11     APPLICANT: SELICK, Harold E.
12     TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
13     NUMBER OF SEQUENCES: 113
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: Townsend and Townsend Khourie and Crew
16     STREET: 379 Lytton Avenue
17     CITY: Palo Alto
18     STATE: California
19     COUNTRY: US
20     ZIP: 94301
21     COMPUTER READABLE FORM:
22     MEDIUM TYPE: Floppy disk
23     COMPUTER: IBM PC compatible
24     OPERATING SYSTEM: PC-DOS/MS-DOS
25     SOFTWARE: PatentIn Release #1.0, Version #1.25
26     CURRENT APPLICATION DATA:
27     APPLICATION NUMBER: US/07/634,278
28     FILING DATE: 19-DEC-1990
29     CLASSIFICATION: 424
30     PRIOR APPLICATION DATA:
31     APPLICATION NUMBER: US 07/590,274
32     FILING DATE: 28-SEP-1990
33     PRIOR APPLICATION DATA:
34     APPLICATION NUMBER: US 07/110,252
35     FILING DATE: 13-FEB-1989
36     PRIOR APPLICATION DATA:
37     APPLICATION NUMBER: US 07/290,975
38     FILING DATE: 28-DEC-1988
39     ATTORNEY/AGENT INFORMATION:
40     NAME: Smith, William M
41     REGISTRATION NUMBER: 30,223
42     REFERENCE/DOCKET NUMBER: 11823-002600
43     TELECOMMUNICATION INFORMATION:
44     TELEPHONE: (415) 326-2400
45     TELEFAX: (415) 326-2422
46     INFORMATION FOR SEQ ID NO: 83:
47     SEQUENCE CHARACTERISTICS:
48     LENGTH: 127 amino acids
49     TYPE: amino acid
50     TOPOLOGY: linear
51     MOLECULE TYPE: protein
52     US-07-634-278-83

```

```

Query Match          95.9%;   Score 634;   DB 1;   Length 127;
Best Local Similarity 96.1%;   Pred. No. 5, 2e-53;
Matches 122;   Conservative 1;   Indels 0;   Gaps 0;

QY      1 MVFPTQIIIGLMFWISASRGDIVLQSPATLISVTPRGDSVLSQCRASQIISNNLHWQOKS 60
      : |||||

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Db      _ MVEPTPLGLMFWISASRSGDIVLTPSPATLISVTPGDSVSISCAASOSISNNLHWQOKS 60
QY      61 HESPPRLIKYASOSISGIPSRFSGSGSGDFTLSINSVETEDFGMYFCOOSNSMPLTFGS 120
        |||||
        |||||
Db      61 HESPRLLIKYASOSISGIPSRFSGSGSGDFTLSNVGVETEDFGMYFCQOSNSMPLHFGG 120
QY      121 GTLLEIK 127
        |||||
        |||||
Db      121 GTLLEIK 127

```

```

1      RESULT 3
2      US-08-477-728-03
3      ; Sequence 03, Application US/08477728
4      ; Patent No. 5585089
5      ; GENERAL INFORMATION:
6      ; APPLICANT: QUEEN, Cary L.
7      ; APPLICANT: SCHNIDER, William P.
8      ; APPLICANT: SELICK, Harold E.
9      ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
10     ; NUMBER OF SEQUENCES: 113
11     ; CORRESPONDENCE ADDRESS:
12     ; ADDRESSEE: Townsend and Townsend and Crew LLP
13     ; STREET: Two Embarcadero Center, 8th Floor
14     ; CITY: Palo Alto
15     ; STATE: California
16     ; COUNTRY: US
17     ; ZIP: 94111
18     ; COMPUTER READABLE FORM:
19     ; MEDIUM TYPE: Floppy disk
20     ; COMPUTER: IBM PC Compatible
21     ; OPERATING SYSTEM: PC-DOS/MS-DOS
22     ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23     ; CURRENT APPLICATION DATA:
24     ; APPLICATION NUMBER: US/08/477,728
25     ; FILING DATE: 07-JUN-1995
26     ; CLASSIFICATION: 424
27     ; PRIOR APPLICATION DATA:
28     ; APPLICATION NUMBER: US 07/634,278
29     ; FILING DATE: 19-DEC-1990
30     ; PRIOR APPLICATION DATA:
31     ; APPLICATION NUMBER: US 07/590,274
32     ; FILING DATE: 28-SEP-1990
33     ; PRIOR APPLICATION DATA:
34     ; APPLICATION NUMBER: US 07/310,252
35     ; FILING DATE: 13-FEB-1989
36     ; PRIOR APPLICATION DATA:
37     ; APPLICATION NUMBER: US 07/290,975
38     ; FILING DATE: 28-DEC-1988
39     ; ATTORNEY/AGENT INFORMATION:
40     ; NAME: Smith, William M
41     ; REGISTRATION NUMBER: 30,223
42     ; REFERENCE/DOCKET NUMBER: 11823-002600
43     ; TELECOMMUNICATION INFORMATION:
44     ; TELEPHONE: (415) 326-2400
45     ; TELEFAX: (415) 326-2422
46     ; INFORMATION FOR SEQ ID NO: 83:
47     ; SEQUENCE CHARACTERISTICS:
48     ; LENGTH: 127 amino acids
49     ; TYPE: amino acid
50     ; TOPOLOGY: linear
51     ; MOLECULE TYPE: protein
52     ; US-08-477-728-03

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Query Match	95.9%	Score 634	DB 1	Length 127
Best Local Similarity	96.1%	Pred. No. 5, 2e-53		
Matches 122	Conservative 1	Mismatches 4	Indels 0	Gaps 0

  

QY	1	MVFPTQIIIGLFWTASASRGDIIVLTQSRATLSYFGSDVSLSCRSQIISNNLHWYQOKS	60
DB	1	MVFPTQIIIGLFWTASASRGDIIVLTQSRATLSYFGSDVSLSCRSQIISNNLHWYQOKS	60
QY	61	HESPLLKIVASQISIGIPSPRSGSGCTDTFLINSVATEDFGMYPCQASNSWPLTTRGS	120



Db 61 HESPRLIKYASQISIGIPSRFGSGGTDFLTLSVNGVETEDFGMYFCOQSNMWPHTFG 120  
 QY 121 GTRLEIK 127  
 Db 121 GTRLEIK 127

RESULT 4

US-08-474-040-83  
 ; Sequence 83, Application US/08474040  
 ; Patent No. 5693761  
 ; GENERAL INFORMATION:  
 ; APPLICANT: QUEEN, Cary L.  
 ; APPLICANT: CO, Man Sung  
 ; APPLICANT: SCHNEIDER, William P.  
 ; APPLICANT: LANDOLFI, Nicholas P.  
 ; APPLICANT: COELINGH, Kathleen L.  
 ; APPLICANT: SELICK, Harold B.  
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 ; NUMBER OF SEQUENCES: 113  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend Knourie and Crew  
 ; STREET: 379 Lytton Avenue  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94301  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/474,040  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/634,278  
 ; FILING DATE: 19-DEC-1990  
 ; APPLICATION NUMBER: US 07/590,274  
 ; FILING DATE: 28-SEP-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/310,252  
 ; FILING DATE: 13-FEB-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/290,975  
 ; FILING DATE: 28-DEC-1988  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 11823-002600  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 326-2400  
 ; TELEFAX: (415) 326-2422  
 ; INFORMATION FOR SEQ ID NO: 83:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 127 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-474-040-83

Query Match 95.9%; Score 634; DB 1; Length 127;  
 Best Local Similarity 96.1%; Pred. No. 5.2e-53;  
 Matches 122; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MWFTPOIIGLMFWISASRGDIVLTOSPATLSVTGDSVSLSCRASQIISNNLHWYQKS 60  
 DB 1 MWFTPOIIGLMFWISASRGDIVLTOSPATLSVTGDSVSLSCRASQIISNNLHWYQKS 60  
 QY 61 HESPRLIKYASQISIGIPSRFGSGGTDFLTLSVNGVETEDFGMYFCOQSNMWPHTFGS 120

Db 61 HESPRLIKYASQISIGIPSRFGSGGTDFLTLSVNGVETEDFGMYFCOQSNMWPHTFG 120  
 QY 121 GTRLEIK 127  
 Db 121 GTRLEIK 127

RESULT 5

US-08-487-200-83  
 ; Sequence 83, Application US/08487200  
 ; Patent No. 5693762  
 ; GENERAL INFORMATION:  
 ; APPLICANT: QUEEN, Cary L.  
 ; APPLICANT: CO, Man Sung  
 ; APPLICANT: SCHNEIDER, William P.  
 ; APPLICANT: LANDOLFI, Nicholas P.  
 ; APPLICANT: COELINGH, Kathleen L.  
 ; APPLICANT: SELICK, Harold B.  
 ; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
 ; NUMBER OF SEQUENCES: 113  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew  
 ; STREET: 379 Lytton Avenue  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: US  
 ; ZIP: 94301  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/487,200  
 ; FILING DATE: 7-JUN-1995  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/634,278  
 ; FILING DATE: 19-DEC-1990  
 ; APPLICATION NUMBER: US 07/590,274  
 ; FILING DATE: 28-SEP-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/310,252  
 ; FILING DATE: 13-FEB-1989  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/290,975  
 ; FILING DATE: 28-DEC-1988  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 11823-002610  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 326-2400  
 ; TELEFAX: (415) 326-2422  
 ; INFORMATION FOR SEQ ID NO: 83:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 127 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-487-200-83

Query Match 95.9%; Score 634; DB 1; Length 127;  
 Best Local Similarity 96.1%; Pred. No. 5.2e-53;  
 Matches 122; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MWFTPOIIGLMFWISASRGDIVLTOSPATLSVTGDSVSLSCRASQIISNNLHWYQKS 60  
 DB 1 MWFTPOIIGLMFWISASRGDIVLTOSPATLSVTGDSVSLSCRASQIISNNLHWYQKS 60  
 QY 61 HESPRLIKYASQISIGIPSRFGSGGTDFLTLSVNGVETEDFGMYFCOQSNMWPHTFGS 120

Db 61 HESPRLLIKYASQISIGIPSRFSGSGSDTFTLSVNGVETEDFGMYFCQGSNSWPHTFGG 120  
QY 121 GTKLEIK 127  
Db 121 GTKLEIK 127

RESULT 6  
US-08-484-537-83  
; Sequence 83, Application US/08484537  
; Patent No. 6180370  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,537  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US/07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 83:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-484-537-83

Query Match 95.9%; Score 634; DB 3; Length 127;  
Best Local Similarity 96.1%; Pred. No. 5.2e-53;  
Matches 122; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MVEFTPOLIGLMLFWISASRGDIVLTOSPATLSVTTPGDSVSLSCRASQIISNNLHWYQOKS 60  
Db 1 MVEFTPOLIGLMLFWISASRGDIVLTOSPATLSVTTPGDSVSLSCRASQIISNNLHWYQOKS 60  
QY 61 HESPRLLIKYASQISIGIPSRFSGSGSDTFTLSINSVETEDFGMYFCQGSNSWPHTFGS 120  
Db 61 HESPRLLIKYASQISIGIPSRFSGSGSDTFTLSINSVETEDFGMYFCQGSNSWPHTFGS 120

QY 121 GTKLEIK 127  
Db 121 GTKLEIK 127

RESULT 7  
US-08-436-463-4  
; Sequence 4, Application US/08436463  
; Patent No. 5760185  
; GENERAL INFORMATION:  
; APPLICANT: KIMACHI, Kazuhiko  
; APPLICANT: MAEDA, Hiroaki  
; APPLICANT: NISHIYAMA, Kiyoko  
; APPLICANT: TOKIYOSHI, Sachio  
; TITLE OF INVENTION: ANTI-FELINE HERPES VIRUS-1 RECOMBINANT  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street, N.W., Suite 400  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/436,463  
; FILING DATE: 26-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 341255/1992  
; FILING DATE: 28-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-737-3528  
; TELEFAX: 202-628-5197  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 127 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-436-463-4

Query Match 94.1%; Score 622; DB 1; Length 127;  
Best Local Similarity 94.5%; Pred. No. 7.2e-52;  
Matches 120; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 MVEFTPOLIGLMLFWISASRGDIVLTOSPATLSVTTPGDSVSLSCRASQIISNNLHWYQOKS 60  
Db 1 MVEFTPOLIGLMLFWISASRGDIVLTOSPATLSVTTPGDSVSLSCRASQIISNNLHWYQOKS 60  
QY 61 HESPRLLIKYASQISIGIPSRFSGSGSDTFTLSINSVETEDFGMYFCQGSNSWPHTFGS 120  
Db 61 HESPRLLIKYASQISIGIPSRFSGSGSDTFTLSINSVETEDFGMYFCQGSNSWPHTFGS 120  
QY 121 GTKLEIK 127  
Db 121 GTKLEIK 127  
RESULT 8  
US-09-232-290-27  
; Sequence 27, Application US/09232290A  
; Patent No. 6815540

GENERAL INFORMATION:  
APPLICANT: PLUCKTHUN, ANDREAS  
APPLICANT: NIEBA, LARS  
APPLICANT: HONEGGER, ANNEMARIE  
TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH  
TITLE OF INVENTION: INCREASED SOLUBILITY  
FILE REFERENCE: MORPHO/7  
CURRENT APPLICATION NUMBER: US/09/232,290A  
CURRENT FILING DATE: 1999-01-15  
EARLIER APPLICATION NUMBER: PCT/EP96/02230  
EARLIER FILING DATE: 1996-05-23  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 27  
LENGTH: 108  
TYPE: PRT  
ORGANISM: Murine  
US-09-232-290-27

Query Match 80.8%; Score 534; DB 4; Length 108;  
Best Local Similarity 95.4%; Pred. No. 1.4e-43;  
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 21 DIVLTQSPATLSVTPGDVSLSGCRASQIISNNLHWYQOKSHSPRLLIKVASQISIGIPS 80  
Db 1 DIVLTQSPATLSVTPGNSVSLSCRASQSIGNNLHWYQOKSHSPRLLIKVASQISIGIPS 60  
Qy 81 RFGSGSGTDFLTLSINSVETEDFGMYFCQOQSNWPLTGGSGTKLEIKR 128  
Db 61 RFGSGSGTDFLTLSINSVETEDFGMYFCQOQSNWPLTGGSGTKLEIKR 108

RESULT 9  
US-07-942-245-4  
Sequence 4, Application US/07942245  
Patent No. 5639641  
GENERAL INFORMATION:  
APPLICANT: PEDERSEN, Jan T.  
APPLICANT: SEARLE, Stephen M.J.  
APPLICANT: REES, Anthony R.  
APPLICANT: ROGUSKA, Michael A.  
APPLICANT: GUILD, Braydon C.  
TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT  
TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 522  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrie, Mion, Zimm, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: HP 9000/700 workstation  
OPERATING SYSTEM: UNIX  
SOFTWARE: In house  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/942,245  
FILING DATE: 09-SEP-1992  
CLASSIFICATION: 530  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7860  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-942-245-4

Query Match 80.8%; Score 534; DB 1; Length 109;  
Best Local Similarity 95.4%; Pred. No. 1.4e-43;  
Matches 103; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 21 DIVLTQSPATLSVTPGDVSLSGCRASQIISNNLHWYQOKSHSPRLLIKVASQISIGIPS 80  
Db 1 DIVLTQSPATLSVTPGNSVSLSCRASQSIGNNLHWYQOKSHSPRLLIKVASQISIGIPS 60  
Qy 81 RFGSGSGTDFLTLSINSVETEDFGMYFCQOQSNWPLTGGSGTKLEIKR 128  
Db 61 RFGSGSGTDFLTLSINSVETEDFGMYFCQOQSNWPLTGGSGTKLEIKR 108

RESULT 10  
US-07-634-278-62  
Sequence 62, Application US/07634278  
Patent No. 5530101  
GENERAL INFORMATION:  
APPLICANT: QUEEN, Cary L.  
APPLICANT: CO, Man Sung  
APPLICANT: SCHNEIDER, William P.  
APPLICANT: LANDOLFI, Nicholas F.  
APPLICANT: SELICK, Kathleen L.  
APPLICANT: COELING, Harold E.  
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/634,278  
FILING DATE: 19-DEC-1990  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-07-634-278-62

Query Match 80.3%; Score 531; DB 1; Length 107;  
Best Local Similarity 95.3%; Pred. No. 2.6e-43;  
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 21 DIVLTQSPATLSVTPGDVSLSGCRASQIISNNLHWYQOKSHSPRLLIKVASQISIGIPS 80  
Db 1 DIVLTQSPATLSVTPGNSVSLSCRASQSIGNNLHWYQOKSHSPRLLIKVASQISIGIPS 60

Db 1 DIVLTGSPATLSTVPDGSVLSRCASQISNNLHMWYQOKSHESPRLIKYASQISIGIPS 60  
QY 81 RFSGSGGTDFTLINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 127  
Db 61 RFSGSGGTDFTLINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 107

RESULT 11  
US-08-477-728-62  
; Sequence 62, Application US/08477728  
; Patent No. 5585089  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,728  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-477-728-62

Query Match 80.3%; Score 531; DB 1; Length 107;  
Best Local Similarity 95.3%; Pred. No. 2,6e-43; Indels 0; Gaps 0;  
Matches 102; Conservative 1; Mismatches 4;  
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Db 1 DIVLTGSPATLSTVPDGSVLSRCASQISNNLHMWYQOKSHESPRLIKYASQISIGIPS 60  
QY 81 RFSGSGGTDFTLINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 127  
Db 61 RFSGSGGTDFTLINSVETEDFGMYFCQOSNSWPLTFGSGTKLEIK 107

RESULT 12  
US-08-474-040-62  
; Sequence 62, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLEI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Knourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 62:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-474-040-62

Query Match 80.3%; Score 531; DB 1; Length 107;  
Best Local Similarity 95.3%; Pred. No. 2,6e-43; Indels 0; Gaps 0;  
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RESULT 13  
US-08-487-200-62  
; Sequence 62, Application US/08487200

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; Patent No. 5693762
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLF, Nicholas P.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,200
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
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; MOLECULE TYPE: peptide
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Best Local Similarity 95.3%; Pred. No. 2.6e-43;
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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DB 61 RPSGSGGTDFTLSTINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 107

RESULT 14
US-08-484-537-62
; Sequence 62, Application US/08484537
; Patent No. 6180370
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
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; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLF, Nicholas P.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,537
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-484-537-62

Query Match      80.3%; Score 531; DB 3; Length 107;
Best Local Similarity 95.3%; Pred. No. 2.6e-43;
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSVTPGDVSLSLCRASQIISNNLHWYQKSHSPRLILKYASQISIGIPS 80
DB 1 DIVLTQSPATLSVTPGDVSLSLCRASQIISNNLHWYQKSHSPRLILKYASQISIGIPS 60

QY 81 RPSGSGGTDFTLSTINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 127
DB 61 RPSGSGGTDFTLSTINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 107

RESULT 15
US-08-436-463-20
; Sequence 20, Application US/08436463
; Patent No. 5760185
; GENERAL INFORMATION:
; APPLICANT: KIMACHI, Kazuhiko
; APPLICANT: MAEDA, Hiroaki
; APPLICANT: NISHIYAMA, Kiyoko
; APPLICANT: TOKIYOSHI, Sachio
; TITLE OF INVENTION: ANTI-BELINE HERPES VIRUS-1 RECOMBINANT
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:37:58 ; Search time 59.0586 Seconds  
(without alignments)  
724.991 Million cell updates/sec

Title: US-10-006-773a-6

Perfect score: 661

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Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

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- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
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- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	661	100.0	128	US-10-006-773-6	Sequence 6, Appl1
2	634	95.9	127	US-10-452-357-83	Sequence 83, Appl1
3	626	94.7	127	US-10-389-155-70	Sequence 70, Appl1
4	626	94.7	127	US-10-389-417-70	Sequence 70, Appl1
5	614	92.9	127	US-10-452-646-28	Sequence 28, Appl1
6	533	80.6	107	US-10-308-817-123	Sequence 123, App
7	533	80.6	107	US-10-453-698-123	Sequence 123, App
8	531	80.3	107	US-10-388-155-21	Sequence 21, Appl1
9	531	80.3	107	US-10-389-417-21	Sequence 21, Appl1
10	531	80.3	107	US-10-452-357-62	Sequence 62, Appl1
11	529	80.0	107	US-10-436-782-17	Sequence 17, Appl1
12	529	80.0	107	US-10-923-068-511	Sequence 511, App
13	529	80.0	107	US-10-920-899-1776	Sequence 1776, App

14	526	79.6	107	US-10-340-189-1	Sequence 1, Appl1
15	526	79.6	107	US-10-325-696-1	Sequence 1, Appl1
16	525	79.4	109	US-10-078-7578-45	Sequence 45, Appl1
17	520	78.7	108	US-09-910-483-38	Sequence 38, Appl1
18	520	78.7	108	US-09-910-483-42	Sequence 42, Appl1
19	518	78.4	108	US-10-223-880-7	Sequence 7, Appl1
20	511	77.3	107	US-08-790-540A-8	Sequence 8, Appl1
21	511	77.3	107	US-08-791-391A-8	Sequence 8, Appl1
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26	511	77.3	107	US-10-959-871-8	Sequence 8, Appl1
27	506	76.6	127	US-10-374-600-15	Sequence 15, Appl1
28	506	76.6	127	US-10-374-531-15	Sequence 15, Appl1
29	493	74.6	127	US-10-374-600-5	Sequence 5, Appl1
30	493	74.6	127	US-10-374-531-5	Sequence 5, Appl1
31	493	74.6	127	US-10-374-600-11	Sequence 11, Appl1
32	493	74.6	127	US-10-374-531-11	Sequence 11, Appl1
33	492.5	74.5	109	US-10-032-482-6	Sequence 6, Appl1
34	492	74.4	264	US-10-207-655-400	Sequence 400, App
35	492	74.4	548	US-10-207-655-272	Sequence 272, App
36	487	73.7	127	US-10-207-655-264	Sequence 264, App
37	484.5	73.3	131	US-10-207-655-244	Sequence 244, App
38	484.5	73.3	267	US-10-207-655-248	Sequence 248, App
39	484.5	73.3	552	US-10-207-655-265	Sequence 265, App
40	471	71.3	768	US-10-207-655-350	Sequence 350, App
41	467	70.7	243	US-10-097-558-2	Sequence 2, Appl1
42	466	70.5	107	US-09-982-464-1	Sequence 1, Appl1
43	466	70.5	107	US-10-697-399-1	Sequence 1, Appl1
44	466	70.5	107	US-10-697-400-1	Sequence 1, Appl1
45	465	70.3	128	US-10-443-466A-74	Sequence 74, Appl1

ALIGNMENTS

RESULT 1  
US-10-006-773-6  
; Sequence 6, Application US/10006773  
; Publication No. US20020132983A1  
; GENERAL INFORMATION:  
; APPLICANT: Junghans, Richard P.  
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Ant.  
; FILE REFERENCE: 003  
; CURRENT APPLICATION NUMBER: US/10/006,773  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/250,089  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-006-773-6

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Best Local Similarity	100.0%	Pred. No. 2.9e-50		
Matches 128	Conservative	0	Mismatches	0
			Indels	0
			Gaps	0
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DB	1	MWFTQIIQLGLMFWISASRGDIVLTQSPATLSVTPGDYSVLSGRASQITISNNLHWYQKS	60	
QY	61	HSSPLTKVYASQISGIPSRFSGSGSDFTLSINSVETEDFGMYFCQSNMPLTFGS	120	
DB	61	HSSPLTKVYASQISGIPSRFSGSGSDFTLSINSVETEDFGMYFCQSNMPLTFGS	120	
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DB	121	GTKLEIKR 128		

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US-10-452-357-83  
; Sequence 83, Application US/10452357  
; Publication No. US20040058414A1  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary  
; APPLICANT: Co, Man Sung  
; APPLICANT: Schneider, William  
; APPLICANT: Landolfi, Nicholas  
; APPLICANT: Coeligh, Kathleen  
; APPLICANT: Selick, Harold  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; FILE REFERENCE: 05882.0078, CNU501  
; CURRENT APPLICATION NUMBER: US/10/452,357  
; CURRENT FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: 09/718,993  
; PRIOR FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: 09/487,200  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 07/634,278  
; PRIOR FILING DATE: 1990-12-19  
; PRIOR APPLICATION NUMBER: 07/590,275  
; PRIOR FILING DATE: 1990-09-28  
; PRIOR APPLICATION NUMBER: 07/310,252  
; PRIOR FILING DATE: 1989-02-13  
; PRIOR APPLICATION NUMBER: 07/290,975  
; PRIOR FILING DATE: 1988-12-28  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 83  
; LENGTH: 127  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: CMV5 light chain antibody  
US-10-452-357-83

Query Match 95.9%; Score 634; DB 15; Length 127;  
Best Local Similarity 96.1%; Pred. No. 6,5e-48;  
Matches 122; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
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RESULT 3  
US-10-389-155-70  
; Sequence 70, Application US/10389155  
; Publication No. US20030229208A1  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary L.  
; APPLICANT: Co, Man Sung  
; APPLICANT: Schneider, William P.  
; APPLICANT: Landolfi, Nicholas F.  
; APPLICANT: Coeligh, Kathleen L.  
; APPLICANT: Selick, Harold E.  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California

COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/389,155  
FILING DATE: 13-Mar-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/325,000  
FILING DATE: 01-JUN-1999  
APPLICATION NUMBER: US 07/290,975  
FILING DATE: 28-DEC-1988  
APPLICATION NUMBER: US 07/310,252  
FILING DATE: 13-FEB-1989  
APPLICATION NUMBER: US 07/590,274  
FILING DATE: 28-SEP-1990  
APPLICATION NUMBER: US 07/634,278  
FILING DATE: 19-DEC-1990  
APPLICATION NUMBER: US 08/484,537  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 011823-002650US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 127 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
US-10-389-155-70

Query Match 94.7%; Score 626; DB 15; Length 127;  
Best Local Similarity 94.5%; Pred. No. 3.3e-47;  
Matches 120; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
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DB 121 GTKLEIK 127

RESULT 4  
US-10-389-417-70  
; Sequence 70, Application US/10389417  
; Publication No. US20040049014A1  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary L.  
; APPLICANT: Co, Man Sung  
; APPLICANT: Schneider, William P.  
; APPLICANT: Landolfi, Nicholas F.  
; APPLICANT: Coeligh, Kathleen L.  
; APPLICANT: Selick, Harold E.  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco



```
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent in Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/389,417
/ FILING DATE: 13-Mar-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/325,000
/ FILING DATE: 01-JUN-1999
/ APPLICATION NUMBER: US 07/290,975
/ FILING DATE: 28-DEC-1988
/ APPLICATION NUMBER: US 07/310,252
/ FILING DATE: 13-FEB-1989
/ APPLICATION NUMBER: US 07/590,274
/ FILING DATE: 28-SEP-1990
/ APPLICATION NUMBER: US 07/634,278
/ FILING DATE: 19-DEC-1990
/ APPLICATION NUMBER: US 08/484,537
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M.
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 011823-002650US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 70:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 127 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-10-389-417-70

Query Match          94.7%; Score 626; DB 15; Length 127;
Best Local Similarity 94.5%; Pred. No. 3.3e-47;
Matches 120; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MWFTPOLGLMFWISASRGDIYLTQSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKS 60
DB 1 MWFTPOLGLMFWISASRGDIYLTQSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKS 60
QY 61 HSPRLIRYASQISIGIPSRFGSGSGTDFTLISNVTEDPGMYFCQOQSNWPLTFGS 120
DB 61 HSPRLIRYASQISIGIPSRFGSGSGTDFTLISNVTEDPGMYFCQOQSNWPLTFGS 120
QY 121 GTKLEIK 127
DB 121 GTKLEIK 127

RESULT 5
US-10-452-646-28
/ Sequence 28, Application US/10452646
/ Publication No. US20040018593A1
/ GENERAL INFORMATION:
/ APPLICANT: Carton, Jill M.
/ APPLICANT: Staquet, Kimberly C.
/ APPLICANT: Scallion, Bernard J.
/ APPLICANT: Jili, Gilles-Komar
/ TITLE OF INVENTION: ANTI-REL P FUSION ANTIBODIES, COMPOSITIONS, METHODS AND USES
/ FILE REFERENCE: CHN296 NP
/ CURRENT APPLICATION NUMBER: US/10/452,646
/ PRIOR FILING DATE: 2003-06-02
/ PRIOR APPLICATION NUMBER: US 60/385,305
/ PRIOR FILING DATE: 2002-06-03
```

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/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 28
/ LENGTH: 127
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-452-646-28

Query Match          92.9%; Score 614; DB 15; Length 127;
Best Local Similarity 91.3%; Pred. No. 3.7e-46;
Matches 116; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 MWFTPOLGLMFWISASRGDIYLTQSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKS 60
DB 1 MWFTPOLGLMFWISASRGDIYLTQSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKS 60
QY 61 HSPRLIRYASQISIGIPSRFGSGSGTDFTLISNVTEDPGMYFCQOQSNWPLTFGS 120
DB 61 HSPRLIRYASQISIGIPSRFGSGSGTDFTLISNVTEDPGMYFCQOQSNWPLTFGS 120
QY 121 GTKLEIK 127
DB 121 GTKLEIK 127

RESULT 6
US-10-308-817-123
/ Sequence 123, Application US/10308817
/ Publication No. US20030219861A1
/ GENERAL INFORMATION:
/ APPLICANT: Roche, Russell
/ APPLICANT: Wu, Dayang
/ TITLE OF INVENTION: HYBRID ANTIBODIES
/ FILE REFERENCE: 1087-37
/ CURRENT APPLICATION NUMBER: US/10/308,817
/ CURRENT FILING DATE: 2002-12-03
/ NUMBER OF SEQ ID NOS: 195
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 123
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: mouse
US-10-308-817-123

Query Match          80.6%; Score 533; DB 15; Length 107;
Best Local Similarity 96.3%; Pred. No. 3.7e-39;
Matches 103; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTQSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIP 80
DB 1 DIVLTQSPATLSTVPDGSVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIP 80
QY 81 RFGSGSGTDFTLISNVTEDPGMYFCQOQSNWPLTFGS 127
DB 81 RFGSGSGTDFTLISNVTEDPGMYFCQOQSNWPLTFGS 127

RESULT 7
US-10-453-698-123
/ Sequence 123, Application US/10453698
/ Publication No. US20040038308A1
/ GENERAL INFORMATION:
/ APPLICANT: Roche, Russell
/ APPLICANT: Roche, Russell
/ TITLE OF INVENTION: HYBRID ANTIBODIES
/ FILE REFERENCE: 82 CIP (1087-37 CIP)
/ CURRENT APPLICATION NUMBER: US/10/453,698
/ CURRENT FILING DATE: 2003-06-03
/ NUMBER OF SEQ ID NOS: 196
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 123
/ LENGTH: 107
/ TYPE: PRT
/ ORGANISM: mouse
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US-10-453-698-123

Query Match 80.6%; Score 533; DB 15; Length 107;  
Best Local Similarity 96.3%; Pred. No. 3,7e-39;  
Matches 109; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTGSPATLSTPGDVSLSGCRASQIISNNLHWYQKSHESPRLIKYASQISGIPS 80  
DB 1 DIVLTGSPATLSTPGDVSLSGCRASQISNNLHWYQKSHESPRLIKYASQISGIPS 60  
QY 81 RFGSGSGTDFTLTINSVETEDFGMYFCQOSNWPPLTFGSGTLEIK 127  
DB 61 RFGSGSGTDFTLTINSVETEDFGMYFCQOSNWPPLTFGSGTLEIK 107

RESULT 8

US-10-389-155-21  
Sequence 21, Application US/10389155  
Publication No. US20030229208A1

GENERAL INFORMATION:

APPLICANT: Queen, Cary L.

Co, Man Sung  
Schneider, William P.  
Landolfi, Nicholas F.  
Coeligh, Kathleen L.  
Selick, Harold E.

TITLE OF INVENTION: Improved Humanized Immunoglobulins

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/389,155

FILING DATE: 13-Mar-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000

FILING DATE: 01-JUN-1999

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 08/484,537

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 011823-002650US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

STRANDEDNESS: &lt;Unknown&gt;

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-389-155-21

Query Match 80.3%; Score 531; DB 15; Length 107;

Best Local Similarity 95.3%; Pred. No. 5.5e-39;  
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTGSPATLSTPGDVSLSGCRASQIISNNLHWYQKSHESPRLIKYASQISGIPS 80  
DB 1 DIVLTGSPATLSTPGDVSLSGCRASQISNNLHWYQKSHESPRLIKYASQISGIPS 60  
QY 81 RFGSGSGTDFTLTINSVETEDFGMYFCQOSNWPPLTFGSGTLEIK 127  
DB 61 RFGSGSGTDFTLTINSVETEDFGMYFCQOSNWPPLTFGSGTLEIK 107

RESULT 9

US-10-389-417-21  
Sequence 21, Application US/10389417  
Publication No. US20040049014A1

GENERAL INFORMATION:

APPLICANT: Queen, Cary L.

Co, Man Sung  
Schneider, William P.  
Landolfi, Nicholas F.  
Coeligh, Kathleen L.  
Selick, Harold E.

TITLE OF INVENTION: Improved Humanized Immunoglobulins

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/389,417

FILING DATE: 13-Mar-2003

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/325,000

FILING DATE: 01-JUN-1999

APPLICATION NUMBER: US 07/290,975

FILING DATE: 28-DEC-1988

APPLICATION NUMBER: US 07/310,252

FILING DATE: 13-FEB-1989

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

APPLICATION NUMBER: US 08/484,537

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 011823-002650US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

STRANDEDNESS: &lt;Unknown&gt;

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-10-389-417-21

Query Match 80.3%; Score 531; DB 15; Length 107;

Best Local Similarity 95.3%; Pred. No. 5.5e-39;  
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 21 DIVTQSPATLSVTPEGDSVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIPS 80  
Db 1 DIVTQSPATLSVTPEGDSVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIPS 60

Qy 81 RFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 127  
Db 61 RFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 107

RESULT 10  
US-10-452-357-62  
; Sequence 62, Application US/10452357  
; Publication No. US20040058414A1  
; GENERAL INFORMATION:  
; APPLICANT: Queen, Cary  
; APPLICANT: Co, Man Sung  
; APPLICANT: Schneider, William  
; APPLICANT: Landolfi, Nicholas  
; APPLICANT: Coeligh, Kathleen  
; APPLICANT: Selick, Harold  
; TITLE OF INVENTION: Improved Humanized Immunoglobulins  
; FILE REFERENCE: 05882.0078.CNUS01  
; CURRENT FILING DATE: 2003-05-30  
; PRIOR FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: 09/718,993  
; PRIOR FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: 09/487,200  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 07/634,278  
; PRIOR FILING DATE: 1990-12-19  
; PRIOR APPLICATION NUMBER: 07/590,275  
; PRIOR FILING DATE: 1990-09-28  
; PRIOR APPLICATION NUMBER: 07/310,252  
; PRIOR FILING DATE: 1989-02-13  
; PRIOR APPLICATION NUMBER: 07/290,975  
; PRIOR FILING DATE: 1988-12-28  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 62  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: murine Cmu5 light chain antibody  
US-10-452-357-62

Query Match 80.3%; Score 531; DB 15; Length 107;  
Best Local Similarity 95.3%; Pred. No. 5.5e-39;  
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 21 DIVTQSPATLSVTPEGDSVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIPS 80  
Db 1 DIVTQSPATLSVTPEGDSVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIPS 60

Qy 81 RFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 127  
Db 61 RFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 107

RESULT 11  
US-10-436-782-17  
; Sequence 17, Application US/10436782  
; Publication No. US20040028685A1  
; GENERAL INFORMATION:  
; APPLICANT: Kinch, Michael  
; APPLICANT: Carles-Kinch, Kelly  
; APPLICANT: Kiener, Peter  
; APPLICANT: Langermann, Solomon  
; TITLE OF INVENTION: EphA2 Monoclonal Antibodies and Methods of Use Thereof  
; FILE REFERENCE: 10271-097

; CURRENT APPLICATION NUMBER: US/10/436,782  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,322  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/418,213  
; PRIOR FILING DATE: 2002-10-14  
; PRIOR APPLICATION NUMBER: 60/418,213  
; PRIOR FILING DATE: 2003-04-03  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 17  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-436-782-17

Query Match 80.0%; Score 529; DB 15; Length 107;  
Best Local Similarity 94.4%; Pred. No. 8.3e-39;  
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIVTQSPATLSVTPEGDSVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIPS 80  
Db 1 DIVTQSPATLSVTPEGDSVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIPS 60

Qy 81 RFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 127  
Db 61 RFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 107

RESULT 12  
US-10-923-068-511  
; Sequence 511, Application US/10923068  
; Publication No. US20050042664A1  
; GENERAL INFORMATION:  
; APPLICANT: Wu, Herren  
; APPLICANT: Dall'Acqua, William  
; APPLICANT: Damschroder, Melissa  
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES  
; FILE REFERENCE: AE600US  
; CURRENT APPLICATION NUMBER: US/10/923,068  
; CURRENT FILING DATE: 2004-08-20  
; NUMBER OF SEQ ID NOS: 518  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 511  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-923-068-511

Query Match 80.0%; Score 529; DB 17; Length 107;  
Best Local Similarity 94.4%; Pred. No. 8.3e-39;  
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 21 DIVTQSPATLSVTPEGDSVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIPS 80  
Db 1 DIVTQSPATLSVTPEGDSVSLSCRASQIISNNLHWYQOKSHSPRLIRYASQISIGIPS 60

Qy 81 RFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 127  
Db 61 RFGSGSGTDFTLINSVETEDFGMYFCQOQSNWPLTFGSGTKLEIK 107

RESULT 13  
US-10-920-899-1776  
; Sequence 1776, Application US/10920899  
; Publication No. US20050048617A1  
; GENERAL INFORMATION:  
; APPLICANT: Wu, Herren  
; APPLICANT: Dall'Acqua, William  
; APPLICANT: Damschroder, Melissa  
; TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES  
; FILE REFERENCE: AE650US  
; CURRENT APPLICATION NUMBER: US/10/920,899

CURRENT FILING DATE: 2004-08-18  
NUMBER OF SEQ ID NOS: 1781  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1776  
LENGTH: 107  
TYPE: PRT  
ORGANISM: Mus musculus  
US-10-920-899-1776

Query Match 80.0%; Score 529; DB 17; Length 107;  
Best Local Similarity 94.4%; Pred. No. 8,3e-39;  
Matches 101; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTOSPATLSTVPDGSVSLSCRAQIISNNLHMWYQOKSHSPRLIKYASQSIGIPS 80  
1 DIVLTOSPATLSTVPDGSVSLSCRAQIISNNLHMWYQOKSHSPRLIKYVPOSIGIPS 60

DB 81 RFGSGSGTDFTLINSVETEDFGMYFCQOSNSWPLTFSGGTLEIK 127  
61 RFGSGSGTDFTLINSVETEDFGMYFCQOSNSWPLTFAGTLEIK 107

## RESULT 14

US-10-340-189-1  
Sequence 1, Application US/10340189  
Publication No. US20030229207A1

## GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains  
NUMBER OF SEQUENCES: 89  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 W. Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/340,189  
FILING DATE: 10-Jan-2003  
CLASSIFICATION: 530

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/245,202A  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/082,842  
FILING DATE: 23-JUN-1993  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11023US07 / 200-71.P2.C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-340-189-1

Query Match 79.6%; Score 526; DB 15; Length 107;

Best Local Similarity 94.4%; Pred. No. 1.5e-38;  
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTOSPATLSTVPDGSVSLSCRAQIISNNLHMWYQOKSHSPRLIKYASQSIGIPS 80  
1 DIVLTOSPATLSTVPDGSVSLSCRAQIISNNLHMWYQOKSHSPRLIKYASQSIGIPS 60

DB 81 RFGSGSGTDFTLINSVETEDFGMYFCQOSNSWPLTFSGGTLEIK 127  
61 RFGSGSGTDFTLINSVETEDFGMYFCQOSNSWPLTFGGTLEIK 107

## RESULT 15

US-10-325-696-1  
Sequence 1, Application US/10325696  
Publication No. US20040005630A1

## GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.  
TITLE OF INVENTION: Modified Antibody Variable Domains  
NUMBER OF SEQUENCES: 67  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: IL  
COUNTRY: United States of America  
ZIP: 60661

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/325,696  
FILING DATE: 18-Dec-2002  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/097,980  
FILING DATE: 16-JUN-1998  
APPLICATION NUMBER: 08/107,669  
FILING DATE: 13-AUG-1993  
APPLICATION NUMBER: PCT/US92/10906  
FILING DATE: 14-DEC-1992  
APPLICATION NUMBER: US 07/808,464  
FILING DATE: 13-DEC-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Janet M. McNicholas, Ph.D.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11023US06/200-71.P1.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9050  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-325-696-1

Query Match 79.6%; Score 526; DB 15; Length 107;  
Best Local Similarity 94.4%; Pred. No. 1.5e-38;  
Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTOSPATLSTVPDGSVSLSCRAQIISNNLHMWYQOKSHSPRLIKYASQSIGIPS 80  
1 DIVLTOSPATLSTVPDGSVSLSCRAQIISNNLHMWYQOKSHSPRLIKYASQSIGIPS 60

DB 81 RFGSGSGTDFTLINSVETEDFGMYFCQOSNSWPLTFSGGTLEIK 127  
61 RFGSGSGTDFTLINSVETEDFGMYFCQOSNSWPLTFGGTLEIK 107

Thu May 26 09:14:28 2005

us-10-006-773a-6.rapb

Page 7

Search completed: May 25, 2005, 16:06:50  
Job time : 60.1836 secs

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## OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 18.096 Seconds  
(without alignments)  
680.480 Million cell updates/sec

Title: US-10-006-773a-6

Perfect score: 661

Sequence: 1 MWFPTQIIGLMLFWISASRG.....QQSNSWPLTFCSGTKLEIKR 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	642	97.1	138	2	A26471
2	592	89.6	123	2	S35479
3	531	80.3	107	2	A45722
4	530	80.2	107	2	B45722
5	524	79.3	104	2	B43413
6	524	79.3	106	2	PL0267
7	507	76.7	102	2	S26346
8	506	76.6	107	2	C45722
9	473	71.6	128	2	PN0445
10	465	70.3	115	1	KWMSL7
11	447	67.6	108	2	C30502
12	425	64.3	103	2	S19975
13	423	64.0	144	2	PL0106
14	422	63.8	128	2	S40343
15	420	63.5	128	2	S40379
16	417.5	63.2	128	1	K3HU41
17	416	62.9	117	2	S40362
18	416	62.9	128	2	A56701
19	409	61.9	96	2	G33730
20	404	61.1	129	2	A32274
21	399	60.4	115	2	S10146
22	398	60.2	114	2	S00996
23	398	60.2	125	2	S40316
24	398	60.2	127	2	S40367
25	398	60.2	128	2	S40345
26	397	60.1	125	2	S40349
27	395	59.8	123	2	S40331
28	395	59.8	234	2	S01320
29	394	59.6	125	2	S40344

30	394	59.6	127	2	S04574	Ig kappa chain pre
31	391.5	59.2	131	2	S40328	Ig kappa chain - h
32	391	59.2	122	2	S40314	Ig kappa chain - h
33	391	59.2	129	2	S49532	anti-5m antibody V
34	391	59.2	132	2	S40334	Ig kappa chain h
35	390	59.0	125	2	S40333	Ig kappa chain V-J
36	389	58.9	129	2	S29627	Ig kappa chain V r
37	389	58.9	130	2	S40360	Ig kappa chain - h
38	388	58.7	108	2	S19674	Ig kappa chain V r
39	388	58.7	129	1	K3HU4A	Ig kappa chain pre
40	388	58.7	145	2	PL0014	Ig kappa chain pre
41	386	58.4	111	2	S23628	Ig kappa chain V r
42	386	58.4	129	2	S40369	Ig kappa chain - h
43	385	58.2	129	1	K3HUH1	Ig kappa chain pre
44	384.5	58.2	136	2	S40357	Ig kappa chain V-J
45	384.5	58.2	215	2	JEB0244	Ig kappa chain NIG

## ALIGNMENTS

```
RESULT 1
A26471
Ig kappa chain precursor V region (MAX33) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: A26471
R:Buckel, P.; Hubner-Parajsz, C.; Matthes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A>Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
A:Reference number: A91572; MUID:87248058; PMID:3110009
A:Accession: A26471
A:Molecule type: mRNA
A:Residues: 1-138 <BUC>
A:Cross-References: GB:M6162; NID:g196893; PIDN:AAA3823.1; PID:g196894
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match          97.1% Score 642; DB 2; Length 138;
Best Local Similarity 96.9%; Pred. No. 1.7e-47;
Matches 124; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MWFPTQIIGLMLFWISASRGDIVLTQSPATLSVTPFGDSVSLCRASQIISNNLHWYQOKS 60
    |||||
Db 1 MWFPTQIIGLMLFWISASRGDIVLTQSPATLSVTPFRDSVSLCRASQIISNNLHWYQOKS 60

QY 61 HESPRLLKRYASQSIISGIPSRPSGSGGNDFTLSINSYETEDFGMYFCQSNWPLTRGS 120
    |||||
Db 61 HESPRLLKRYASQSIISGIPSRPSGSGGNDFTLSINSYETEDFGMYFCQSNWPLTRGA 120

QY 121 GTKLEIKR 128
    |||||
Db 121 GTKLEIKR 128

RESULT 2
S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S35479
R:Takeuchi, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A>Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from a m
A:Reference number: S35479; MUID:92375706; PMID:1387203
A:Accession: S35479
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-References: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
```

A:Map position: 6  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>  
F:13-13/Domain: signal sequence (fragment) #status predicted <SIG>  
F:28-102/Domain: immunoglobulin homology <IMM>

Query Match 89.6%; Score 592; DB 2; Length 123;  
Best Local Similarity 95.8%; Pred. No. 2.5e-43;  
Matches 115; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 9 GMLFMISASRGIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQKSHSPRLIK 68  
DB 1 GMLFMISASRGIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQKSHSPRLIK 60  
QY 69 KYVASISGICRPSRFGSGSGTDFTLINSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 128  
DB 61 KYVASISGICRPSRFGSGSGTDFTLINSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 120

## RESULT 3

A45722  
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fr  
C:Species: Mus musculus (house mouse)  
C>Date: 03-Mar-1994 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C/Accession: A45722  
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vaeg  
J. Virol. 67, 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu  
A:Reference number: A45722; MUID:93100833; PMID:7677958  
A/Accession: A45722  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-107 <SIM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 531; DB 2; Length 107;  
Best Local Similarity 95.3%; Pred. No. 3.1e-38;  
Matches 102; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQKSHSPRLIKYASQISGIRPS 80  
DB 1 DIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQKSHSPRLIKYASQISGIRPS 60  
QY 81 RFGSGSGTDFTLINSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 127  
DB 61 RFGSGSGTDFTLINSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 107

## RESULT 4

B45722  
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr  
C:Species: Mus musculus (house mouse)  
C>Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C/Accession: B45722  
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vaeg  
J. Virol. 67, 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu  
A:Reference number: A45722; MUID:93100833; PMID:7677958  
A/Accession: B45722  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-107 <SIM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:120590)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 530; DB 2; Length 107;  
Best Local Similarity 95.3%; Pred. No. 3.8e-38;

Matches 102; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 21 DIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQKSHSPRLIKYASQISGIRPS 80  
DB 1 DIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQKSHSPRLIKYASQISGIRPS 60  
QY 81 RFGSGSGTDFTLINSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 127  
DB 61 RFGSGSGTDFTLINSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 107

## RESULT 5

B43413  
Ig kappa chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 27-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C/Accession: B43413  
R:Tomiyama, Y.; Brojer, E.; Ruggieri, Z.M.; Shattil, S.J.; Smilneck, J.; Gorzki, J.; Ku  
J. Biol. Chem. 267, 18085-18092, 1992  
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific  
A:Reference number: A43413; MUID:92388177; PMID:1517241  
A/Accession: B43413  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-104 <DOM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:13-87/Domain: immunoglobulin homology <IMM>

Query Match 79.3%; Score 524; DB 2; Length 104;  
Best Local Similarity 96.2%; Pred. No. 1.2e-37;  
Matches 100; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 24 LTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQKSHSPRLIKYASQISGIRPS 83  
DB 1 LTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQKSHSPRLIKYASQISGIRPS 60  
QY 84 GSGSGTDFTLINSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 127  
DB 61 GSGSGTDFTLINSVETEDFGMYFCQOQNSWPLTFGSGTKLEIK 104

## RESULT 6

PL0267  
Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 21-Jan-2000  
C/Accession: PL0267  
R:Shlomchik, M.; Maccelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J  
J. Exp. Med. 171, 265-297, 1990  
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic  
A:Reference number: PL0231; MUID:90111618; PMID:2104919  
A/Accession: PL0267  
A:Molecule type: mRNA  
A:Residues: 1-106 <SHL>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:1-23/Region: framework 1  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:24-34/Region: complementarity-determining 1  
F:35-49/Region: complementarity-determining 2  
F:50-56/Region: complementarity-determining 2  
F:57-88/Region: framework 3  
F:89-97/Region: complementarity-determining 3  
F:98-106/Region: framework 4

Query Match 79.3%; Score 524; DB 2; Length 106;  
Best Local Similarity 96.2%; Pred. No. 1.2e-37;  
Matches 102; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 21 DIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQKSHSPRLIKYASQISGIRPS 80  
DB 1 DIVLTOSPATLSVTPGDSVSLSCRASQIISNNLHWYQKSHSPRLIKYASQISGIRPS 60



Db 1 DIVLTQSPATLSVTPGDRLVSLCRASQISINYLHWYQOKSHSPRLIKYASQISIGIPRS 60  
QY 81 RFSSGSGGTDFTLINSVEDTPEFGMYFCQQSNMWPLTFGGGTKEIK 126  
Db 61 RFSSGSGGTDFTLINSVEDTPEFGMYFCQQSNMWPLTFGGGTKEIK 106

RESULT 7  
S26346  
Ig kappa chain V region - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 20-Jun-2000  
C:Accession: S26346  
R:Stark, S.E.; Caton, A.J.  
J. Exp. Med. 174, 613-624, 1991  
A:Title: Antibodies that are specific for a single amino acid interchange in a protein  
A:Reference number: S26309; MUID:91341421; PMID:1908510  
A:Accession: S26346  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-102 <STA>  
A:Cross-references: EMBL:X59211; NID:952338; PIDN:CAA41921.1; PID:91334075  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; Immunoglobulin  
F:14-88/Domain: immunoglobulin homology <IMM>

Query Match 76.7%; Score 507; DB 2; Length 102;  
Best Local Similarity 95.1%; Pred. No. 3.1e-36;  
Matches 97; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 23 VLTPSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKSHSPRLIKYASQISIGIPRS 82  
Db 1 VLTPSPATLSVTPGDSVSLSCRASQISINLHWYQOKSHSPRLIKYASQISIGIPRS 60  
QY 83 SSGSGGTDFTLINSVEDTPEFGMYFCQQSNMWPLTFGGGTKEIK 124  
Db 61 SSGSGGTDFTLINSVEDTPEFGMYFCQQSNMWPLTFGGGTKEIK 102

RESULT 8  
C45722  
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse (H  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
C:Accession: C45722  
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasequ  
J. Virol. 67, 489-496, 1993  
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu  
A:Reference number: A45722; MUID:93100833; PMID:7677958  
A:Accession: C45722  
A:Status: preliminary, not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-107 <SIM>  
A:Note: sequence extracted from NCBI backbone (NCBIP:120591)  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: glycoprotein  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.6%; Score 506; DB 2; Length 107;  
Best Local Similarity 89.6%; Pred. No. 4e-36;  
Matches 95; Conservative 8; Mismatches 3; Indels 0; Gaps 0;  
QY 22 IVLTSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKSHSPRLIKYASQISIGIPRS 81  
Db 2 VLTPSPATLSVTPGDSVSLSCRASQISNNLHWYQOKSHSPRLIKYASQISIGIPRS 61  
QY 82 FSSGSGGTDFTLINSVEDTPEFGMYFCQQSNMWPLTFGGGTKEIK 127  
Db 62 FSSGSGGTDFTLINSVEDTPEFGMYFCQQSNMWPLTFGGGTKEIK 107

RESULT 9  
PN0445

Ig kappa chain precursor V-I region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PN0445  
R:Kaluzza, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.  
Gene 122, 321-328, 1992  
A:Title: A general method for chimerization of monoclonal antibodies by inverse polymera  
A:Reference number: PN0444; MUID:93138402; PMID:1339379  
A:Accession: PN0445  
A:Molecule type: mRNA  
A:Residues: 1-128 <KAL>  
A:Cross-references: GB:L02347  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-10/Domain: signal sequence #status predicted <SIG>  
F:11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>  
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 71.6%; Score 473; DB 2; Length 128;  
Best Local Similarity 74.6%; Pred. No. 3e-33;  
Matches 88; Conservative 15; Mismatches 15; Indels 0; Gaps 0;  
QY 11 MLFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKSHSPRLIKY 70  
Db 1 LLSWIPASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKSHSPRLIKY 60  
QY 71 ASQISIGIPRSFSSGSGGTDFTLINSVEDTPEFGMYFCQQSNMWPLTFGGGTKEIK 128  
Db 61 ASQISIGIPRSFSSGSGGTDFTLINSVEDTPEFGMYFCQQSNMWPLTFGGGTKEIK 118

RESULT 10  
KXMS17  
Ig kappa chain precursor V region (L7) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Dec-1981 #sequence\_revision 18-Dec-1981 #text\_change 09-Jul-2004  
C:Accession: A01925  
R:Bech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.  
Nature 291, 668-670, 1981  
A:Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequ  
A:Reference number: A93259; MUID:81220975; PMID:6264318  
A:Accession: A01925  
A:Molecule type: DNA  
A:Residues: 1-115 <PDC>  
A:Cross-references: UNIPROT:P01642; GB:V01564; GB:J00574; NID:951718; PIDN:CAA24884.1; P  
A:Note: the sequence was determined from the germline gene  
A:Note: there appear to be two possible splice junctions at the 3' end of the intron; th  
C:Genetics: 17/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into la  
C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>  
F:36-110/Domain: immunoglobulin homology <IMM>  
F:43-108/Disulfide bonds: #status predicted

Query Match 70.3%; Score 465; DB 1; Length 115;  
Best Local Similarity 76.5%; Pred. No. 1.3e-32;  
Matches 88; Conservative 12; Mismatches 15; Indels 0; Gaps 0;  
QY 1 MWFTPIIGLMLFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60  
Db 1 MWSTPQFLVFLFWIPASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKS 60  
QY 61 HESPRLLIKYASQISIGIPRSFSSGSGGTDFTLINSVEDTPEFGMYFCQQSNMW 115  
Db 61 NGSFRLIKYASQISIGIPRSFSSGSGGTDFTLINSVEDTPEFGMYFCQQSNMW 115

RESULT 11  
C30502



Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chl genes and their hypermutation..  
A;Reference number: S40313. MIMD.94090991. PMID.9259241

A;Accession: S40379  
A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Status: preliminary

A; molecule type: mRNA

A;Residues: 1-128 <KLE>

A; Cross-references: EMB

C; Superfamily: immunoglobulin V region; immunoglobulin homology

**Keywords:** heterotetramer; immunoglobulin

F;36-110/Domain: immunoglobulin homology <IMM>

[illegible]

Query Match

Best Local Similarity 62.6%; Pred. No. 9e-29;  
Matches 17; Correlation 0.33; W-matches 0

Matches 77; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 6 QILGLMLFWISASRGDIVLTQSPATLSVTPGDSVSLSCRASQIISNNLHWYQOKSHESPR 65

Db 6 QLLFLLLLWLPDTTGEFVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQPPR 65

66 LLIKASQISGIPRFGSGGSDFTLSINSVETEDFGMYFCQSQNSWPLTFGGSTKLE 125

Db 66 LIYYASNRATGIPARFSGGAGTDFLLTIISSLEPEDFAVYYCQQRSKWPWTFGGGTKE 125

QY 126 IKR 128

Db 126 IKR 128

Search completed: May 25, 2005, 16:48:37  
Job time : 18.0986 secs

Job time : 18.0986 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 62.3926 Seconds  
(without alignments)  
1050.544 Million cell updates/sec

Title: US-10-006-773A-6

Perfect score: 661

Sequence: 1 MWFTPOLGLMFMISASRG.....QQSNMPLTFSGSKLEIKR 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_03:\*  
2: uniprot\_sprot:\*  
3: uniprot\_crembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	72.2	262	2	Q65Z11
2	465	70.3	115	1	KV5I_MOUSE
3	430.5	65.1	235	2	Q6GMW0
4	417.5	62.2	128	1	KV3K_HUMAN
5	411.5	62.3	129	1	KV3H_HUMAN
6	392	59.3	236	2	Q6GMX8
7	388	58.7	129	1	KV3L_HUMAN
8	387	58.5	235	2	Q6GMV9
9	385	58.2	236	2	Q6PIH7
10	385	58.2	129	1	KV3M_HUMAN
11	385	58.2	236	2	Q6GMW1
12	384.5	58.2	239	2	Q6NEK0
13	384	58.1	108	2	Q9UL83
14	384	58.1	236	2	Q6GMX0
15	380.5	57.6	109	2	Q9UL85
16	380	57.5	238	2	Q6GUS7
17	379.5	57.4	236	2	Q6P5S8
18	379	57.3	240	2	Q6P5F2
19	379	57.3	240	2	Q6PIH6
20	378	57.2	129	1	KV1W_HUMAN
21	376.5	57.0	239	2	Q6TCD0
22	375.5	56.8	109	1	KV3F_HUMAN
23	374.5	56.7	236	2	Q6PIL8
24	372	56.3	236	2	Q723Y4
25	370	56.0	236	2	Q6GMX9
26	369	55.8	115	1	KV3I_HUMAN
27	368	55.7	234	2	Q72473
28	368	55.7	236	2	Q6PIT5
29	366.5	55.4	133	1	KV2F_HUMAN
30	360.5	54.5	109	1	KV3D_HUMAN
31	359	54.3	236	2	Q6PIH4

32	357	54.0	134	1	KV4C_HUMAN	P06314 homo sapien
33	353.5	53.5	109	2	KV3B_HUMAN	P01620 homo sapien
34	353.5	53.5	109	2	Q9UL78	Q9UL78 homo sapien
35	353	53.4	132	1	KV3F_MOUSE	P01658 mus musculus
36	352.5	53.3	128	1	KV3E_MOUSE	P01637 mus musculus
37	352	53.3	131	1	KV3I_MOUSE	P01631 mus musculus
38	351.5	53.2	133	1	KV4B_HUMAN	P06313 homo sapien
39	351	53.1	237	2	Q7S236	Q7S236 xenopus lae
40	348	52.6	108	2	Q9UL77	Q9UL77 homo sapien
41	347.5	52.6	107	2	Q9ESA9	Q9ESA9 homo sapien
42	346.5	52.4	109	1	KV3E_HUMAN	P01623 homo sapien
43	346.5	52.4	114	2	Q8KIF1	Q8KIF1 mus musculus
44	346	52.3	108	1	KV1S_HUMAN	P01611 homo sapien
45	346	52.3	108	2	Q9UL79	Q9UL79 homo sapien

## ALIGNMENTS

### RESULT 1

ID	Q65Z11	PRELIMINARY	PRT	262 AA.
AC	Q65Z11			
DT	25-OCT-2004 (TREMBLrel. 28, Created)			
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)			
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)			
DE	Anti-HIV-1 reverse transcriptase single-chain variable.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hybridoma;			
RX	MEDLINE=96211469; PubMed=8648670;			
RA	Shahen F., Duan L., Zhu M., Bagasra O., Pomerantz R.J.;			
RT	"Targeting human immunodeficiency virus type 1 reverse transcriptase			
RT	by intracellular expression of single-chain variable fragments to			
RT	inhibit early stages of the viral life cycle."			
RL	J. Virol. 70:3392-3400(1996).			
DR	EMBL; U48716; AAB64342.1; -			
DR	GO; GO:0003964; F:RNA-directed DNA polymerase activity; IEA.			
DR	InterPro; IPR003599; IG_1-like.			
DR	InterPro; IPR003598; IG_C2.			
DR	InterPro; IPR003596; IG_V.			
DR	Pfam; PF00047; IG_2.			
DR	SMART; SM00409; IG_2.			
DR	SMART; SM00408; IGC2; 2.			
DR	SMART; SM00406; IGV_2.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
KW	RNA-directed DNA polymerase.			
SQ	SEQUENCE 262 AA; 27842 MW; 7DF20138E53865E4 CRC64;			

Query Match 72.2%; Score 477; DB 2; Length 262;

Best Local Similarity 84.3%; Pred. No. 2e-38; 7; Indels 0; Gaps 0;

Matches 91; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY	21	DIVLTQSPATLSVTPGDVSLS	CRASQITISNNIMHWYQOKSHSPRLTIKVASQSIGIPS	80
DB	2	DIMTQSPATLSVTPGDVSL	SCRASQISDFLHWYQOKSHSPRLTIKVASQSIGIPS	61
QY	81	RFGSGSGDTFTLSINSVETED	FGMYFCQGSNSWPLTFSGSKLEIKR	128
DB	62	RFGSGSGSDFTLSINSVETED	FGMYFCQGSNSWPLTFSGSKLEIKR	109

### RESULT 2

ID	KV5I_MOUSE	STANDARD	PRT	115 AA.
AC	KV5I_MOUSE			
ID	P01642;			
DT	21-JUL-1966 (Rel. 01, Created)			
DT	21-JUL-1966 (Rel. 01, Last sequence update)			

```
DT 25-OCT-2004 (Rel. 45, last annotation update)
DE Ig kappa chain V-V region L7 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=81220975; PubMed=6264318;
RX Pech M., Hochst J., Schnell H., Zachau H.G.;
RT "differences between germ-line and rearranged immunoglobulin V kappa
RL coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1991).
CC -1- MISCELLANEOUS: There appears to be two possible splice junctions
CC at the 3' end of the intron. The alternate would code for a
CC protein lacking residues 17-19.
CC
DR PIR; A01925; KYMSL7.
DR PDB; 1J10; X-ray; L=21-115.
DR PDB; 1J1P; X-ray; L=21-115.
DR PDB; 1J1X; X-ray; L=21-115.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG_1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR 3D-structure; Immunoglobulin V region; Signal.
KW STGNL 1 20
FT CHAIN 21 >115 Ig kappa chain V-V region L7.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 54 Complementarity-determining-1.
FT DOMAIN 55 69 Framework-2.
FT DOMAIN 70 76 Complementarity-determining-2.
FT DOMAIN 77 108 Framework-3.
FT DOMAIN 109 >115 Complementarity-determining-3.
FT DISUFID 43 108 By similarity.
FT STRAND 24 27
FT STRAND 30 33
FT STRAND 35 36
FT STRAND 39 45
FT STRAND 50 51
FT STRAND 53 58
FT STRAND 60 61
FT STRAND 65 69
FT STRAND 70 72
FT STRAND 73 74
FT STRAND 76 77
FT TURN 80 81
FT STRAND 82 87
FT TURN 88 89
FT STRAND 90 95
FT HELIX 100 102
FT STRAND 104 110
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577BE00 CRC64;

Query Match 70.3%; Score 465; DB 1; Length 115;
Best Local Similarity 76.5%; Pred. No. 1,1e-37;
Matches 88; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 MVEPTQILGLMFWISARGDIVLTQSPATLSVTPGDVSLSGSAQIISNNLHWYQOKS 60
DB 1 MVEPTQFLVFLFWIPASRGDILTQSPALISVSPGERVSPSCRASQISGTSIHWYQORT 60
QY 61 HESPRLLIKYASQISGIPSRFSGSGGTDTFTLSINSEVEDFGMTFCQGSNSWP 115
DB 61 NSPRLLIKYASISGIPSRFSGSGGTDTFTLSINSEVEDIADYVCOGSNSWP 115

RESULT 3
O6GMMO PRELIMINARY; PRT; 235 AA.
AC O6GMMO;
ID O6GMMO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
```

```
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Spleen.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.T., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Spleen;
RC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RX EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-sect 1.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; IG_2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36BD4133F5 CRC64;

Query Match 65.1%; Score 430.5; DB 2; Length 235;
Best Local Similarity 66.9%; Pred. No. 6,1e-34;
Matches 83; Conservative 19; Mismatches 21; Indels 1; Gaps 1;

QY 6 QILGLMFWISARGDIVLTQSPATLSVTPGDVSLSGSAQIISNNLHWYQOKSHESPR 65
DB 6 QILGLMFWIPASRGDILTQSPALISVSPGERATISCAQSIISNNLHWYQORPQAR 65
QY 66 LIIKYSQISGIPSRFSGSGGTDTFTLSINSEVEDFGMTFCQGSNSWPL-TFGSGTKL 124
DB 66 LIIKYSQISGIPSRFSGSGGTDTFTLSINSEVEDFAVYCCQYNDMLVTFGGGTRK 125
QY 125 EIKR 128
DB 126 EIKR 129

RESULT 4
KV3K_HUMAN STANDARD; PRT; 128 AA.
ID KV3K_HUMAN
AC P06311;
```

```

DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RL III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
CC -----
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CC or send an email to license@isb-sb.ch).
CC -----
DR EMBL, Z00021; CAAT7316.1; -.
DR PIR, A01899; K3H041.
DR HSP, P01625; IIE0.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KV Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 Ig kappa chain V-III region IARC/BL41.
FT DOMAIN 21 43 Framework-1.
FT DOMAIN 44 54 Complementarity-determining-1.
FT DOMAIN 55 69 Framework-2.
FT DOMAIN 70 76 Complementarity-determining-2.
FT DOMAIN 77 108 Framework-3.
FT DOMAIN 109 117 Complementarity-determining-3.
FT DOMAIN 118 128 JkI segment.
FT DISULFID 43 108 By similarity.
FT NON TER 128
SQ SEQUENCE 128 AA; 14070 MW; CCG957F0FE3B9012 CRC64;
Query Match 63.2%; Score 417.5; DB 1; Length 128;
Best Local Similarity 64.3%; Pred. No. 5; 7e-33;
Matches 81; Conservative 20; Mismatches 24; Indels 1; Gaps 1,
QY 4 TP-QILGLMLWMISMRGDIYVLTGSPALSTVTPGDSVSLSCRASQIISNNLHWYQKSH 62
DB 3 TPAQLFLFLMLLPDTGBIVLTGSPGLTSLPGESATLSCRASQSVSNLAWYQKXGQ 62
QY 63 SPRLILIKYASQISIGIPRFGSGSGCTDFTLSINVERTEDFGMYCCQOQNSMWPLTFGSGT 122
DB 63 SPRLILIRASBRANQIPDRFGSGSGCTDFTLISLNFEDPAVYVYCCQYISPTPTGGCT 122
QY 123 KLEIKR 128
DB 123 KLEIKR 128

```

[illegible]

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Matsuda K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,  
 RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywicki M.I., Skalka U., Smalhus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Matra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.L.  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073764; AAH73764.1; -  
 DR InterPro; IPR003599; IG\_-like.  
 DR InterPro; IPR007110; IG\_-like.  
 DR InterPro; IPR003597; IG\_-like.  
 DR InterPro; IPR003066; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00654; C1-set; 1.  
 DR Pfam; PF00047; IG; 2.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGc1; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KM Hypothetical protein\_  
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;  
 Query Match 59.3%; Score 392; DB 2; Length 236;  
 Best Local Similarity 60.2%; Pred. No. 3.6e-30;  
 Matches 74; Conservative 25; Mismatches 24; Indels 0; Gaps 0;  
 QY 6 QILGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCPASQIISNNLHWYQOKSHSPR 65  
 DB 8 QLLGLLMLPFGSSCDIQMTQSPSSVSASVGDRTVITCRASQGISMLAWYQOKPGKAPK 67  
 QY 66 LLIKYASQISGIPSRFSGSGCTDFTLSINSVETEDFGMYFCQGSNSMPLTFGSGTKLR 125  
 DB 68 LLITYAASSLSQSVPSRFSGSGCTDFTLTISLQPEDPATYYCOQANSFFPTGPGTKVD 127  
 QY 126 IKR 128  
 DB 128 IKR 130  
 RESULT 7  
 KVI3L\_HUMAN STANDARD; PRT; 129 AA.  
 ID KVI3L\_HUMAN  
 AC P18135;  
 DT 01-NOV-1990 (Ref. 16, Created)  
 DT 01-NOV-1990 (Ref. 16, Last sequence update)  
 DT 15-JUL-1999 (Ref. 38, Last annotation update)  
 DE Ig kappa chain V-II region HAH precursor.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OX Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=68171307; PubMed=3127527;  
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.,  
 RT "Autoantibody-associated kappa light chain variable region gene  
 expressed in chronic lymphocytic leukemia with little or no somatic  
 mutation. Implications for etiology and immunotherapy."  
 RT J. Exp. Med. 167:840-852(1988).  
 RL CC -1- DISASE: The protein is one of the surface immunoglobulin M  
 autoantibodies expressed in patients with chronic lymphocytic  
 leukemia.  
 CC PIR; P10622; KAHUHA.  
 DR HSSP; P01625; 1EEQ.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; P:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; IG\_-like.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF00047; IG; 1.  
 DR SMART; SM00406; IGv; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129 IG kappa chain V-II region HAH.  
 FT DOMAIN 21 43 Framework-1.  
 FT DOMAIN 44 55 Complementarity-determining-1.  
 FT DOMAIN 56 70 Framework-2.  
 FT DOMAIN 71 77 Complementarity-determining-2.  
 FT DOMAIN 78 109 Framework-3.  
 FT DOMAIN 110 118 Complementarity-determining-3.  
 FT DOMAIN 119 129 JKL segment.  
 FT DISUFID 43 109 By similarity.  
 FT NON\_TER 129 129  
 SQ SEQUENCE 129 AA; 14073 MW; D3C5529272774D0 CRC64;  
 Query Match 58.7%; Score 388; DB 1; Length 129;  
 Best Local Similarity 60.6%; Pred. No. 4.4e-30;  
 Matches 77; Conservative 22; Mismatches 26; Indels 2; Gaps 2;  
 QY 4 TP-QILGLMFWISASRGDIVLTQSPATLSVTPGDSVSLSCPASQIISNNLHWYQOKSH 61  
 DB 3 TPAQLLLMLPDTTGTGIVLTQSPGTLISLSPGERATLSCPASQSVSSYLAWYQOKSG 62  
 QY 62 ESPRLIKYASQISGIPSRFSGSGCTDFTLSINSVETEDFGMYFCQGSNSMPLTFGSG 121  
 DB 63 QARLLIYASGSRATGIPSRFSGSGCTDFTLTISLQPEDPATYYCOQYGTSPRTFGGQ 122  
 QY 122 TKLEIKR 128  
 DB 123 TKVEIKR 129  
 RESULT 8  
 OEGMV9 PRELIMINARY; PRT; 235 AA.  
 ID OEGMV9;  
 AC OEGMV9;  
 DT 05-JUL-2004 (TrEMBL;rel. 27, Created)  
 DT 05-JUL-2004 (TrEMBL;rel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBL;rel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,



RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopline R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Bosh S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Richards S., Morley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimmutz J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [12]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strubeberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073793; AAH73793.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR Hypothetical protein.  
 KW SEQUENCE 235 AA; 25646 MW; DF32B560BAD19E4B CRC64;  
 SQ  
 Query Match 58.7%; Score 388; DB 2; Length 235;  
 Best Local Similarity 61.4%; Pred. No. 8.8e-30;  
 Matches 78; Conservative 20; Mismatches 27; Indels 2; Gaps 2;  
 QY 4 TP-OLGLMFWISASRGDIYVLTOSPATLSTVPDGSVSLSCASASDIT-SNNLHWYQKSH 61  
 DB 3 TPAQLFLFLMLLPDITGIVLTQSPGTLSLSPGERAAALSCASQSVNSKYLAWYQKPG 62  
 QY 62 ESPRLILIKYASQISGIPSRFSGSGGTDFTLINSVETEDFGMYFCQGSNSMPLTFGSG 121  
 DB 63 QAPRLMLAAASIRATGIPDRFSGSGGTDFTLITRLSEDPALYFCQGYGSPITFGG 122  
 QY 122 TKLEIKR 128  
 DB 123 TKVEIKR 129

## RESULT 9

OPHI7 PRELIMINARY; PRT; 236 AA.  
 ID O6PIH7;  
 AC O6PIH7;  
 DT 05-JUL-2004 (TREMblrel. 27, Created)  
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_Taxid=9606;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopline R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Bosh S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Richards S., Morley K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimmutz J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 [12]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strubeberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC034141; AAH34141.1; -.  
 DR HSP; P01607; IAR2.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_v.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR SMART; SM00409; Ig; 2.  
 DR SMART; SM00407; IGcl; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 KV SEQUENCE 236 AA; 25603 MW; 8BC561106661213F CRC64;  
 SQ  
 Query Match 58.5%; Score 387; DB 2; Length 236;  
 Best Local Similarity 61.8%; Pred. No. 1.1e-29;  
 Matches 76; Conservative 20; Mismatches 27; Indels 0; Gaps 0;  
 QY 6 QILGLMFWISASRGDIYVLTOSPATLSTVPDGSVSLSCASASDIT-SNNLHWYQKSHESR 65  
 DB 8 QILGLLMLLPDITGIVLTQSPGTLSLSPGERAAALSCASQSVNSKYLAWYQKPGKAPN 67  
 QY 66 LLIKVASQISGIPSRFSGSGGTDFTLINSVETEDFGMYFCQGSNSMPLTFGSGTKLE 125  
 DB 68 LLIYAASTLQSGVSRFSGSGGTDFTLITSLDPEDPATYICQGLNSPPTFGGCTIVE 127  
 QY 126 IKR 128  
 DB 128 IKR 130

## RESULT 10

KV3M HUMAN STANDARD; PRT; 129 AA.  
 ID KV3M HUMAN  
 AC P18136;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region HIC precursor.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NCBI\_Taxid=9606;  
 RX MEDLINE=8817107; PubMed=3127527;  
 Kipps T.J., Tomhave E., Chen P.P., Carson D.A.,

"Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy." J. Exp. Med. 167:840-852(1988).  
 -1- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.  
 CC PIR; PL0021; K3HUI.  
 DR HSP; P01625; IIEQ.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0003823; F:antigen binding; NAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 129 Ig kappa chain V-III region HIC.  
 FT DOMAIN 21 43 Framework-1.  
 FT DOMAIN 44 55 Complementarity-determining-1.  
 FT DOMAIN 56 70 Framework-2.  
 FT DOMAIN 71 77 Complementarity-determining-2.  
 FT DOMAIN 78 109 Framework-3.  
 FT DOMAIN 110 118 Complementarity-determining-3.  
 FT DOMAIN 119 129 JKL segment.  
 FT DISULFID 43 109 By similarity.  
 FT NON TER 129 129  
 SQ SEQUENCE 129 AA; 14070 MW; 7395528BA2B74D6 CRC64;

Query Match 58.2%; Score 385; DB 1; Length 129;  
 Best Local Similarity 60.6%; Pred. No. 8.6e-30;  
 Matches 77; Conservative 21; Mismatches 27; Indels 2; Gaps 2;

QY 4 TP-QILGLMFWISASRGDIYVLTQSPATLSVTPGDSDSLSCASQIISNN-LHWYQKSH 61  
 DB 3 TPQQLFLFLMLPDTTGTGLVLTQSPETLSLSPERRATLSCRASQVSSSYLAWYQKPG 62  
 QY 62 ESRRLLIKYASQISIGIPSRFGSGGTDFTLINSVETEDPCMYFCQGSNSMPLTFGSG 121  
 DB 63 QARLLIYKASRATGIPDRFSSGSGTDTLTITSLRLEPDAFYVYCOQYSSPMTFGG 122  
 QY 122 TKLEIKR 128  
 DB 123 TKVEIKR 129

## RESULT 11

Q6GMW1 PRELIMINARY; PRT; 236 AA.  
 AC O6GMW1; 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A., Pehly J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzyzanski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E., Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073791; AAH73791.1; -.  
 DR InterPro; IPR003599; Ig.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003597; Ig\_c1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF07654; Cl-set; 1.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00409; IGV; 2.  
 DR SMART; SM00407; IGV; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC37 CRC64;

Query Match 58.2%; Score 385; DB 2; Length 236;  
 Best Local Similarity 59.3%; Pred. No. 1.7e-29;  
 Matches 73; Conservative 24; Mismatches 26; Indels 0; Gaps 0;

QY 6 QILGLMFWISASRGDIYVLTQSPATLSVTPGDSDSLSCASQIISNN-LHWYQKSHESPR 65  
 DB 8 QILGLLMLPGRCAIQMTQSPSSASAVGGRVITTCRASQGISNDLGMWYQKPGKAPK 67  
 QY 66 LTIKYASQISIGIPSRFGSGGTDFTLINSVETEDPCMYFCQGSNSMPLTFGSGTKLE 125  
 DB 68 LTIYASQISIGIPSRFGSGGTDFTLITSLQPDFAFYVYCOQYSSPMTFGGQKVE 127  
 QY 126 IKR 128  
 DB 128 IKR 130

## RESULT 12

Q8NEKO PRELIMINARY; PRT; 239 AA.  
 AC Q8NEKO; 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Klausner R.D., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences",  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RA Strausberg R.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC030814; AAH30814.1; -.  
 DR PIR; S23638; S23638.  
 DR PIR; S34091; S34091.  
 DR PIR; S40342; S40342.  
 DR PIR; S40357; S40357.  
 DR HSSP; P01634; I172.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; Cl-sec; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 2.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 58.1%; Score 384.5; DB 2; Length 239;  
 Best Local Similarity 57.8%; Pred. No. 28-29;  
 Matches 74; Conservative 17; Mismatches 32; Indels 5; Gaps 1;

QY 6 QILGMLTWISAKRDIVLTGSPATLSTPGDSVLSGRASGIT-----SNNTLHWYQOKS 60  
 DB 6 QILGMLTWISAKRDIVLTGSPATLSTPGDSVLSGRASGIT-----SNNTLHWYQOKS 65  
 QY 61 HESPLLLIKYASQSISGIPRSGSGSGDFTLINSYETEDFGMYFCQGSNSWPLTSGS 120  
 DB 66 GOSPLLLIYLSGNRSGVDPDRSGSGSGDFTLTKISKYEAADVGLIYCCQGLQDTPTREQ 125  
 QY 121 GTKLEIKR 128  
 DB 126 GTKVEIKR 133

RESULT 13  
 ID Q9ULB3 PRELIMINARY; PRT; 108 AA.  
 AC Q9ULB3;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Myosin-reactive immunoglobulin light chain variable region  
 DE (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073775; AAH73775.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus",  
 RT Clin. Immunol. Immunopathol. 87:184-192 (1998).  
 DR EMBL; AF035031; AAD56267.1; -.

DR PIR; B30609; B30609.  
 DR PIR; C30609; C30609.  
 DR PIR; D30609; D30609.  
 DR PIR; S34098; S34098.  
 DR PIR; S34099; S34099.  
 DR HSSP; P01625; I1VE.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003596; IG\_V.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS50835; IG\_LIKE; 1.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 58.1%; Score 384; DB 2; Length 108;  
 Best Local Similarity 64.8%; Pred. No. 8-30;  
 Matches 70; Conservative 21; Mismatches 17; Indels 0; Gaps 0;

QY 21 DIVLTGSPATLSTPGDSVLSGRASGITSNNTLHWYQOKSHESPLLLIKYASQSISGIPS 80  
 DB 1 EIVMTGSPATLSTPGDSVLSGRASGITSNNTLHWYQOKSHESPLLLIKYASQSISGIPS 60  
 QY 81 RFGSGSGDFTLINSYETEDFGMYFCQGSNSWPLTSGSGTKLEIKR 128  
 DB 61 RFGSGSGDFTLINSYETEDFGMYFCQGSNSWPLTSGSGTKLEIKR 108

RESULT 14  
 ID Q6GKX0 PRELIMINARY; PRT; 236 AA.  
 AC Q6GKX0;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences",  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073775; AAH73775.1; -.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-1like.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003006; IG\_MHC.

DR InterPro: IPR003596; IG\_V.  
DR Pfam: PF07654; Cl-set; 1.  
DR Pfam: PF00047; IG; 2.  
DR SMART: SM00409; IG; 2.  
DR SMART: SM00407; IG; 1.  
DR SMART: SM00406; IG; 1.  
DR PROSITE: PSS0835; IG\_LIKE; 2.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
DR Hypothetical protein.  
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 58.1%; Score 384; DB 2; Length 236;  
Best Local Similarity 59.3%; Pred. No. 2.2e-29;  
Matches 73; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 6 QIIGLMFWISARGLIVLTOSPATLVTPEGSVSLSCRASQITSNLHWYQOKSHESPR 65  
DB 8 QILGLLIMRGARCDIQMTQSPSSLSASVGDVITTCRASQINNYIMWYQJLKPGRAP 67  
QY 66 LLIKVASQISIGIPSNRPSGSGGTPTLSINSVETEDFGMYFCQGSNSWPLTFGSGTKLE 125  
DB 68 LLIIYAASLSIQSGVPSRPSGSGGTPTLTITSLRPDPFATYYCQGSYNIPLTFGCGTNVE 127  
QY 126 IKR 128  
DB 128 IKR 130

RESULT 15  
O9UL85 PRELIMINARY; PRT; 109 AA.

AC O9UL85;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Myosin-reactive immunoglobulin kappa chain variable region  
DE (Fragment).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/cjln.1998.4531;  
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berny S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus".  
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).  
DR EMBL; AF035029; AAD56265.1; -.  
DR PIR; D30609; D30609.  
DR HSSP; P01625; 1EK3.  
DR InterPro: IPR007110; IG-like.  
DR InterPro: IPR003596; IG\_V.  
DR SMART; SM00406; IG; 1.  
DR PROSITE; PSS0835; IG\_LIKE; 1.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 109 AA; 11761 MW; FBIE43E7C7AFACC CRC64;

Query Match 57.6%; Score 380.5; DB 2; Length 109;  
Best Local Similarity 67.9%; Pred. No. 2e-29;  
Matches 74; Conservative 18; Mismatches 16; Indels 1; Gaps 1;

QY 21 DIVLTOSPATLSTPDSVSLSCRASQITSNLHWYQOKSHESPRLLIKVASISIGIPS 80  
DB 1 EIVMTOSPATLSTPDSVSLSCRASQITSNLHWYQOKSHESPRLLIKVASISIGIPS 60  
QY 81 RPSGSGSGTPTLSINSVETEDFGMYFCQGSNSW-PLTFGSGTKLEIKR 128  
DB 61 RPSGSGSGTPTLSINSVETEDFGMYFCQGSNSW-PLTFGSGTKLEIKR 109

Search completed: May 25, 2005, 15:56:03  
Job time : 63.3926 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 25, 2005, 15:35:17 ; Search time 62.6028 Seconds  
(without alignments)  
821.675 Million cell updates/sec

Title: US-10-006-773A-9

Perfect score: 684

Sequence: 1 NNFGSLIFLVVLKVGQCE.....YCARDLFRWGQGITLVSS 133

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A\_Geneseq\_16dec04:\*  
1: geneeqp1980s:\*  
2: geneeqp1990s:\*  
3: geneeqp2000s:\*  
4: geneeqp2001s:\*  
5: geneeqp2002s:\*  
6: geneeqp2003as:\*  
7: geneeqp2003bs:\*  
8: geneeqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	100.0	133	6	ABG74243
2	610.5	89.3	138	5	ABG76924
3	609.5	89.1	138	8	ADR88408
4	590	86.3	139	6	ABG74247
5	569.5	83.3	462	7	AAO29869
6	569.5	83.3	462	7	ADJ79787
7	569.5	83.3	464	5	AAU72801
8	559.5	81.8	144	5	ABR79730
9	559	81.7	137	2	AAW57592
10	559	81.7	137	3	AAW89625
11	559	81.7	137	3	AAW77513
12	559	81.7	137	4	AAW67102
13	559	81.7	137	4	AAW64775
14	559	81.7	137	4	AAW63393
15	559	81.7	137	6	ABR95208
16	559	81.7	137	6	ABR95208
17	559	81.7	137	8	ADO33883
18	552.5	80.8	138	5	AAO20064
19	550.5	80.5	138	5	ABG76928
20	550.5	80.5	138	5	ADR88412
21	550.5	80.5	140	6	ABG74241
22	549.5	80.3	468	6	ABP58275
23	548.5	80.2	138	5	ABG76932
24	548.5	80.2	138	8	ADR88416
25	547.5	80.0	139	2	AAO30460

#### ALIGNMENTS

26	545.5	79.8	138	2	AAW03722
27	543.5	79.5	139	2	AAO27053
28	542.5	79.3	477	2	AAO47450
29	542.5	79.3	477	2	AAO47453
30	541.5	79.2	138	3	AAO32404
31	539	78.8	141	8	AAO43551
32	538.5	78.7	136	2	AAO6251
33	536.5	78.4	140	5	AAU76122
34	536	78.4	141	8	AAO43555
35	534.5	78.1	136	2	AAO43555
36	534.5	78.1	136	2	AAO43555
37	533.5	78.0	142	2	AAO30882
38	533	77.9	139	1	AAO90480
39	533	77.9	139	2	AAO52773
40	533	77.9	139	2	AAO52791
41	532.5	77.9	140	2	AAO21841
42	531.5	77.7	140	5	AAU76132
43	529.5	77.4	138	8	ADR47397
44	529.5	77.4	140	5	AAU76133
45	527.5	77.1	158	2	AAO19579

RESULT 1  
ABG74243 standard, protein, 133 AA.  
ID ABG74243

AC ABG74243;

DT 22-APR-2003 (first entry)

DE Mouse antibody 3D8 heavy chain variable region.

KW T-cell receptor; cytosolic; dermatological; neuroprotective;

KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;

KW 3E11; prostate-specific membrane antigen; zeta signalling chain;

KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;

OS small cell lung cancer; heavy chain variable region; mouse.

XX Mus sp.

XX US2002132983-A1.

XX 19-SEP-2002.

XX 10-DEC-2001; 2001US-00006773.

XX 30-NOV-2000; 2000US-0250087P.

XX 30-NOV-2000; 2000US-0250089P.

XX (JUNG/) JUNGHANS R P.

XX Jungmans RP;

XX WPI; 2003-208946/20.

XX N-PSDB; ABX16569.

XX New chimeric molecule useful in treating patients with disorders, such as

XX melanoma, neuroendocrine disorders, prostate and small cell lung cancer

XX comprises GD3 and/or PSMA binding domains of antibody.

XX Disclosure; Page 12; 35pp; English.

CC The invention relates to a chimeric molecule comprising the GD3  
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3  
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)  
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene  
CC sequences, the zeta signalling chain of the T cell receptor and an  
CC intervening CD8alpha hinge in which cysteine residues have been mutated.  
CC The chimeric molecules expressed in T cells or NK cells or other  
CC effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),  
 CC and/or together with each other or with heterologous constructs to engage  
 CC additional stimulatory and functional properties of the effector cells to  
 CC enhance the antitumour therapeutic efficacy (claimed). They are  
 CC particularly useful in disorders including melanoma, neuroendocrine  
 CC tumours and prostate and small cell lung cancer. The present sequence  
 CC represents the mouse antibody 3D8 heavy chain variable region  
 XX

SQ Sequence 133 AA;

Query Match 100.0%; Score 684; DB 6; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 1e-54; Indels 0; Gaps 0;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNFGSLIFLVYLVKGVQCEVKVBSGGGLVYKPGASLKLSCAASGFTFSNYGMSWYRQTS 60  
 DB 1 MNFGSLIFLVYLVKGVQCEVKVBSGGGLVYKPGASLKLSCAASGFTFSNYGMSWYRQTS 60  
 QY 61 DKRLVNASISGGGSTFYADNVKGRFTTSRENANKTLYLQMSLKSSEDTALYYCARDDL 120  
 DB 61 DKRLVNASISGGGSTFYADNVKGRFTTSRENANKTLYLQMSLKSSEDTALYYCARDDL 120  
 QY 121 FNMGGTTLTVSS 133  
 DB 121 FNMGGTTLTVSS 133

RESULT 2

ABG76924 standard; protein; 138 AA.

AC ABG76924;  
 DT 05-NOV-2002 (first entry)  
 XX

DE Mouse 3D6 VH protein.

XX Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;  
 KW variable region complementarity determining region; 3D6; 10D5;  
 KW variable framework region; amyloidogenic disease; Alzheimer's disease;  
 KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;  
 KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;  
 KW Abeta.

XX Mus musculus.

XX WO200246237-A2.

XX 13-JUN-2002.

XX 06-DEC-2001; 2001WO-US046587.

XX 06-DEC-2000; 2000US-0251892P.

XX (NEUR-) NEURALAB LTD.

XX (AMHP) WYETH.

XX Basi G, Saldanha J, Yednock T;

XX WPI; 2002-519658/55.

XX N-PSDB; ABS59427.

XX Novel light/heavy chain of humanized immunoglobulin for treating

XX amyloidogenic disease, has 3D6/10D5 variable region complementarity

XX determining regions and variable framework region from human acceptor

XX immunoglobulin.

XX Claim 68; Fig 2; 171pp; English.

XX The present invention relates to new humanized immunoglobulin (Ig) light

XX chain (LC) or heavy chain (HC) comprising variable region complementarity

XX determining regions from 3D6/10D5 Ig LC or HC variable region sequence,

XX and variable framework region from human acceptor Ig LC or HC sequence.

CC The invention is useful for preventing or treating an amyloidogenic  
 CC disease or Alzheimer's disease in a patient. The invention is also useful  
 CC for in vivo imaging amyloid deposits in a patient. The present amino acid  
 CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or  
 CC variable heavy (VH) chain protein of the invention  
 XX

SQ Sequence 138 AA;

Query Match 89.3%; Score 610.5; DB 5; Length 138;  
 Best Local Similarity 87.0%; Pred. No. 5.6e-48;  
 Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVYLVKGVQCEVKVBSGGGLVYKPGASLKLSCAASGFTFSNYGMSWYRQTS 60  
 DB 1 MNFGSLIFLVYLVKGVQCEVKVBSGGGLVYKPGASLKLSCAASGFTFSNYGMSWYRQTS 60  
 QY 61 DKRLVNASISGGGSTFYADNVKGRFTTSRENANKTLYLQMSLKSSEDTALYYCARDDL 120  
 DB 61 DKRLVNASISGGGSTFYADNVKGRFTTSRENANKTLYLQMSLKSSEDTALYYCARDDL 120  
 QY 121 FNMGGTTLTVSS 133  
 DB 121 FNMGGTTLTVSS 133

RESULT 3

ADR88408 standard; protein; 138 AA.

AC ADR88408;

DT 16-DEC-2004 (first entry)

DE Murine 3D6 immunoglobulin heavy chain variable region SEQ ID NO:4.

XX 3D6; heavy chain variable region; immunoglobulin;  
 KW complementarity determining region; CDR; 10D5; variable framework region;  
 KW neuroprotective; nootropic; gene therapy; amyloidogenic disease;  
 KW Alzheimer's disease.

XX Mus musculus.

XX Key

XX Peptide 1..19

XX Protein /label= signal peptide

XX WO2004080419-A2.

XX 23-SEP-2004.

XX 12-MAR-2004; 2004WO-US007503.

XX 12-MAR-2003; 2003US-00388389.

XX (NEUR-) NEURALAB LTD.

XX (AMHP) WYETH.

XX Basi G, Saldanha JW, Yednock T;

XX WPI; 2004-668880/65.

XX N-PSDB; ADR88407.

XX New humanized antibodies that recognize beta amyloid peptides, useful for

XX preventing or treating amyloidogenic diseases, such as Alzheimer's

XX disease.

XX Claim 2; SEQ ID NO 4; 176pp; English.

XX The invention relates to a novel humanised immunoglobulin light or heavy

XX chain. The humanised immunoglobulin light or heavy chain comprises:

XX variable region complementarity determining regions (CDR's) from the 3D6

immunoglobulin light chain variable region sequence of 132 amino acids fully defined in the specification (ADR88406), or heavy chain variable region sequence of 138 amino acids fully defined in the specification (ADR88408); or from the 1005 immunoglobulin light chain variable region sequence of 131 amino acids given in the specification (ADR88418) or heavy chain variable region sequence of 142 amino acids fully defined in the specification (ADR88420); and a variable framework region from a human acceptor immunoglobulin light or heavy chain sequence, provided that at least one framework residue is substituted with the corresponding amino acid residue from the mouse 3D6 or 10D5 light or heavy chain variable region sequence, where the framework residue is a residue that non-covalently binds antigen directly, a residue adjacent to a CDR, a CDR-intersecting residue or a residue participating in the VL-VH interface. An antibody of the invention has neuroprotective and neurotropic activity, and may have a use in gene therapy. The composition and methods are useful for preventing or treating an amyloidogenic disease, such as Alzheimer's disease. The variable region sequence is useful in producing a three-dimensional image of a 3D6 or 10D5 immunoglobulin, immunoglobulin chain, or its domain. The present sequence represents the murine 3D6 immunoglobulin heavy chain variable region.

Sequence 138 AA;

Query Match Best Local Similarity 89.1%; Score 609.5; DB 8; Length 138;  
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVLYLVKGVQCEVKVVGSGGLVPGASLKLSCAAGFTFSNYGMSVNRQTS 60  
DB 1 MNFGSLIFLVLYLVKGVQCEVKVVGSGGLVPGASLKLSCAAGFTFSNYGMSVNRQTS 60  
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRANKTYLQMSLSKSDTALYYCARDL 120  
DB 61 DKRLWVASISGGDSTFYADNVKGRFTISRANKTYLQMSLSKSDTALYYCARDL 120  
QY 121 FN-----WGQGTTLTVSS 133  
DB 121 YGSSSDVWGQGTTLTVSS 138

RESULT 4  
ABG74247  
ID ABG74247 standard; protein; 139 AA.

AC ABG74247;

DT 22-APR-2003 (first entry)

DE Mouse antibody 3E11 heavy chain variable region.

XX T-cell receptor; cytosolic; dermatological; neuroprotective;  
XX immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D6; 4D4;  
XX 3E11; prostate-specific membrane antigen; zeta signalling chain;  
XX CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;  
XX small cell lung cancer; heavy chain variable region; mouse.

OS Mus sp.

PN US2002132983-A1.

PD 19-SEP-2002.

PP 10-DEC-2001; 2001US-00006773.

PR 30-NOV-2000; 2000US-0250087P.

PR 30-NOV-2000; 2000US-0250089P.

PA (JUNG/) JUNGHANS R P.

PI Jungmans RP;

DR MPI; 2003-208946/20.

DR N-PSDB; ABX16573.

XX New chimeric molecule useful in treating patients with disorders, such as  
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer  
PT comprises GD3 and/or PSMA binding domains of antibody.

PS Disclosure; Page 17; 35pp; English.

XX The invention relates to a chimeric molecule comprising the GD3  
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3  
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)  
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene  
CC sequences, the zeta signalling chain of the T cell receptor and an  
CC intervening CD8alpha hinge in which cysteine residues have been mutated.  
CC The chimeric molecules expressed in T cells or NK cells or other  
CC effector cells are useful in treating patients with cancers expressing  
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),  
CC and/or together with each other or with heterologous constructs to engage  
CC additional stimulatory and functional properties of the effector cells to  
CC enhance the antitumour therapeutic efficacy (claimed). They are  
CC particularly useful in disorders including melanoma, neuroendocrine  
CC tumours and prostate and small cell lung cancer. The present sequence  
CC represents the mouse antibody 3E11 heavy chain variable region

Sequence 139 AA;

Query Match Best Local Similarity 86.3%; Score 590; DB 6; Length 139;  
Matches 116; Conservative 8; Mismatches 9; Indels 6; Gaps 1;

QY 1 MNFGSLIFLVLYLVKGVQCEVKVVGSGGLVPGASLKLSCAAGFTFSNYGMSVNRQTS 60  
DB 1 MNFGSLIFLVLYLVKGVQCEVKVVGSGGLVPGASLKLSCAAGFTFSNYGMSVNRQTS 60  
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRANKTYLQMSLSKSDTALYYCARDL 119  
DB 61 DKRLWVASISGGDSTFYADNVKGRFTISRANKTYLQMSLSKSDTALYYCARDL 120  
QY 120 -----LFWGQGTTLTVSS 133  
DB 121 SVGCMFATWGQGTTLTVSSA 139

RESULT 5  
AAO29869  
ID AAO29869 standard; protein; 462 AA.

AC AAO29869;

DT 27-AUG-2003 (first entry)

DE Mouse anti-human DR5 antibody (TR8-8) heavy chain.

XX Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;  
XX inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;  
XX Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;  
XX multiple sclerosis; graft-versus-host disease; arteriosclerosis; actina;  
XX Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;  
XX Crohn's disease; diabetes mellitus; antibody; mouse.

OS Mus sp.

PN WO2003037913-A2.

PD 08-MAY-2003.

PP 01-NOV-2002; 2002WO-US035333.

PR 01-NOV-2001; 2001US-0346402P.

PA (UABR-) UAB RES FOUND.

PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;

DR WPI, 2003-441350/41.  
 XX N-PSDB; AAL60477.  
 XX  
 PT New purified antibody that specifically binds a TNF-related apoptosis-  
 PT inducing ligand receptor DR4 or DR5, useful for treating cancer,  
 PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or  
 PT rheumatoid arthritis.  
 XX  
 PS Example 16; Page 224-225; 251pp; English.  
 XX  
 CC The invention relates to an antibody that specifically binds a tumour  
 CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor  
 CC DR4 or DR5. Antibodies of the invention are useful for selectively  
 CC inducing apoptosis in target cells expressing DR4, for inhibiting  
 CC proliferation of target cells expressing DR4 or for treating cancer,  
 CC inflammatory disease or autoimmune disease in a subject e.g. systemic  
 CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-  
 CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple  
 CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or  
 CC glomerular nephritis. The present sequence is mouse anti-human DR5  
 CC antibody (TRA-8) heavy chain  
 CC  
 SQ Sequence 462' AA:  
 Query Match 83.3%; Score 569.5; DB 6; Length 462;  
 Best Local Similarity 81.9%; Pred. No. 1.2e-43;  
 Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;  
 QY 1 MNFGSLIFLVVLKGVQCEVKEVSGGLVPRGASLKLSCAASGFTPSNYGMSWVRQTS 60  
 DB 1 MNFGSLIFLVVLKGVQCEVMEVSGGLVPRGSLKLSCAASGFTFSSYVMSWVRQTP 60  
 QY 61 DKRLWVASISGSGDSTFYADVNGKRFITISRENAKTLYLQMSLSKSEPTALYYCAR--D 118  
 DB 61 EKRLWVAITISGSGSTYYPDVSKGRFTISRDNAKTLYLQMSLSKSEPTAMYYCARRGD 120  
 QY 119 DLFN--WGQGTTLTVSS 133  
 DB 121 SMITTDYWGQGTTLTVSS 138  
 RESULT 6  
 ADJ79787  
 ID ADJ79787 standard; protein; 462 AA.  
 XX  
 AC ADJ79787;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE TRA-8 antibody heavy chain.  
 XX  
 KM nephrotic; antiarteriosclerotic; cardiac; antiasthmatic;  
 KM antiatherogenic; antiinflammatory; antidiabetic; haemostatic;  
 KM neuroprotective; antiinfectivity; immunosuppressive; dermatological;  
 KM antianemic; antitrematic; antiarthritic; thyromimetic; apoptosis;  
 KM proliferation;  
 KM tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;  
 KM TRAIL; synovial cell; lymphocyte; neutrophil;  
 KM systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;  
 KM graft-versus-host disease; Sjogren's syndrome; pernicious anemia;  
 KM Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;  
 KM autoimmune hemolytic anemia; sterility; myasthenia gravis;  
 KM multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;  
 KM thrombopenia purpura; insulin dependent diabetes mellitus; allergy;  
 KM asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;  
 KM glomerular nephritis; hypoplastic anemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003038043-A2.  
 XX  
 PD 08-MAY-2003.  
 XX

PF 25-OCT-2002; 2002WO-US034420.  
 XX  
 XX 01-NOV-2001; 2001US-0346402P.  
 XX 24-JUN-2002; 2002US-0391478P.  
 XX  
 PA (UABR-) UAB RES FOUND.  
 XX  
 PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;  
 PI Lobuglio AF, Buchsbaum DJ;  
 XX  
 DR WPI, 2003-421518/39.  
 XX  
 PT Inducing apoptosis and inhibiting proliferation of target cells  
 PT expressing DR5, by contacting the target cell with an antibody that binds  
 PT TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic  
 PT agents.  
 XX  
 PS Example 16; SEQ ID NO 23; 274pp; English.  
 XX  
 CC The invention relates to a method of selectively inducing apoptosis in  
 CC and inhibiting (M1) proliferation of target cells expressing DR5,  
 CC comprising contacting the cell with an antibody that specifically binds  
 CC tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)  
 CC receptor DR5, where the antibody, in its soluble form, has in vivo and in  
 CC vitro apoptosis-inducing activity in the cell expressing DR5, and  
 CC contacting the cell with one or more therapeutic agents. M1 is useful for  
 CC inducing apoptosis in target cell and inhibiting proliferation of target  
 CC cell expressing DR5, where the target cell is an abnormally proliferating  
 CC synovial cells (e.g. rheumatoid arthritis synovial cell), activated  
 CC immune cell (e.g. activated lymphocyte), neutrophil, or virally infected  
 CC cell. M2 is useful for treating a subject having inflammatory and  
 CC autoimmune diseases. The inflammatory or autoimmune disease are selected  
 CC from systemic lupus erythematosus, Hashimoto's disease, rheumatoid  
 CC arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious  
 CC anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's  
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,  
 CC multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,  
 CC asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,  
 CC glomerular nephritis, and hypoplastic anemia. This sequence represents a  
 CC protein used in the method of the invention.  
 CC  
 SQ Sequence 462 AA:  
 Query Match 83.3%; Score 569.5; DB 7; Length 462;  
 Best Local Similarity 81.9%; Pred. No. 1.2e-43;  
 Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;  
 QY 1 MNFGSLIFLVVLKGVQCEVKEVSGGLVPRGASLKLSCAASGFTPSNYGMSWVRQTS 60  
 DB 1 MNFGSLIFLVVLKGVQCEVMEVSGGLVPRGSLKLSCAASGFTFSSYVMSWVRQTP 60  
 QY 61 DKRLWVASISGSGDSTFYADVNGKRFITISRENAKTLYLQMSLSKSEPTALYYCAR--D 118  
 DB 61 EKRLWVAITISGSGSTYYPDVSKGRFTISRDNAKTLYLQMSLSKSEPTAMYYCARRGD 120  
 QY 119 DLFN--WGQGTTLTVSS 133  
 DB 121 SMITTDYWGQGTTLTVSS 138  
 RESULT 7  
 AAU72801  
 ID AAU72801 standard; protein; 464 AA.  
 XX  
 AC AAU72801;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE TRA-8 heavy chain.  
 XX  
 KM Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;  
 KM TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;  
 KM



autoimmune disease; systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia; Addison disease; scleroderma; Goodpasture's syndrome; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes; allergy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.

Mus musculus.

WO200183560-A1.

08-NOV-2001.

02-MAY-2001; 2001WO-US014151.

02-MAY-2000; 2000US-0201344P.

(UABR-) UAB RES FOUND.

Zhou T, Ichikawa K, Kimberly RP, Koopman WJ; WPI; 2002-049338/06. N-PSDB; AAS97062.

Novel antibody specific for tumor necrosis factor-related apoptosis-inducing ligand, useful for inhibiting cell proliferation in cancer.

Claim 26; Page 198-199; 229pp; English.

The invention describes a novel antibody which recognizes a tumour necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing activity to a cell expressing DR5 in vivo. It is also useful for preparing a therapeutic for selective apoptosis of abnormal or dysregulated cells, and for inhibiting cell proliferation in a cell, preferably a human breast, ovary, colon, haematopoietic, prostate, lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may also be administered e.g. paclitaxel, taxol or cycloheximide. The antibody is used to treat an autoimmune disease, systemic lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, rejection after organ transplantation, and numerous malignancies of lung, prostate, liver, ovary, lymphatic or breast tissue. Peptides used to design primers for isolating heavy and light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are shown in AAU72799 and AAU72800

Sequence 464 AA;

Query Match 83.3%; Score 569.5; DB 5; Length 464; Best Local Similarity 81.9%; Pred. No. 1.2e-43; Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;

QY 1 MNFGSLIFLVVLKGVCEVNVBSGGGLVPGASLKLSKASGFTFSNYGMSWVRQTS 60  
DB 1 MNFGSLIFLVVLKGVCEVNVBSGGGLVPGASLKLSKASGFTFSNYGMSWVRQTS 60  
QY 61 DKRLWVASISGGSTFYADNVKGRFTISRENANKTLYLQMSLSKSEDTALYYCAR--D 118  
DB 61 DKRLWVASISGGSTFYADNVKGRFTISRENANKTLYLQMSLSKSEDTALYYCAR--D 120  
QY 119 DLFN---WGQGTTLTVSS 133  
DB 121 SMITTDYWGQGTTLTVSS 138

RESULT 8  
ABR79730  
ID ABR79730 strand; protein; 144 AA.

AC ABR79730;  
DT 29-OCT-2002 (first entry)  
DE Anti-Streptococcus mutans surface antigen MAb SWIA3 VH.  
KW Streptococcus mutans; monoclonal antibody; Mab; mouse; chimeric antibody; antibody; anticaries; transgenic plant; transgenic animal; carries; immunotherapy; therapy.  
XX Mus musculus.  
XX US2002068066-A1.  
XX 06-JUN-2002.  
XX 15-JUN-2001; 2001US-00881823.  
XX 20-AUG-1999; 99US-00378577.  
XX (SHI W.) SHI W.  
XX (MORR/) MORRISON S L.  
XX (TRIN/) TRINH K.  
XX (WIMS/) WIMS L.  
XX (CHEN/) CHEN L.  
XX (ANDE/) ANDERSON M H.  
XX Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH; WPI; 2002-565838/60. N-PSDB; ABR84611.  
XX Treatment and prevention of dental caries in mammals, in particular PT humans by orally administering genetically engineered or purified PT antibodies that bind to surface antigens of cariogenic organisms.  
XX Claim 14; Fig 3B; 30pp; English.  
XX The present sequence is the protein sequence of the heavy chain variable CC region (VH) of the murine monoclonal antibody SWIA3 (IgG), which binds CC specifically to the surface antigens of cariogenic type c Streptococcus CC mutans (ATCC 25175). The monoclonal antibody is produced by SWIA3 (ATCC CC HB 12558) hybridoma cells. In an example from the invention, chimeric CC monoclonal antibody TERE was produced comprising SWIA3 variable regions CC and human antibody constant regions. Such chimeric monoclonal antibodies CC can be used to prevent or treat dental caries in humans. The antibodies CC engage the effector apparatus of the human immune system when they bind CC cariogenic organisms, resulting in their destruction. The chimeric CC antibodies may be produced in edible plants, in transgenic animals, or in CC chicken eggs for oral ingestion  
XX  
XX Sequence 144 AA;

Query Match 81.8%; Score 559.5; DB 5; Length 144; Best Local Similarity 76.1%; Pred. No. 2.7e-43; Matches 108; Conservative 15; Mismatches 10; Indels 9; Gaps 1;

QY 1 MNFGSLIFLVVLKGVCEVNVBSGGGLVPGASLKLSKASGFTFSNYGMSWVRQTS 60  
DB 1 MNFGSLIFLVVLKGVCEVNVBSGGGLVPGASLKLSKASGFTFSNYGMSWVRQTS 60  
QY 61 DKRLWVASISGGSTFYADNVKGRFTISRENANKTLYLQMSLSKSEDTALYYCARD-- 119  
DB 61 DKRLWVASISGGSTFYADNVKGRFTISRENANKTLYLQMSLSKSEDTALYYCARD-- 120  
QY 120 -----LFNWGQGTTLTVSS 133  
DB 121 SYGSYYAMDYWGQGTSTVTVSS 142

RESULT 9  
AAM57592



RESULT 11  
 ID AAY77513  
 AC AAY77513 standard; protein; 137 AA.  
 XX  
 XX AAY77513;  
 DT 26-APR-2000 (first entry)  
 XX  
 XX Mouse antibody H chain V region.  
 DE  
 XX Hypercalcaemic crisis; parathyroid hormone related peptide; PTHrP; tumour.  
 XX  
 XX Mus musculus.  
 OS  
 XX WO200000219-A1.  
 XX  
 XX PD 06-JAN-2000.  
 XX  
 XX PF 25-JUN-1999; 99WO-JP003433.  
 XX  
 XX PR 26-JUN-1998; 98JP-00180143.  
 XX  
 XX PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 XX PI Sato K, Tsunenari T;  
 XX  
 XX DR WPI: 2000-117115/10.  
 XX  
 XX DR N-PSDB; AA258913.  
 XX  
 XX PT Treatment of hypercalcaemic crisis with a substance inhibiting binding of  
 XX  
 XX PT parathyroid hormone related peptide to its receptor.  
 XX  
 XX PS Example 2; Page 96-97; 120pp; Japanese.  
 XX  
 XX CC The invention relates to a method of treatment of hypercalcaemic crisis. A  
 XX  
 XX CC composition for the treatment of hypercalcaemic crisis contains as active  
 XX  
 XX CC component a substance which inhibits the binding of parathyroid hormone  
 XX  
 XX CC related peptide (PTHrP) to its receptor. The inhibitor is used for the  
 XX  
 XX CC treatment of hypercalcaemic crisis, such as that associated with a  
 XX  
 XX CC malignant tumour  
 XX  
 XX SQ Sequence 137 AA;

Query Match 81.7%; Score 559; DB 3; Length 137;  
 Best Local Similarity 78.1%; Pred. No. 2.8e-43;  
 Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;

QY 1 MNFGSLIFLVVLKGVCEVAVVSGGLVYKPGASLKLSCAASGFTFSNYGMSWVROT 60  
 DB 1 MNFGSLIFLVVLKGVCEVAVVSGGLVYKPGASLKLSCAASGFTFSNYGMSWVROT 60  
 QY 61 DKRLKLVASISGGSDTFYADVVKGRFTISRANAKNTLYLQMSLKSSEDTALYCARDDL 120  
 DB 61 DKRLKLVASISGGSDTFYADVVKGRFTISRANAKNTLYLQMSLKSSEDTALYCARDDL 120  
 QY 121 FN---WGQGTLLTVSS 133  
 DB 121 MTFYFAYWGQGTLLTVSA 137

RESULT 12  
 ID AAG67102  
 AC AAG67102 standard; protein; 137 AA.  
 XX  
 XX AAG67102;  
 DT 13-NOV-2001 (first entry)  
 XX  
 XX Amino acid sequence of a murine antibody directed against PTH.  
 DE  
 XX Tissue decomposition inhibitor; parathyroid hormone; cancer cachexia;  
 XX  
 XX KM septicemia; injury; muscular dystrophy; cytokine; interleukin-6;

KW granulocyte colony stimulating factor; interleukin-11;  
 KM leukemia inhibitory factor; weight loss.  
 XX  
 XX OS Mus musculus.  
 XX  
 XX FH Key Location/Qualifiers  
 XX FT Peptide 1..19  
 XX FT /note="signal peptide"  
 XX FT Protein 20..137  
 XX FT /note="mature protein; this sequence given as sequence  
 XX FT number 45 in the specification"  
 XX  
 XX PN WO200164249-A1.  
 XX  
 XX PD 07-SEP-2001.  
 XX  
 XX PF 30-AUG-2000; 2000WO-JP005886.  
 XX  
 XX PR 28-FEB-2000; 2000JP-00052414.  
 XX  
 XX PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 XX PI Saito H, Tsunenari T, Onuma E, Sato K;  
 XX  
 XX DR WPI: 2001-550131/61.  
 XX  
 XX DR N-PSDB; AAH75106..  
 XX  
 XX PT Tissue decomposition inhibitor that prevents parathyroid hormone  
 XX  
 XX PT associated proteins from binding to its receptor.  
 XX  
 XX PS Example 1; Page 106; 132pp; Japanese.  
 XX  
 XX CC The specification describes a tissue decomposition inhibitor, which  
 XX  
 XX CC comprises a substance that inhibits peptides associated with parathyroid  
 XX  
 XX CC hormone (PTH) from binding with their receptor. The method is used to  
 XX  
 XX CC inhibit tissue decomposition caused by cancer cachexia, septicemia, heavy  
 XX  
 XX CC external injury or muscular dystrophy, and for treating patients with  
 XX  
 XX CC elevated cytokine (interleukin-6, granulocyte colony stimulating factor,  
 XX  
 XX CC interleukin-11 and leukemia inhibitory factor) levels. It may also be  
 XX  
 XX CC used for preventing weight loss caused by cancer cachexia. The present  
 XX  
 XX CC sequence represents a murine antibody fragment which is directed against  
 XX  
 XX CC PTH  
 XX  
 XX SQ Sequence 137 AA;

Query Match 81.7%; Score 559; DB 4; Length 137;  
 Best Local Similarity 78.1%; Pred. No. 2.8e-43;  
 Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;

QY 1 MNFGSLIFLVVLKGVCEVAVVSGGLVYKPGASLKLSCAASGFTFSNYGMSWVROT 60  
 DB 1 MNFGSLIFLVVLKGVCEVAVVSGGLVYKPGASLKLSCAASGFTFSNYGMSWVROT 60  
 QY 61 DKRLKLVASISGGSDTFYADVVKGRFTISRANAKNTLYLQMSLKSSEDTALYCARDDL 120  
 DB 61 DKRLKLVASISGGSDTFYADVVKGRFTISRANAKNTLYLQMSLKSSEDTALYCARDDL 120  
 QY 121 FN---WGQGTLLTVSS 133  
 DB 121 MTFYFAYWGQGTLLTVSA 137

RESULT 13  
 ID AAG64775  
 AC AAG64775 standard; protein; 137 AA.  
 XX  
 XX AAG64775;  
 DT 08-OCT-2001 (first entry)  
 XX  
 XX Mouse anti-PTHrP mAb 23-57-137-1 VH precursor.  
 DE  
 XX Parathyroid hormone-related peptide; PTHrP; antagonist;

KW calcium regulation disorder; serum calcium concentration; VH;  
 KM humoral hypercalcaemia of malignancy; cytostatic; analgesic; mouse;  
 KM murine; monoclonal antibody 23-57-137-1; heavy chain variable region.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= signal\_peptide  
 FT 20..137  
 FT Protein /note= "Mature VH"  
 FT  
 PN WO200147554-A1.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 27-DEC-2000; 2000WO-JP009339.  
 XX  
 PR 28-DEC-1999; 99JP-00375203.  
 XX  
 PA (CHUGAI ) CHUGAI SEIYAKU KK.  
 XX  
 PI Yamazaki T, Hayaaka A, Koga A;  
 DR WPI; 2001-425590/45.  
 DR N-PSDB; AAH76644.  
 XX  
 PT Composition for treating diseases of calcium regulation and for use as an  
 PT analgesic, comprises an antibody recognizing parathyroid hormone related  
 PT peptide.  
 PS Disclosure; Page 103-104; 128pp; Japanese.  
 XX  
 CC The invention relates to a stabilised composition of an antibody which  
 CC recognises parathyroid hormone-related peptide (PTHrP) - see AAG64793.  
 CC The composition consists of a solution of the antibody in a buffer of pH  
 CC 5-8 containing one or more of acetic acid, phosphoric acid, citric acid  
 CC and their salts. The composition has increased storage stability,  
 CC especially at elevated temperatures. The composition antagonises the  
 CC action of PTHrP, and may be used in the treatment of diseases involving  
 CC disturbances of calcium regulation (high or low serum calcium  
 CC concentration) such as humoral hypercalcaemia of malignancy and as an  
 CC analgesic. The present sequence represents the heavy chain variable  
 CC region (VH) precursor of anti-human PTHrP murine monoclonal antibody 23-  
 CC 57-137-1  
 CC  
 SQ Sequence 137 AA.  
 Query Match 81.7%; Score 559; DB 4; Length 137;  
 Best Local Similarity 78.1%; Pred. No. 2.8e-43;  
 Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;  
 QY 1 MNFGSLIFLVYLVKGVCEVKNVYSGGGLVYKPGASLKLSGASGTFPSNYGMSWRQTS 60  
 DB 1 MNFGSLIFLVYLVKGVCEVKNVYSGGGLVYKPGASLKLSGASGTFPSNYGMSWRQTS 60  
 QY 61 DKRLWVASISGGSDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCARDDL 120  
 DB 61 DKRLWVASISGGSDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCARDDL 120  
 QY 121 FN---WGQGTTLTVSS 133  
 DB 121 MTYFAWVGQGTTLTVSSA 137  
 RESULT 14  
 AAG63393  
 ID AAG63393 standard; protein; 137 AA.  
 XX  
 AC AAG63393;  
 XX  
 DT 15-OCT-2001 (first entry)  
 XX

DE Amino acid sequence of a murine polypeptide.  
 XX  
 KM Parathyroid hormone-associated peptide; PTHrP; dental disease.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /note= "mature protein"  
 FT  
 PN WO200154725-A1.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 14-DEC-2000; 2000WO-JP008875.  
 XX  
 PR 25-JAN-2000; 2000JP-00083034.  
 XX  
 PA (CHUGAI ) CHUGAI SEIYAKU KK.  
 XX  
 PI Kato A, Suzuki M, Sugimoto T;  
 DR WPI; 2001-465459/50.  
 DR N-PSDB; AAH74284.  
 XX  
 PT Parathyroid hormone-associated peptide binding inhibitors useful for  
 PT treating dental disease.  
 PS Disclosure; Page 111-112; 140pp; Japanese.  
 XX  
 CC The specification describes a treatment for dental diseases. The  
 CC treatment comprises a substance that inhibits binding between parathyroid  
 CC hormone-associated peptide and its receptor. The present sequence  
 CC represents a murine protein, which is used in the course of the invention  
 CC  
 SQ Sequence 137 AA;  
 Query Match 81.7%; Score 559; DB 4; Length 137;  
 Best Local Similarity 78.1%; Pred. No. 2.8e-43;  
 Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;  
 QY 1 MNFGSLIFLVYLVKGVCEVKNVYSGGGLVYKPGASLKLSGASGTFPSNYGMSWRQTS 60  
 DB 1 MNFGSLIFLVYLVKGVCEVKNVYSGGGLVYKPGASLKLSGASGTFPSNYGMSWRQTS 60  
 QY 61 DKRLWVASISGGSDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCARDDL 120  
 DB 61 DKRLWVASISGGSDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSEDTALYYCARDDL 120  
 QY 121 FN---WGQGTTLTVSS 133  
 DB 121 MTYFAWVGQGTTLTVSSA 137  
 RESULT 15  
 ABB95208  
 ID ABB95208 standard; protein; 137 AA.  
 XX  
 AC ABB95208;  
 XX  
 DT 17-JUN-2002 (first entry)  
 XX  
 DE Mouse joint disease related protein SEQ ID NO 57.  
 XX  
 KM Joint disease, PTHrP; parathyroid hormone-related peptide;  
 KM parathyroid hormone; osteopathic; rheumatoid arthritis; arthritis.  
 OS Mus musculus.  
 XX  
 PN WO200213865-A1.  
 XX  
 PD 21-FEB-2002.  
 XX

PF 15-AUG-2001; 2001WO-JP007044.

XX 16-AUG-2000; 2000JP-00247013.

PR (CHUS ) CHUGAI SEIYAKU KK.

XX Yoshikawa H;

PI MPI: 2002-257551/30.

DR N-PSDB; ABL94765.

XX Agents for ameliorating symptoms caused by joint diseases relating to PTH  
PT or PTHrP e.g. chronic rheumatoid arthritis, containing inhibitors on  
PT receptor binding of parathyroid hormone-related peptide.

XX Discloure; Page 88-89; 112pp; Japanese.

CC The invention relates to agents for ameliorating symptoms causing joint  
CC diseases, containing a substance inhibiting the binding of a parathyroid  
CC hormone-related peptide to its receptor as active ingredient. The agents  
CC have osteopathic activity are useful for ameliorating symptoms caused by  
CC joint diseases relating to PTH or PTHrP e.g. chronic rheumatoid arthritis  
CC and arthritis deformans. The agents particularly improve the lowering of  
CC bone amount or suppression of bone reduction. The present sequence is  
CC that of a joint disease related protein, useful to the invention

XX Sequence 137 AA;

Query Match 81.7%; Score 559; DB 5; Length 137;

Best Local Similarity 78.1%; Pred. No. 2.8e-43;

Matches 107; Conservative 13; Mismatches 13; Indels 4; Gaps 1;

OY 1 MNFGSLIFLVVAKGVQCEVKVNESGGGLVPRGASLKSCAASGFTFENYGMWVRQTS 60

DB 1 MNFGSLIFLVVAKGVQCEVKVNESGGGLVPRGASLKSCAASGFTFENYGMWVRQTS 60

OY 61 DKRLFMVASISSGGDSTFYADNVKGRFTISRANAKVTLYLQMSLKSDEPTALYCARDDL 120

DB 61 DKRLFMVASISSGGDSTFYADNVKGRFTISRANAKVTLYLQMSLKSDEPTALYCARDDL 120

OY 121 FN---WGQGTTLTVSS 133

DB 121 MTFAYWGGTTLTVSA 137

Search completed: May 25, 2005, 15:47:16  
Job time : 62.6028 secs

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OM protein - protein search, using SW model

Run on: May 25, 2005, 15:37:02 ; Search time 16.5786 Seconds  
(without alignments)  
598.864 Million cell updates/sec

Title: US-10-006-773A-9

Perfect score: 684  
Sequence: 1 MNFGSLIFLVVLKGVQCE.....YCARDLFFMGCGITLVSS 133

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	559	81.7	135	3	US-08-579-378A-16
2	545.5	79.8	138	2	US-08-379-057-14
3	544.5	79.6	136	3	US-08-976-183A-33
4	543.5	79.5	136	3	US-08-976-183A-31
5	540.5	79.0	136	3	US-08-976-183A-32
6	539.5	78.9	136	3	US-08-976-183A-34
7	538.5	78.7	136	1	US-08-253-877C-57
8	538.5	78.7	136	2	US-08-452-164A-57
9	534.5	78.1	247	5	PCT-US94-07659-2
10	532.5	77.9	140	3	US-08-836-561-23
11	532.5	77.9	140	4	US-09-434-122-23
12	529	77.3	135	3	US-08-579-378A-20
13	527.5	77.1	158	2	US-08-653-402B-6
14	522.5	76.4	138	1	US-08-053-171-7
15	522.5	76.4	138	1	US-08-053-171-11
16	515	75.3	139	1	US-08-129-930B-96
17	515	75.3	139	3	US-08-134-346A-51
18	515	75.3	139	3	US-08-976-288A-96
19	511.5	74.8	158	2	US-08-653-402B-10
20	499	73.0	159	2	US-08-653-402B-2
21	498	72.8	255	2	US-07-690-192-4
22	496.5	72.6	170	2	US-08-652-558-40
23	495	72.4	135	5	PCT-US95-07302-8
24	487	71.2	135	4	US-08-619-491-8
25	486.5	71.1	130	4	US-09-225-322B-8
26	486.5	71.1	130	4	US-09-764-304-8
27	484.5	70.8	130	4	US-09-225-322B-18

28	484.5	70.8	130	4	US-09-764-304-18	Sequence 18, Appl
29	483	70.6	135	3	US-08-619-491-4	Sequence 4, Appl
30	483	70.6	135	5	PCT-US95-07302-4	Sequence 4, Appl
31	482.5	70.5	121	1	US-08-339-582-2	Sequence 2, Appl
32	480	70.2	131	1	US-08-259-372A-4	Sequence 4, Appl
33	480	70.2	131	1	US-08-468-671-4	Sequence 4, Appl
34	474	69.3	144	1	US-08-026-320A-2	Sequence 2, Appl
35	474	69.3	463	4	US-09-472-087-64	Sequence 4, Appl
36	474	69.3	463	4	US-09-472-087-68	Sequence 68, Appl
37	473.5	69.2	470	4	US-09-859-053-32	Sequence 32, Appl
38	471.5	68.9	470	4	US-09-859-053-36	Sequence 36, Appl
39	471	68.9	463	4	US-09-472-087-1	Sequence 1, Appl
40	471	68.9	463	4	US-09-472-087-63	Sequence 63, Appl
41	471	68.9	463	4	US-09-472-087-64	Sequence 64, Appl
42	470.5	68.8	217	5	PCT-US94-14106-59	Sequence 59, Appl
43	470.5	68.8	464	4	US-09-472-087-2	Sequence 2, Appl
44	470.5	68.8	464	4	US-09-472-087-66	Sequence 66, Appl
45	470	68.7	141	1	US-08-259-372A-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-08-579-378A-16  
Sequence 16, Application US/08579378A  
Patent No. 6210671  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/579,378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: A24  
PRIOR APPLICATION NUMBER: US 08/160,074  
FILING DATE: 30-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95114696.8  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebescheut, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
FAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-579-378A-16

Query Match 81.7%; Score 559; DB 3; Length 135;  
Best Local Similarity 82.4%; Pred. No. 4,8e-53;  
Matches 112; Conservative 11; Mismatches 9; Indels 4; Gaps 3;

QY 1 MNFGSLIFLVLVKGVQCEVKVVGSGGGLVKPGASIKLSGCAASGFTFSNYGMSWVRQTS 60  
DB 1 MNFGSLIFLVLVKGVQCEVKVVGSGGGLVKPGASIKLSGCAASGFTFSNYGMSWVRQTS 60

QY 61 DKRLWVASISSGGDSTFYADVNGKRFITSRNNAKNTLYLQMSLSKSEDTALYYCAR--D 118  
DB 61 EKRLWVASISTGG-STYPPDSVGRFTISRDNARILYLQMSLSRSEDTAMYYCARHYD 119

QY 119 DLFN-WGQGTTLTVSS 133  
DB 120 GYFDYWGQGTTLTVSS 135

## RESULT 2

US-08-379-057-14-  
Sequence 14, Application US/08379057  
Patent No. 5876950

GENERAL INFORMATION:

APPLICANT: Siadak, Anthony W.

APPLICANT: Hollenbaugh, Diane L.

APPLICANT: Gilliland, Lisa K.

APPLICANT: Gordon, Marcia L.

APPLICANT: Bajorath, Jürgen

APPLICANT: Aruffo, Alejandro A.

TITLE OF INVENTION: Monoclonal Antibodies Specific For

TITLE OF INVENTION: Different Epitopes of Human gp39 and Methods For Their Use

NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bristol-Myers Squibb Company

STREET: 3005 First Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 26-JAN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Poor, Brian W.

REGISTRATION NUMBER: 32,928

REFERENCE/DOCKET NUMBER: ON0133-

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 727-3670

TELEFAX: (206) 727-3601

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 138 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: N-terminal

US-08-379-057-14

Query Match 79.8%; Score 545.5; DB 2; Length 138;  
Best Local Similarity 77.0%; Pred. No. 1,4e-51;  
Matches 107; Conservative 14; Mismatches 11; Indels 7; Gaps 2;

QY 1 MNFGSLIFLVLVKGVQCEVKVVGSGGGLVKPGASIKLSGCAASGFTFSNYGMSWVRQTS 60  
DB 1 MNFGSLIFLVLVKGVQCEVKVVGSGGGLVKPGASIKLSGCAASGFTFSNYGMSWVRQTS 60

QY 61 DKRLWVASISSGGDSTFYADVNGKRFITSRNNAKNTLYLQMSLSKSEDTALYYCARDDL 120  
DB 61 EKRLWVASISS-GDSTYPPDSVGRFTISRDNARILYLQMSLSRSEDTAMYYCARHYD 119

QY 121 FN-----WGQGTTLTVSS 133  
DB 120 YDSYAMDYWGQGTSTVTVSS 138

## RESULT 3

US-08-976-183A-33  
Sequence 33, Application US/08976183A  
Patent No. 6307026

GENERAL INFORMATION:

APPLICANT: King, David J.

APPLICANT: Adair, John R.

APPLICANT: Owens, Raymond J.

TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33

TITLE OF INVENTION: ANTIGEN

NUMBER OF SEQUENCES: 55

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY &amp; LARDNER

STREET: 3000 K. Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,183A

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/595,848

FILING DATE: 02-FEB-1996

APPLICATION NUMBER: PCT/GB93/02529

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9225853.2

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9315249.4

FILING DATE: 22-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Bernhard D. Saxe

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 40283/151/CABA

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 136 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-976-183A-33

Query Match 79.6%; Score 544.5; DB 3; Length 136;  
Best Local Similarity 77.9%; Pred. No. 1,8e-51;  
Matches 106; Conservative 13; Mismatches 14; Indels 3; Gaps 1;

QY 1 MNFGSLIFLVLVKGVQCEVKVVGSGGGLVKPGASIKLSGCAASGFTFSNYGMSWVRQTS 60  
DB 1 MNFGSLIFLVLVKGVQCEVKVVGSGGGLVKPGASIKLSGCAASGFTFSNYGMSWVRQTS 60

QY 61 DKRLWVASISSGGDSTFYADVNGKRFITSRNNAKNTLYLQMSLSKSEDTALYYCARDDL 120  
DB 61 EKRLWVASISSGGDSTFYADVNGKRFITSRNNAKNTLYLQMSLSKSEDTALYYCARDDL 120



Db 61 EXRLEWVATISSGGSTYTYLDSVKGRFTISRDSARNTLYLQWSSLKSEDTALYYCAPTTV 120  
QY 121 F---NWGGTTLTVSS 133  
Db 121 VPFAYWGQTLVTVSA 136

RESULT 4  
US-08-976-183A-31  
Sequence 31, Application US/08976183A  
Patent No. 6307026  
GENERAL INFORMATION:  
APPLICANT: King, David J.  
APPLICANT: Adair, John R.  
APPLICANT: Owens, Raymond J.  
TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K. Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/976,183A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/595,848  
FILING DATE: 02-FEB-1996  
APPLICATION NUMBER: PCT/GB93/02529  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9225853.2  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9315249.4  
FILING DATE: 22-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bernhard D. Saxe  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 40283/151/CARA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-976-183A-31

Query Match 79.5%; Score 543.5; DB 3; Length 136;  
Best Local Similarity 77.2%; Pred. No. 2.3e-51;  
Matches 105; Conservative 14; Mismatches 14; Indels 3; Gaps 1;  
QY 1 MNFGSLIFLVILKGVQCEVAVESGGGLVYKPGASIKLSKSCAASGFTSNYGMWVRQTS 60  
Db 1 MNFGSLIFLVILKGVQCEVAVESGGGLVYKPGASIKLSKSCAASGFTSNYGMWVRQTS 60  
QY 61 DKRLWVASISSGGSTFYADNVKGRFTISRDNKNTLYLQWSSLKSEDTALYYCARDL 120  
Db 61 EXRLEWVATISSGGSTYTYLDSVKGRFTISRDSARNTLYLQWSSLKSEDTALYYCAPTTV 120  
QY 121 F---NWGGTTLTVSS 133

Db 121 VPFAYWGQTLVTVSA 136

RESULT 5  
US-08-976-183A-32  
Sequence 32, Application US/08976183A  
Patent No. 6307026  
GENERAL INFORMATION:  
APPLICANT: King, David J.  
APPLICANT: Adair, John R.  
APPLICANT: Owens, Raymond J.  
TITLE OF INVENTION: HUMANISED ANTIBODIES DIRECTED AGAINST A33  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 55  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY & LARDNER  
STREET: 3000 K. Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/976,183A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/595,848  
FILING DATE: 02-FEB-1996  
APPLICATION NUMBER: PCT/GB93/02529  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GB 9225853.2  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9315249.4  
FILING DATE: 22-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bernhard D. Saxe  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 40283/151/CARA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-976-183A-32

Query Match 79.0%; Score 540.5; DB 3; Length 136;  
Best Local Similarity 77.2%; Pred. No. 4.9e-51;  
Matches 105; Conservative 13; Mismatches 15; Indels 3; Gaps 1;  
QY 1 MNFGSLIFLVILKGVQCEVAVESGGGLVYKPGASIKLSKSCAASGFTSNYGMWVRQTS 60  
Db 1 MNFGSLIFLVILKGVQCEVAVESGGGLVYKPGASIKLSKSCAASGFTSNYGMWVRQTS 60  
QY 61 DKRLWVASISSGGSTFYADNVKGRFTISRDNKNTLYLQWSSLKSEDTALYYCARDL 120  
Db 61 EXRLEWVATISSGGSTYTYLDSVKGRFTISRDSARNTLYLQWSSLKSEDTALYYCAPTTV 120  
QY 121 F---NWGGTTLTVSS 133  
Db 121 VPFAYWGQTLVTVSA 136



TITLE OF INVENTION: Conjugates of Methylcrithio Antitumor  
TITLE OF INVENTION: Agents and Intermediates for Their Synthesis  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: American Home Products Corporation  
STREET: One Campus Drive  
CITY: Parsippany  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07054  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,164A  
FILING DATE: 26-MAY-1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhard, Elizabeth M.  
REGISTRATION NUMBER: 31,088  
REFERENCE/DOCKET NUMBER: 32,368-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-683-2158  
TELEFAX: 201-683-4117  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-452-164A-57

Query Match 78.7%; Score 538.5; DB 2; Length 136;  
Best Local Similarity 76.5%; Pred. No. 8.1e-51;  
Matches 104; Conservative 14; Mismatches 15; Indels 3; Gaps 1;

QY 1 MNFGSLFLVLVLTGKGVCEYKVVESGGGLVKGASLKLSCAASGFTSNYGMVNRQTS 60  
DB 1 MNFGSLFLVLVLTGKGVCEYKVVESGGGLVKGASLKLSCAASGFTSNYGMVNRQTS 60  
QY 61 DKRLWVASISSGGDSTFYADNVKGRFTISRBNKNTLYLQMSLSKSDTLALYYCARDL 120  
DB 61 EKRLWVAIVISSGGSYTYLLDSVKGRFTISRDPNTLYLQMSLSKSDTLALYYCAPTV 120  
QY 121 F---NMGGGTLTVVSS 133  
DB 121 VPPAVWGQGLTVTVSA 136

RESULT 9  
PCT-US94-07659-2  
Sequence 2, Application PC/TUS9407659  
GENERAL INFORMATION:  
APPLICANT: Young, Peter  
APPLICANT: Gross, Mitchell  
APPLICANT: Jonak, Zdenka L.  
APPLICANT: Thelsen, Timothy  
APPLICANT: Hurle, Mark  
APPLICANT: Jackson, Jeffrey R.  
TITLE OF INVENTION: Recombinant and Humanized IL-1 beta  
TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SmithKline Beecham Corporation - Corp.  
ADDRESSEE: Intellectual Property  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-2799

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/07659  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/090,534  
FILING DATE: 09-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Suton, Jeffrey A.  
REGISTRATION NUMBER: 34,028  
REFERENCE/DOCKET NUMBER: P50171-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 270-5024  
TELEFAX: (610) 270-5090  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 247 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US94-07659-2

Query Match 78.1%; Score 534.5; DB 5; Length 247;  
Best Local Similarity 76.8%; Pred. No. 4.7e-50;  
Matches 106; Conservative 12; Mismatches 15; Indels 5; Gaps 2;

QY 1 MNFGSLFLVLVLTGKGVCEYKVVESGGGLVKGASLKLSCAASGFTSNYGMVNRQTS 60  
DB 1 MNFGSLFLVLVLTGKGVCEYKVVESGGGLVKGASLKLSCAASGFTSNYGMVNRQTS 60  
QY 61 DKRLWVASISSGGDSTFYADNVKGRFTISRBNKNTLYLQMSLSKSDTLALYYCARDL 120  
DB 61 EKRLWVAIVISSGGGTYPTVVKGRFTISRDNKNTLYLQMSLSKSDTLALYYHCRAGV 120  
QY 121 ---FN-WGGGTLTVVSS 133  
DB 121 RRGYFDVWGAGTVTVSS 138

RESULT 10  
US-08-836-561-23  
Sequence 23, Application US/08836561  
Patent No. 6018032  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Masamichi  
APPLICANT: FURUYA, Akiko  
APPLICANT: NAKAMURA, Kazuyasu  
APPLICANT: IIDA, Akihito  
APPLICANT: ANAZAWA, Hideharu  
APPLICANT: HANAI, No. 6018032uo  
TITLE OF INVENTION: Kiyoshi  
TITLE OF INVENTION: Antibody Against Human Interleukin-5  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/836,561

FILING DATE: 09-MAY-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 232384/95  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, IIT, Stanton T  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-115-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-836-561-23

Query Match 77.9%; Score 532.5; DB 3; Length 140;  
Best Local Similarity 72.1%; Pred. No. 3.8e-50;  
Matches 101; Conservative 17; Mismatches 15; Indels 7; Gaps 1;  
QY 1 MNFGSLIFLVLYLKGQCEVKVSGGLVPRGASLKISCAAGFTFSNYGMSVVRQTS 60  
1 MNFGSLIFLVLYLKGQCEVKVSGGLVPRGASLKISCAAGFTFSNYGMSVVRQTS 60  
DB 1 MNFGSLIFLVLYLKGQCEVKVSGGLVPRGASLKISCAAGFTFSNYGMSVVRQTS 60  
QY 61 DKLEWVASISSGGDSFTYADVNGKRFITSRNARKTLYLQMSLKSEPTALYYCARDDL 120  
61 DKLEWVASISSGGDSFTYADVNGKRFITSRNARKTLYLQMSLKSEPTALYYCARDDL 120  
DB 61 DKLEWVASISSGGDSFTYADVNGKRFITSRNARKTLYLQMSLKSEPTALYYCARDDL 120  
QY 121 FN-----WGQTTLVSS 133  
121 FN-----WGQTTLVSS 133  
DB 121 YGNRYAMDYWGQTSVTVSS 140

RESULT 11  
US-09-434-122-23  
Sequence 23, Application US/09434122  
Patent No. 6538111  
GENERAL INFORMATION:  
APPLICANT: KOIKE, Masamichi  
FURUYA, Akiko  
NAKAMURA, Kazuyasu  
IIDA, Akihito  
ANAZAWA, Hideharu  
HANAI, No. 6538111  
TAKATSU, Kiyoshi  
TITLE OF INVENTION: Antibody Against Human Interleukin-5  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/434,122  
FILING DATE: 05-NO. 6538111-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/836,561  
FILING DATE: 09-MAY-1997

APPLICATION NUMBER: JP 232384/95  
FILING DATE: 11-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lawrence, IIT, Stanton T  
REGISTRATION NUMBER: 25,736  
REFERENCE/DOCKET NUMBER: 7005-115-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 140 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-434-122-23

Query Match 77.9%; Score 532.5; DB 4; Length 140;  
Best Local Similarity 72.1%; Pred. No. 3.8e-50;  
Matches 101; Conservative 17; Mismatches 15; Indels 7; Gaps 1;  
QY 1 MNFGSLIFLVLYLKGQCEVKVSGGLVPRGASLKISCAAGFTFSNYGMSVVRQTS 60  
1 MNFGSLIFLVLYLKGQCEVKVSGGLVPRGASLKISCAAGFTFSNYGMSVVRQTS 60  
DB 1 MNFGSLIFLVLYLKGQCEVKVSGGLVPRGASLKISCAAGFTFSNYGMSVVRQTS 60  
QY 61 DKLEWVASISSGGDSFTYADVNGKRFITSRNARKTLYLQMSLKSEPTALYYCARDDL 120  
61 DKLEWVASISSGGDSFTYADVNGKRFITSRNARKTLYLQMSLKSEPTALYYCARDDL 120  
DB 61 DKLEWVASISSGGDSFTYADVNGKRFITSRNARKTLYLQMSLKSEPTALYYCARDDL 120  
QY 121 FN-----WGQTTLVSS 133  
121 FN-----WGQTTLVSS 133  
DB 121 YGNRYAMDYWGQTSVTVSS 140

RESULT 12  
US-08-579-378A-20  
Sequence 20, Application US/08579378A  
Patent No. 6210671  
GENERAL INFORMATION:  
APPLICANT: Co, Man Sung  
TITLE OF INVENTION: Humanized Antibodies Reactive with  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew  
STREET: One Market Plaza, Stewart Tower, Suite 2000  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/579,378A  
FILING DATE: 27-DEC-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/160,074  
FILING DATE: 30-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/983,946  
FILING DATE: 01-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95112895.8  
FILING DATE: 17-AUG-1995  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95114696.8  
FILING DATE: 19-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebescheut, Joe O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 11823-002220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 135 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-579-378A-20

Query Match 77.3%; Score 529; DB 3; Length 135;  
Best Local Similarity 77.9%; Pred. No. 8.7e-50;  
Matches 106; Conservative 14; Mismatches 12; Indels 4; Gaps 3;

QY 1 MNFGSLIFLVYLVKGVQCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSVWROT 60  
DB 1 MNFGSLIFLVYLVKGVQCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSVWROT 60  
QY 61 DKRLFWASISGGSDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR--D 118  
DB 61 GKGLEWVASISITGG-STYIPDSVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR--D 119  
QY 119 DLFW-NWGGQFTLVVSS 133  
DB 120 GYFDYWGQGLTVVSS 135

RESULT 13  
US-08-653-402B-6  
Sequence 6, Application US/08653402B  
Patent No. 5969107  
GENERAL INFORMATION:  
APPLICANT: CARCELLER, Ana  
APPLICANT: ROSELL, Elisabet  
APPLICANT: GOMEZ, Alicia  
APPLICANT: ADEN, Jaume  
APPLICANT: PUJOLAS, Jaume  
TITLE OF INVENTION: Anti-idiotypic antibodies which induce an  
TITLE OF INVENTION: Immune response against epidermal growth factor receptor.  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Millen, White, Zelano & Branigan, P.C.  
STREET: 2200 Clarendon Boulevard, Suite 1400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/653,402B  
FILING DATE: 24-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95107967.2  
FILING DATE: 26-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Lebovitz, Richard M.  
REGISTRATION NUMBER: 37,067  
REFERENCE/DOCKET NUMBER: MERCK 1781  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 158 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-653-402B-6

Query Match 77.1%; Score 527.5; DB 2; Length 158;  
Best Local Similarity 74.3%; Pred. No. 1.5e-49;  
Matches 107; Conservative 12; Mismatches 14; Indels 11; Gaps 1;

QY 1 MNFGSLIFLVYLVKGVQCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSVWROT 60  
DB 1 MDGFLIFLVYLVKGVQCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSVWROT 60  
QY 61 DKRLFWASISGGSDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR--D 118  
DB 61 EKRLFWASISGGSDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR--D 120  
QY 119 -----DLFW-NWGGQFTLVVSS 133  
DB 121 RDSSGYVGYAIDYWGQGLTVVSS 144

RESULT 14  
US-08-053-171-7  
Sequence 7, Application US/08053171  
Patent No. 5562903  
GENERAL INFORMATION:  
APPLICANT: Co, Loibner  
TITLE OF INVENTION: Antibody Derivatives  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend Hourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,171  
FILING DATE: 22-APR-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-54-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-053-171-7

Query Match 76.4%; Score 522.5; DB 1; Length 138;  
Best Local Similarity 74.6%; Pred. No. 4.5e-49;  
Matches 103; Conservative 14; Mismatches 16; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVYLVKGVQCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSVWROT 60  
DB 1 MNFGSLIFLVYLVKGVQCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSVWROT 60  
QY 61 DKRLFWASISGGSDSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR--D 120

Db 61 EKRLWVAIYISNGSGSHYDSYKGRFTISRDNKNTLYLQMSRLNSEDTAMTHCARAMD 120  
QY 121 FN-----WGQGTTLTVSS 133  
Db 121 YGAMFAFWGQGTTLTVTSA 138

RESULT 15  
US-08-053-171-11  
; Sequence 11, Application US/08053171  
; Patent No. 5562903  
; GENERAL INFORMATION:  
; APPLICANT: Co, Loibner  
; TITLE OF INVENTION: Antibody Derivatives  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,171  
; FILING DATE: 22-APR-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-54-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 138 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-053-171-11

Query Match 76.4%; Score 522.5; DB 1; Length 138;  
Best Local Similarity 74.6%; Pred. No. 4.5e-49;  
Matches 103; Conservative 14; Mismatches 16; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVLYLKGVQCEVKVVGSGGLVKPGLKLSGASGFTFSNRYGMSWVROT 60  
Db 1 MNGLSLIFLVLYLKGVQCEVKLVESGGGLVPGSLKLSGATSGFTFSNRYGMSWVROT 60

QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRDNKNTLYLQMSRLNSEDTALYYCARDL 120  
Db 61 EKRLWVAIYISNGSGSHYDSYKGRFTISRDNKNTLYLQMSRLNSEDTAMTHCARAMD 120

QY 121 FN-----WGQGTTLTVSS 133  
Db 121 YGAMFAFWGQGTTLTVTSA 138

Search completed: May 25, 2005, 15:58:23  
Job time : 16.5786 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: May 25, 2005, 15:37:58 ; Search time 61.3656 Seconds  
(without alignments)  
724.991 Million cell updates/sec

Title: US-10-006-773A-9

Perfect score: 684  
Sequence: 1 MNFGSLFLVLVLRGVQCE.....YCARDLFFMGQTTLVSS 133

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	100.0	133	13	US-10-006-773-9
2	609.5	89.1	138	14	US-10-010-942B-4
3	609.5	89.1	138	15	US-10-388-389-8
4	609.5	89.1	138	16	US-10-703-713-8
5	609.5	89.1	138	17	US-10-704-070-4
6	609.5	89.1	138	16	US-10-232-030-4
7	590	86.3	139	13	US-10-006-773-17
8	569.5	83.3	146	14	US-10-281-479A-23
9	569.5	83.3	462	14	US-10-286-132A-23
10	569.5	83.3	464	14	US-10-275-180A-23
11	559.5	81.8	144	9	US-09-881-823-12
12	559	81.7	137	9	US-09-423-800-76
13	559	81.7	137	14	US-10-337-981-76

14	550.5	80.5	138	14	US-10-010-942B-8	Sequence 8, Appli
15	550.5	80.5	138	15	US-10-388-389-8	Sequence 8, Appli
16	550.5	80.5	138	16	US-10-703-713-8	Sequence 8, Appli
17	550.5	80.5	138	16	US-10-704-070-8	Sequence 8, Appli
18	550.5	80.5	138	17	US-10-232-030-8	Sequence 8, Appli
19	550.5	80.5	140	13	US-10-006-773-4	Sequence 4, Appli
20	549.5	80.3	468	17	US-10-476-265-20	Sequence 20, Appli
21	548.5	80.2	138	14	US-10-010-942B-12	Sequence 12, Appli
22	548.5	80.2	138	15	US-10-388-389-12	Sequence 12, Appli
23	548.5	80.2	138	16	US-10-703-713-12	Sequence 12, Appli
24	548.5	80.2	138	16	US-10-704-070-12	Sequence 12, Appli
25	548.5	80.2	138	17	US-10-232-030-12	Sequence 12, Appli
26	536.5	78.4	140	9	US-09-286-240-4	Sequence 4, Appli
27	532.5	77.9	140	14	US-10-283-349-23	Sequence 23, Appli
28	526.5	77.0	158	15	US-10-226-795-32	Sequence 32, Appli
29	516.5	75.5	143	15	US-10-469-104-17	Sequence 17, Appli
30	515	75.3	139	10	US-09-947-839-96	Sequence 96, Appli
31	510.5	74.6	140	15	US-10-365-123-51	Sequence 51, Appli
32	509	74.4	137	9	US-09-423-800-77	Sequence 77, Appli
33	509	74.4	137	14	US-10-337-981-77	Sequence 77, Appli
34	507.5	74.2	465	14	US-10-401-344-2	Sequence 2, Appli
35	506	74.0	143	10	US-09-791-551-117	Sequence 117, App
36	506	74.0	177	16	US-10-633-629-64	Sequence 64, Appli
37	504.5	73.8	159	9	US-10-291-265-333	Sequence 333, App
38	503.5	73.6	470	15	US-10-038-591-46	Sequence 46, Appli
39	502.5	73.5	138	9	US-09-796-744-15	Sequence 15, Appli
40	502.5	73.5	138	14	US-10-231-452-62	Sequence 62, Appli
41	502.5	73.5	461	17	US-10-938-353-70	Sequence 70, Appli
42	502.5	73.5	474	10	US-09-848-832-3	Sequence 3, Appli
43	502.5	73.5	474	14	US-10-225-108A-3	Sequence 3, Appli
44	502.5	73.5	474	15	US-10-461-148-1	Sequence 1, Appli
45	502	73.4	461	17	US-10-938-353-34	Sequence 34, Appli

#### ALIGNMENTS

RESULT 1  
US-10-006-773-9  
; Sequence 9, Application US/10006773  
; Publication No. US20020132983A1  
; GENERAL INFORMATION:  
; APPLICANT: Junghans, Richard P.  
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti.  
; FILE REFERENCE: 003  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: 60/250,089  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-10-006-773-9

Query Match 100.0%; Score 684; DB 13; Length 133;  
Best Local Similarity 100.0%; Pred. No. 7.6e-57;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNFGSLFLVLVLRGVQCEVKVVGGLTKPKASLTKSCAASGFTFSNYGMVNRQTS	60
DB	1	MNFGSLFLVLVLRGVQCEVKVVGGLTKPKASLTKSCAASGFTFSNYGMVNRQTS	60
QY	61	DKRLWVASISSGGSTFYADNVKGRFTISRENAKNTLYLQMSLSKSDTALYYCARDL	120
DB	61	DKRLWVASISSGGSTFYADNVKGRFTISRENAKNTLYLQMSLSKSDTALYYCARDL	120
QY	121	FNMGQTTLVSS 133	
DB	121	FNMGQTTLVSS 133	

RESULT 2  
 US-10-010-942B-4  
 ; Sequence 4, Application US/10010942B  
 ; Publication No. US20030165496A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Basi, Gurig  
 ; APPLICANT: Saldanha, Jose  
 ; APPLICANT: Yednock, Ted  
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
 ; TITLE OF INVENTION: BETA AMYLOID PEPTIDE  
 ; FILE REFERENCE: ELN-002  
 ; CURRENT APPLICATION NUMBER: US/10/010,942B  
 ; CURRENT FILING DATE: 2002-12-06  
 ; PRIOR APPLICATION NUMBER: US 60/251,892  
 ; PRIOR FILING DATE: 2000-12-06  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 138  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: SIGNAL  
 ; LOCATION: (1)...(19)  
 US-10-010-942B-4

Query Match 89.1%; Score 609.5; DB 14; Length 138;  
 Best Local Similarity 87.0%; Pred. No. 8.5e-50;  
 Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVKEGASLKLSCAAGFTFSNYGMSWVRQTS 60  
 DB 1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVKEGASLKLSCAAGFTFSNYGMSWVRQTS 60  
 QY 61 DKRLWVASISGGGSTFYADVVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCVRYDH 120  
 DB 61 DKRLWVASIRSGGGRFTYSDNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCVRYDH 120  
 QY 121 FN-----WGQGTTLTVSS 133  
 DB 121 YGSSSDYWGQGTTLTVSS 138

RESULT 3  
 US-10-388-389-4  
 ; Sequence 4, Application US/10388389  
 ; Publication No. US2004008777A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Basi, Gurig  
 ; APPLICANT: Saldanha, Jose  
 ; APPLICANT: Yednock, Ted  
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
 ; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
 ; FILE REFERENCE: ELN-002CP  
 ; CURRENT APPLICATION NUMBER: US/10/388,389  
 ; CURRENT FILING DATE: 2003-03-12  
 ; PRIOR APPLICATION NUMBER: US 10/010,942  
 ; PRIOR FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: US 60/251,892  
 ; PRIOR FILING DATE: 2000-12-06  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 138  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: SIGNAL  
 ; LOCATION: (1)...(19)  
 US-10-388-389-4

Query Match 89.1%; Score 609.5; DB 15; Length 138;

Best Local Similarity 87.0%; Pred. No. 8.5e-50;  
 Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;  
 QY 1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVKEGASLKLSCAAGFTFSNYGMSWVRQTS 60  
 DB 1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVKEGASLKLSCAAGFTFSNYGMSWVRQTS 60  
 QY 61 DKRLWVASISGGGSTFYADVVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCVRYDH 120  
 DB 61 DKRLWVASIRSGGGRFTYSDNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCVRYDH 120  
 QY 121 FN-----WGQGTTLTVSS 133  
 DB 121 YGSSSDYWGQGTTLTVSS 138

RESULT 4  
 US-10-703-713-4  
 ; Sequence 4, Application US/10703713  
 ; Publication No. US20040171815A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Basi, Gurig  
 ; APPLICANT: Saldanha, Jose  
 ; APPLICANT: Yednock, Ted  
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
 ; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
 ; FILE REFERENCE: ELN-002CP  
 ; CURRENT APPLICATION NUMBER: US/10/703,713  
 ; CURRENT FILING DATE: 2003-11-07  
 ; PRIOR APPLICATION NUMBER: US/10/388,389  
 ; PRIOR FILING DATE: 2003-03-12  
 ; PRIOR APPLICATION NUMBER: US 10/010,942  
 ; PRIOR FILING DATE: 2001-12-06  
 ; PRIOR APPLICATION NUMBER: US 60/251,892  
 ; PRIOR FILING DATE: 2000-12-06  
 ; NUMBER OF SEQ ID NOS: 63  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 4  
 ; LENGTH: 138  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; FEATURE:  
 ; NAME/KEY: SIGNAL  
 ; LOCATION: (1)...(19)  
 US-10-703-713-4

Query Match 89.1%; Score 609.5; DB 16; Length 138;  
 Best Local Similarity 87.0%; Pred. No. 8.5e-50;  
 Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVKEGASLKLSCAAGFTFSNYGMSWVRQTS 60  
 DB 1 MNFGSLIFLVYLVKGVCEVKEVSGGGLVKEGASLKLSCAAGFTFSNYGMSWVRQTS 60  
 QY 61 DKRLWVASISGGGSTFYADVVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCVRYDH 120  
 DB 61 DKRLWVASIRSGGGRFTYSDNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCVRYDH 120  
 QY 121 FN-----WGQGTTLTVSS 133  
 DB 121 YGSSSDYWGQGTTLTVSS 138

RESULT 5  
 US-10-704-070-4  
 ; Sequence 4, Application US/10704070  
 ; Publication No. US20040171816A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Basi, Gurig  
 ; APPLICANT: Saldanha, Jose  
 ; APPLICANT: Yednock, Ted  
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
 ; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
 US-10-704-070-4



FILE REFERENCE: ELN-002CP  
CURRENT APPLICATION NUMBER: US/10/704,070  
CURRENT FILING DATE: 2003-11-07  
PRIOR APPLICATION NUMBER: 10/388,389  
PRIOR FILING DATE: 2003-03-12  
PRIOR APPLICATION NUMBER: US 10/010,942  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US 60/251,892  
PRIOR FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 138  
TYPE: PRT  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)...(19)  
US-10-704-070-4

Query Match 89.1%; Score 609.5; DB 16; Length 138;  
Best Local Similarity 87.0%; Pred. No. 8,5e-50;  
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MNFGSLFLVLYLKGVCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSWVRQTS 60  
DB 1 MNFGSLFLVLYLKGVCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRBNANTLYLQMSLKSSEDTALYYCARDL 120  
DB 61 DKRLWVASISGGRTYSDNVKGRFTISRBNANTLYLQMSLKSSEDTALYYCVRD 120  
QY 121 FN-----WGCGTTLTVSS 133  
DB 121 YGSSDYWGCGTTLTVSS 138

RESULT 6  
US-10-232-030-4  
Sequence 4, Application US/10232030  
Publication No. US20050009150A1  
GENERAL INFORMATION:  
APPLICANT: Dale Schenk  
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE  
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE  
FILE REFERENCE: ELN-002CN  
CURRENT APPLICATION NUMBER: US/10/232,030  
CURRENT FILING DATE: 2002-08-30  
PRIOR APPLICATION NUMBER: US 09/201,430  
PRIOR FILING DATE: 1998-11-30  
PRIOR APPLICATION NUMBER: US 09/723,713  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: US 09/322,289  
PRIOR FILING DATE: 1999-05-28  
PRIOR APPLICATION NUMBER: US 10/010,942  
PRIOR FILING DATE: 2001-12-06  
PRIOR APPLICATION NUMBER: US 60/251,892  
PRIOR FILING DATE: 2000-12-06  
NUMBER OF SEQ ID NOS: 63  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 138  
TYPE: PRT  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)...(19)  
US-10-232-030-4

Query Match 89.1%; Score 609.5; DB 17; Length 138;  
Best Local Similarity 87.0%; Pred. No. 8,5e-50;  
Matches 120; Conservative 6; Mismatches 7; Indels 5; Gaps 1;

QY 1 MNFGSLFLVLYLKGVCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSWVRQTS 60  
DB 1 MNFGSLFLVLYLKGVCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSWVRQNS 60  
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRBNANTLYLQMSLKSSEDTALYYCARDL 120  
DB 61 DKRLWVASISGGRTYSDNVKGRFTISRBNANTLYLQMSLKSSEDTALYYCVRD 120  
QY 121 FN-----WGCGTTLTVSS 133  
DB 121 YGSSDYWGCGTTLTVSS 138

RESULT 7  
US-10-006-773-17  
Sequence 17, Application US/10006773  
Publication No. US20020132983A1  
GENERAL INFORMATION:  
APPLICANT: Junghans, Richard P.  
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti  
FILE REFERENCE: 003  
CURRENT FILING DATE: 2001-12-10  
PRIOR APPLICATION NUMBER: 60/250,089  
PRIOR FILING DATE: 2000-11-30  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 17  
LENGTH: 139  
TYPE: PRT  
ORGANISM: Mus sp.  
US-10-006-773-17

Query Match 86.3%; Score 590; DB 13; Length 139;  
Best Local Similarity 83.5%; Pred. No. 6e-48;  
Matches 116; Conservative 8; Mismatches 9; Indels 6; Gaps 1;

QY 1 MNFGSLFLVLYLKGVCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSWVRQTS 60  
DB 1 MNFGSLFLVLYLKGVCEVYVSGGGLVYKPGASLKLSCAASGFTFSNYGMSWVRQTS 60  
QY 61 DKRLWVASISGGDSTFYADNVKGRFTISRBNANTLYLQMSLKSSEDTALYYCARDL 119  
DB 61 DKRLWVASISGGRTYSDNVKGRFTISRBNANTLYLQMSLKSSEDTALYYCARD 120  
QY 120 -----LFNWGGTTLTVSS 133  
DB 121 SVGCWPAFWGCGTTLTVSSA 139

RESULT 8  
US-10-281-479A-23  
Sequence 23, Application US/10281479A  
Publication No. US20030133932A1  
GENERAL INFORMATION:  
APPLICANT: The UAB Research Foundation  
APPLICANT: Zhou, Tong  
APPLICANT: Ichikawa, Kimihisa  
APPLICANT: Kimberly, Robert P.  
APPLICANT: Koopman, William J.  
APPLICANT: Oshumi, Jun  
APPLICANT: Lobuglio, Albert S.  
APPLICANT: Buchsbaum, Donald J.  
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS  
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER  
FILE REFERENCE: 21085,0029U6  
CURRENT APPLICATION NUMBER: US/10/281,479A  
CURRENT FILING DATE: 2003-01-28  
PRIOR APPLICATION NUMBER: 60/391,478  
PRIOR FILING DATE: 2002-06-24  
PRIOR APPLICATION NUMBER: 60/346,402  
PRIOR FILING DATE: 2001-11-01

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; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 462
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US2003013932A1e = Synthe
US-10-281-479a-23
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Query Match      83.3%; Score 569.5; DB 14; Length 462;
Best Local Similarity 81.9%; Pred. No. 1,9e-45;
Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;

QY      1 MNFGSLIFLVYLKGVQCEVKVSGGGLVKPGASLKSCAASGFTFSNYGMSWVRQTS 60
      1 MNFGSLIFLVYLKGVQCEVMVLVESGGGLVKPGGSLKLSCAASGFTFSYVMSWVRQTP 60
DB      61 DKLEWVASISSGGSDSTFFADVNVKGRFTISRBNKNTLYLQMSLSKSEPTALYYCAR--D 118
      61 EKRLWVATISSGGSYTYPPDSYKGRFTISRDNKNTLYLQMSLSLSEDTAMYYCARRGD 120
QY      119 DLFN---WGCGTTLTYVSS 133
      121 SMITTDYWGCGTTLTYVSS 138
DB
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RESULT 9
US-10-286-132a-23
; Sequence 23, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Lohbuglio, Albert S.
; APPLICANT: Buchbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002917
; CURRENT APPLICATION NUMBER: US/10/286,132A
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 462
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132a-23
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Query Match      83.3%; Score 569.5; DB 14; Length 462;
Best Local Similarity 81.9%; Pred. No. 1,9e-45;
Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;

QY      1 MNFGSLIFLVYLKGVQCEVKVSGGGLVKPGASLKSCAASGFTFSNYGMSWVRQTS 60
      1 MNFGSLIFLVYLKGVQCEVMVLVESGGGLVKPGGSLKLSCAASGFTFSYVMSWVRQTP 60
DB      61 DKLEWVASISSGGSDSTFFADVNVKGRFTISRBNKNTLYLQMSLSKSEPTALYYCAR--D 118
      61 EKRLWVATISSGGSYTYPPDSYKGRFTISRDNKNTLYLQMSLSLSEDTAMYYCARRGD 120
DB
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QY      119 DLFN---WGCGTTLTYVSS 133
      121 SMITTDYWGCGTTLTYVSS 138
DB
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RESULT 10
US-10-275-180a-23
; Sequence 23, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTO-
; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.002905
; CURRENT APPLICATION NUMBER: US/10/275,180A
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
US-10-275-180a-23
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Query Match      83.3%; Score 569.5; DB 14; Length 464;
Best Local Similarity 81.9%; Pred. No. 2e-45;
Matches 113; Conservative 10; Mismatches 10; Indels 5; Gaps 2;

QY      1 MNFGSLIFLVYLKGVQCEVKVSGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQTS 60
      1 MNFGSLIFLVYLKGVQCEVMVLVESGGGLVKPGGSLKLSCAASGFTFSYVMSWVRQTP 60
DB      61 DKLEWVASISSGGSDSTFFADVNVKGRFTISRBNKNTLYLQMSLSKSEPTALYYCAR--D 118
      61 EKRLWVATISSGGSYTYPPDSYKGRFTISRDNKNTLYLQMSLSLSEDTAMYYCARRGD 120
QY      119 DLFN---WGCGTTLTYVSS 133
      121 SMITTDYWGCGTTLTYVSS 138
DB
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RESULT 11
US-09-881-823-12
; Sequence 12, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-12
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Db 121 YSGSSDIYWGQGLTVVSS 138

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RESULT 15
US-10-388-389-8
; Sequence 8, Application US/10388389
; Publication No. US2004008777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurliq
; APPLICANT: Saldanha, Jose
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized 3d6 heavy chain variable region
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-10-388-389-8
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Query Match 80.5%; Score 550.5; DB 15; Length 138;
Best Local Similarity 76.8%; Pred. NO. 3.2e-44;
Matches 106; Conservative 15; Mismatches 12; Indels 5; Gaps 1;

QY 1 MNFGSLIFLVLVKGVQCEVKVVESSGGGLVKPGASIKLSCAASGFTFSNYGMSWVRQTS 60
Db 1 MNFGSLIFLVLVKGVQCEVGLFESSGGGLVQPGGSLRUSCAASGFTFSNYGMSWVRQAP 60

QY 61 DKRLVNAVASTSSGGDSTFTADNVKGRFTIRSNKAKNTLYIQMSLSKSEDTALYYCARDL 120
Db 61 GKGLVNAVASTSSGGGRTYSDNVKGRFTISRDNKNSLYIQMNSLRAPDTALYYCVRYDH 120

QY 121 FN----WGQGLTVVSS 133
Db 121 YSGSSDIYWGQGLTVVSS 138
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Search completed: May 25, 2005, 16:06:51  
Job time : 62.4906 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2005, 15:56:18 ; Search time 18.8056 Seconds  
(without alignments)  
680.480 Million cell updates/sec

Title: US-10-006-773a-9

Perfect score: 684

Sequence: 1 MNFGSLIFLVLVKGVQCE.....YCARDDLFNMGQTTLVSS 133

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	553.5	80.9	152	B26471	Ig heavy chain pre
2	552.5	80.8	138	S09258	Ig heavy chain V r
3	546	79.8	139	S38808	Ig heavy chain - m
4	517	75.6	117	HVMS84	Ig heavy chain pre
5	515.5	75.4	142	C34903	Ig heavy chain pre
6	515	75.3	117	HVMS34	Ig heavy chain pre
7	510	74.6	117	HVMS39	Ig heavy chain pre
8	503.5	73.6	134	S31699	Ig heavy chain V r
9	502.5	73.5	140	S31588	Ig heavy chain V r
10	501.5	73.3	160	S05271	Ig heavy chain pre
11	498.5	72.9	138	S31666	Ig heavy chain V r
12	498	72.8	140	S70442	Ig heavy chain pre
13	493	72.1	117	HVMSRF	Ig heavy chain pre
14	491	71.8	117	HVMS57	Ig heavy chain pre
15	490.5	71.7	140	S22657	Ig heavy chain pre
16	489	71.5	139	S31674	Ig heavy chain V r
17	488.5	71.4	140	S31686	Ig heavy chain V r
18	485.5	71.0	134	S31679	Ig heavy chain V r
19	483.5	70.7	139	I37781	Ig heavy chain V r
20	482	70.5	136	G1MS21	Ig heavy chain pre
21	481	70.3	140	S31587	Ig heavy chain V r
22	479.5	70.1	136	A30532	Ig heavy chain pre
23	476.5	69.7	136	S31615	hypothetical prote
24	476	69.6	141	S31669	Ig heavy chain V r
25	475	69.4	137	S31701	Ig heavy chain V r
26	474	69.3	151	A60943	Ig heavy chain pre
27	472	69.0	147	I37780	Ig variable region
28	471.5	68.9	132	S31603	Ig heavy chain V r
29	470	68.7	117	A34964	Ig heavy chain pre

30	469	68.6	117	2	A45953	Ig heavy chain pre
31	469	68.6	119	2	P27888	Ig heavy chain V r
32	469	68.6	137	2	S78054	Ig heavy chain pre
33	468.5	68.5	130	2	P10098	Ig heavy chain pre
34	468.5	68.5	138	2	A30561	Ig heavy chain pre
35	466.5	68.2	122	2	E27888	Ig heavy chain V r
36	466.5	68.2	135	2	S31598	Ig heavy chain V r
37	466	68.1	254	2	B31790	Ig heavy chain V r
38	465	68.0	117	1	H3H26	Ig heavy chain pre
39	465	68.0	117	2	B34964	Ig heavy chain pre
40	465	68.0	118	2	PH0097	Ig heavy chain V r
41	464	67.8	135	2	I37778	Ig variable region
42	461	67.4	118	2	PH0096	Ig heavy chain V r
43	459.5	67.2	120	2	S5536	Ig heavy chain V r
44	459	67.1	121	2	I27887	Ig heavy chain V r
45	459	67.1	548	2	S38864	Ig epsilon chain C

## ALIGNMENTS

RESULT 1  
B26471  
Ig heavy chain precursor V region (MAX33) - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 23-Jul-1999  
C:Accession: B26471; S70410  
R:Buckel, P.; Hubner-Parafisz, C.; Mates, R.; Lenz, H.; Haug, H.; Beaucamp, K.  
Gene 51, 13-19, 1987  
A>Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine  
A:Reference number: A91572; MUID:87248058; PMID:3110009  
A:Accession: B26471  
A:Molecule type: mRNA  
A:Residues: 1-152 <BUC>  
A:Cross-references: GB:M6163; NID:9195405; PIDN:AAA38292.1; PID:9195406  
R:Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 172, 1717-1727, 1990  
A>Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5' boundary  
A:Reference number: S70410; MUID:91079775; PMID:2258702  
A:Accession: S70410  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-19 <LEB>  
A:Cross-references: EMBL:X53776; NID:952475; PIDN:CAA37792.1; PID:952476  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-152/Product: Ig heavy chain V region MAX33 #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match  
Best Local Similarity 80.9%; Score 553.5; DB 2; Length 152;  
Matches 109; Conservative 11; Mismatches 13; Indels 9; Gaps 1;

QY 1 MNFGSLIFLVLVKGVQCEVYVSGGGLVYPPGASLKLSCAASGFTSNTGMSVRCRS 60  
|||||  
DB 1 MNFGSLIFLVLVKGVQCEVGVSGGLVYPPGSLKLSCAASGFTSDYMYWRQTP 60  
|||||

QY 61 DRLRPMVASISGGSTFYADNVKGRFTISRNAKNTLYLQWSLKSEDTALYCARDDL 120  
:|||||  
DB 61 EKRLEKVAATISDGGSYTTPDSVKGRFTISRDNANLTLQWSLKSEDTATMYTCARDA 120  
:|||||

QY 121 F-----NWGGTTLVSS 133  
:|||||  
DB 121 YGNGVGDAMDYWGQGTSTVTS 142  
:|||||

RESULT 2  
S09258  
Ig heavy chain V region precursor - mouse (fragment)  
C:Species: Mus musculus (house mouse)



C>Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C/Accession: J0502  
Riley, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A>Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A/Reference number: J0501; MUID:89279149; PMID:2499654  
A/Accession: J0502  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-117 <LEV>  
A/Cross-references: UNIPROT:P18526  
A/Experimental source: strain BALB/cJ  
A/Note: this sequence belongs to the VH7183 subfamily  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:41-115/Diulfide bonds: #status predicted

Query Match 75.3%; Score 515; DB 1; Length 117;  
Best Local Similarity 84.6%; Pred. No. 1.6e-38;  
Matches 99; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MNFGSLIFLVVLKGVCEVAVESGGGLVPGASLKLSCAAGFTFSNTGMSVWVROT 60  
Db 1 MNFGSLIFLVVLKGVCEVAVESGGGLVPGASLKLSCAAGFTFSNTGMSVWVROT 60  
Qy 61 DKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 117  
Db 61 EKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 117

## RESULT 7

HVMS39  
Ig heavy chain precursor V region (7-39) - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004  
C/Accession: J0507  
Riley, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.  
J. Exp. Med. 169, 2007-2019, 1989  
A>Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary  
A/Reference number: J0501; MUID:89279149; PMID:2499654  
A/Accession: J0507  
A/Status: translation not shown  
A/Molecule type: mRNA  
A/Residues: 1-117 <LEV>  
A/Cross-references: UNIPROT:P18530  
A/Experimental source: strain BALB/cJ  
A/Note: this sequence belongs to the VH7183 subfamily  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-117/Product: Ig heavy chain V region (7-39) #status predicted <MAT>  
F:34-117/Domain: immunoglobulin homology <IMM>  
F:41-115/Diulfide bonds: #status predicted

Query Match 74.6%; Score 510; DB 1; Length 117;  
Best Local Similarity 84.6%; Pred. No. 4.4e-38;  
Matches 99; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MNFGSLIFLVVLKGVCEVAVESGGGLVPGASLKLSCAAGFTFSNTGMSVWVROT 60  
Db 1 MNFGSLIFLVVLKGVCEVAVESGGGLVPGASLKLSCAAGFTFSNTGMSVWVROT 60  
Qy 61 DKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 117  
Db 61 EKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR 117

RESULT 8  
S31699  
Ig heavy chain V region - human (fragment)

C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31699  
R. Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31699  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-134 <CU>  
A/Cross-references: EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.6%; Score 503.5; DB 2; Length 134;  
Best Local Similarity 71.6%; Pred. No. 1.9e-37;  
Matches 96; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

Qy 1 MNFGSLIFLVVLKGVCEVAVESGGGLVPGASLKLSCAAGFTFSNTGMSVWVROT 60  
Db 1 MNFGSLIFLVVLKGVCEVAVESGGGLVPGASLKLSCAAGFTFSNTGMSVWVROT 60  
Qy 61 DKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR-DD 119  
Db 61 GKLEWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR-DD 120  
Qy 120 LFNWGGFTLVVSS 133  
Db 121 LDYWGCGTLVTVSS 134

## RESULT 9

S31588  
Ig heavy chain V region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C/Accession: S31588  
R. Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.  
submitted to the EMBL Data Library, June 1992  
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A/Reference number: S31585  
A/Accession: S31588  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-140 <CU>  
A/Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958  
C/Superfamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 73.5%; Score 502.5; DB 2; Length 140;  
Best Local Similarity 68.6%; Pred. No. 2.4e-37;  
Matches 96; Conservative 22; Mismatches 15; Indels 7; Gaps 2;

Qy 1 MNFGSLIFLVVLKGVCEVAVESGGGLVPGASLKLSCAAGFTFSNTGMSVWVROT 60  
Db 1 MNFGSLIFLVVLKGVCEVAVESGGGLVPGASLKLSCAAGFTFSNTGMSVWVROT 60  
Qy 61 DKRLWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR-D 119  
Db 61 GKLEWVASISGGSTFYADNVKGRFTISRDNKNTLYLQMSLSKSDTALYYCAR-D 120  
Qy 120 LFNWGGFTLVVSS 133  
Db 121 YSNYTFDYWGCGTLVTVSS 140

RESULT 10  
S05271  
Ig heavy chain precursor - human (fragment)  
C/Species: Homo sapiens (man)





## RESULT 14

HVMSS7

Ig heavy chain precursor V region (5-76) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence\_revision 30-Jun-1990 #text\_change 09-Jul-2004

C:Accession: J05056

R:Levy, N.S.; Malpiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: J05051; MUID:89279149; PMID:249654

A:Accession: J05056

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 &lt;LEV&gt;

A:Cross-references: UNIPROT:P18529

A:Experimental source: strain BALB/cJ

A&gt;Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F:20-117/Product: Ig heavy chain V region (5-76) #status predicted &lt;MAT&gt;

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

F:41-115/Disulfide bonds: #status predicted

Query Match 71.8%; Score 491; DB 1; Length 117;

Best Local Similarity 80.3%; Pred. No. 2.1e-36;

Matches 94; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 MNFGSLIFLVVLKGVQCEVAVESGGGLVPGASLKLSKSCAAGFTFSNYGMSWVRQTS 60  
DB 1 MNFVSLIFLAILKGVQCEVAVESGGGLVPGASLKLSKSCVSGFTFNKAMSWVRQTP 60  
QY 61 DKRLWVASISSGGSTFPADNVKGRFTSRNNAKNTLYLQMSLKSEPTALYYCAR 117  
DB 61 EKRLWVATISSGGSTFYTPDSVKGRFTSRDNAGNTLYLQMSLSRSEPTALYYCAR 117

## RESULT 15

S22657

Ig heavy chain precursor V region (0-81VH) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 06-Feb-1998

C:Accession: S22657

R:Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A:Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-a

A:Reference number: S22657; MUID:92285150; PMID:1598223

A:Accession: S22657

A:Molecule type: mRNA

A:Residues: 1-140 &lt;HIR&gt;

A:Cross-references: EMBL:X59134

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F:20-140/Product: Ig heavy chain (fragment) #status predicted &lt;MAT&gt;

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

Query Match 71.7%; Score 490.5; DB 2; Length 140;

Best Local Similarity 67.9%; Pred. No. 2.8e-36;

Matches 91; Conservative 24; Mismatches 18; Indels 1; Gaps 1;

QY 1 MNFGSLIFLVVLKGVQCEVAVESGGGLVPGASLKLSKSCAAGFTFSNYGMSWVRQTS 60  
DB 1 MEFGLSWVFLVAILRGVQCEVQLVESGGGLVQPGSLRLSKCAAGFTFSHMTWVRQTP 60  
QY 61 DKRLWVASISSGGSTFPADNVKGRFTSRNNAKNTLYLQMSLKSEPTALYYCAR-D 119  
DB 61 GRRLWVANVKKODGSARYYADSVGRFTSRDNKNSLYLQMSLRADTAVYYCARSTG 120  
QY 120 LFNMGQGTTLTVSS 133  
: ||||| : |||||

DB 121 IDYMGQGTTLTVSS 134

Search completed: May 25, 2005, 16:48:38  
Job time : 19.8056 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: May 25, 2005, 15:36:17 ; Search time 64.8298 Seconds  
(without alignments)  
1050.544 Million cell updates/sec

Title: US-10-006-773a-9

Perfect score: 684

Sequence: 1 MNFGLSLIFLVVLKVGQCE.....YCARDLLEFVWGGQTLTVSS 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	567	82.9	487	2	Q09KA4
2	533.5	78.0	479	2	Q01WP5
3	527.5	77.1	486	2	Q01Z07
4	523	76.5	196	2	Q05ZL8
5	517	75.6	117	1	HV5A_MOUSE
6	515	75.3	117	1	HV55_MOUSE
7	510	74.6	117	1	HV59_MOUSE
8	510	74.6	473	2	Q01Z05
9	502.5	73.5	480	2	Q01X01
10	494.5	72.3	485	2	Q06PDB8
11	493	72.1	117	1	HV53_MOUSE
12	492	71.9	613	2	Q08WU1
13	491	71.8	117	1	HV58_MOUSE
14	488	71.3	606	2	Q06MW2
15	487.5	71.3	597	2	Q06SB9
16	485.5	71.0	464	2	Q06WU6
17	483.5	70.7	470	2	Q06PU4
18	483.5	70.7	499	2	Q08NSK4
19	482	70.5	136	1	HV16_MOUSE
20	480.5	70.2	478	2	Q061B1
21	480.5	70.2	493	2	Q06MK2
22	474.5	69.4	119	2	Q020E7
23	470.5	68.8	255	2	Q06KB05
24	470	68.7	573	2	Q08WU38
25	467.5	68.3	472	2	Q06N089
26	467	68.3	494	2	Q06K68
27	465	68.0	117	1	HV3C_HUMAN
28	464	67.8	475	2	Q06WZ06
29	454	66.4	465	2	Q06PC4
30	452	66.1	487	2	Q06ZVX0
31	450	65.8	544	2	Q06PJ95

32	449.5	65.7	493	2	Q08NCL6	Q08NCL6 homo sapien
33	449	65.6	479	2	Q06MZV6	Q06MZV6 homo sapien
34	448.5	65.6	466	2	Q061N78	Q061N78 homo sapien
35	447	65.4	475	2	Q06CMW7	Q06CMW7 homo sapien
36	446.5	65.3	466	2	Q06N096	Q06N096 homo sapien
37	445	65.1	473	2	Q06MZV7	Q06MZV7 homo sapien
38	439.5	64.3	470	2	Q07ZSW1	Q07ZSW1 homo sapien
39	438.5	64.1	116	1	HV05_CARAU	P19181 carassius a
40	438.5	64.1	480	2	Q06N054	Q06N094 homo sapien
41	438	64.0	483	2	Q06MZX9	Q06MZX9 homo sapien
42	431.5	63.1	519	2	Q06N092	Q06N092 homo sapien
43	429.5	62.8	97	1	HV56_MOUSE	Q06N092 mus sapien
44	427.5	62.5	487	2	Q080Z17	P18527 mus musculus
45	426.5	62.4	493	2	Q068CN4	Q068CN4 homo sapien

## ALIGNMENTS

RESULT 1  
Q09KA4 PRELIMINARY; PRT; 487 AA.  
AC Q09KA4;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)  
DE Igh-VJ558 protein.  
GN Name=Igh-VJ558;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II; TISSUE=Mammary tumor;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stalcup M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Urdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shoychenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,  
RT Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II; TISSUE=Mammary tumor;  
RA Director MGC Project;  
RU Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
EMBL BC004786; AAH04786.1; --  
DR HSP; P01810; 2FBJ.  
DR MGD; MGI:96486; Igh-VJ558.  
DR InterPro; IPR007110; Iq-1ike.  
DR InterPro; IPR003597; Iq-1c.  
DR InterPro; IPR003006; Iq-1MHC.  
DR InterPro; IPR003596; Iq-1V.  
DR Pfam; PF07654; C1-set; 2.  
DR SMART; SM00406; IGV; 1.  
DR PROSITE; PS50835; Iq-1like; 4.  
DR PROSITE; PS00290; Iq-1MHC; UNKNOWN 2.  
SQ SEQUENCE 487 AA; 52554 MW; 7DC8B96DB333077B CRC64;

Query Match Similarity 82.9%; Score 567; DB 2; Length 487;  
Best Local Similarity 78.3%; Pred. No. 4,7e-47;  
Matches 112; Conservative 10; Mismatches 11; Indels 10; Gaps 2;

Qy 1 MNFGSLIFLVVLKGVOCCEVKVBSGGGLVYKPGASLKLSCAASGFTFSNMGMSVWRQTS 60  
Db 1 MNFGSLIFLVVLKGVOCCEVQLVBSGGGLVYKPGASLKLSCAASGFTFSYAMSVMWRQTP 60

Qy 61 DKRLKLEWVASISSGGSTFYADNVKCRFTTISRENACTLYLQMSLSKSDTLYLYAAR-- 118  
Db 61 EKRLKLEWVATISDGGSTFYTPDVVKCRFTTISRDNARNLNYLQMSLSKSDTLYLYAARDMG 120

Qy 119 -----DLFN-WGGGTLTVSS 133  
Db 121 GSPYGYGRFDPVWGGGTLTVSS 143

RESULT 2  
Q91WPS PRELIMINARY; PRT; 479 AA.

ID Q91WPS  
AC Q91WPS  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Igh-VJ558 protein.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Alechski S.F., Zeeberg B., Buetow K.H., Scheiner C.F., Bhat N.K.,  
RA Hopfman R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Murusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Vallon J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Buterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalusi D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/genbank/DBJ databases.  
DR EMBL, BC013656; AAH13656.1; --  
DR HSSP, F01789; IMCP.  
DR Pfam, PF07654; Cl-set; 2.  
DR SMART, SMO0406; IGV; 1.  
DR PROSITE, PS00835; IG LIKE; 4.  
DR PROSITE, PS00290; IG MHC; UNKNOWN 2.  
SQ SEQUENCE 479 AA; 51603 MW; ECG2D0877748584F CRC64;

Query Match 78.0%; Score 533.5; DB 2; Length 479;  
Best Local Similarity 75.4%; Pred. No. 8,9e-44;  
Matches 101; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

Qy 1 MNFGSLIFLVVLKGVOCCEVKVBSGGGLVYKPGASLKLSCAASGFTFSNMGMSVWRQTS 60  
Db 1 MNFGSLIFLVVLKGVOCCEVQLVBSGGGLVYKPGASLKLSCAASGFTFSYAMSVMWRQTP 60

Db	1	MMFGLITLFLVTLTKGVQCEVQVLVBSSGGGLVKPGSLKLVSCAASGLTFSNVAMS	VRQSP	60
Qy	61	DKRLIEWASISGGSDSTFYADNNVKGRRFTISRENAKNTLYLQWSSLSKSDTLYAYCARBDL		120
Db	61	EKRLEIEMVAAINSGNTIYSDTMMKGRFPTISRDNAKSTLYLQWSSLSKSDTLYAYCVRGXY		120
Qy	121	FN-WGQGGFTLVSS	133	
Db	121	FDWMAGTAIVTSS	134	
RESULT 3				
ID	Q91207	PRELIMINARY;	PRT;	486 AA.
AC	Q91207			
DT	01-DEC-2001	(TREMBLrel. 19, Created)		
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	Igh-VJ558	protein.		
CN	Name=Igh-VJ558;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CZECH II; TISSUE=Mammary tumor;			
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Sores M.B., Bonaldo M.F., Caavaant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ueidi T.B., Toshlyuk S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Foley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buttefield Y.S.,			
RA	Krzywnski J., Skalski U., Smallie D.E., Scherch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CZECH II; TISSUE=Mammary tumor;			
RA	Director MGC Project;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC010324; AAH10324.1; -			
DR	HSSP; P01789; IMCP.			
DR	Pfam; PF07654; Cl-sect; 2.			
DR	SMART; SMO0406; IGV; 1.			
DR	PROSITE; PS00835; IG_LIKE; 4.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN.2.			
DR	SEQUENCE 486 AA; 52681 MW; 4EEF83515DA870B CRC64;			
SO	Query Match	77.1%; Score 527.5; DB 2; Length 486;		
	Best Local Similarity	71.3%; Pred. No. 3.5e-43;		
	Matches 102; Conservative 17; Mismatches 13; Indels 11; Gaps 2			
Qy	1	MMFGLITLFLVTLTKGVQCEVQVLVBSSGGGLVKPGASLKSAAAGFTTSNTGMSVNRQTS		60
Db	1	MMFGLITLFLVTLTKGVQCEVQVLVBSSGGGLVKPGASLKSAAAGFTTSNTGMSVNRQTS		60
Qy	61	DKRLIEWASISGGSDSTFYADNNVKGRRFTISRENAKNTLYLQWSSLSKSDTLYAYCARBDL		120
Db	61	EKRLEIEMVAAINSGNTIYSDTMMKGRFPTISRDNAKSTLYLQWSSLSKSDTLYAYCVRGXY		120
Qy	121	FN-WGQGGFTLVSS		133
Db	121	FDWMAGTAIVTSS		134

Qy 121 -----FNMGGTTLTVSS 133  
 Db 120 PIIYYSGSYFDSMGCTITVSS 142

## RESULT 4

065ZL8 PRELIMINARY; PRT; 196 AA.  
 AC 065ZL8; 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE VH7183-DSP2-JH3-CH1 protein (Fragment).  
 GN Name=VH7183-DSP2-JH3-CH1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=95362300; PubMed=7635518;  
 RA Komori T., Sugiyama H.;  
 RT "An aberrant splicing using a 3' cryptic splice site within the CH1  
 exon induces truncated mu-chain production.";  
 RL Immunology 85:166-170(1995).  
 DR EMBL, S79401, AAB35023.2; -.  
 DR InterPro; IPR003599; I9.  
 DR InterPro; IPR007110; I9-1like.  
 DR InterPro; IPR003596; I9\_v.  
 DR Pfam; PF00047; I9; 1.  
 DR SMART; SM00409; I9; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; I9\_LIKE; 1.  
 FT NON\_TER 196  
 SQ SEQUENCE 196 AA; 21429 MW; 12A381018944B268 CRC64;

Query Match 76.5%; Score 523; DB 2; Length 196;  
 Best Local Similarity 86.2%; Pred. No. 3.6e-43;

Matches 100; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MNFGSLIFLVVLKGVCEVKEVSGGLVPGASLKISCAASGFTFSNYGMSWVRQTS 60  
 Db 1 MNFGSLIFLVVLKGVCEVKEVSGGLVPGASLKISCAASGFTFSNYGMSWVRQTP 60  
 61 DKRLFWASISGSDSTFYADVNGKRFITSRNAXNTLYLQMSLSKSEDTALYYCA 116  
 61 EKRLFWATISGSGSYTYPPDVKGRFTISRDNAXNTLYLQMSLSKSEDTALYYCA 116

## RESULT 5

HV54\_MOUSE STANDARD; PRT; 117 AA.  
 ID HV54\_MOUSE  
 AC P18525;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 5-84 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the  
 primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -1- MISCELLANEOUS; This sequence belongs to the VH7183 subfamily.  
 DR PIR; J0505; HVMS4.  
 DR HSSP; P01810; 2FBU.

DR InterPro; IPR007110; I9-1like.  
 DR InterPro; IPR003596; I9\_v.  
 DR Pfam; PF00047; I9; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; I9\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.

FT CHAIN 1 19 Ig heavy chain V region 5-84.  
 FT SIGNAL 20 117  
 FT DOMAIN 20 49 Framework-1.  
 FT DOMAIN 50 54 Complementarity-determining-1.  
 FT DOMAIN 55 68 Framework-2.  
 FT DOMAIN 69 85 Complementarity-determining-2.  
 FT DOMAIN 86 117 Framework-3.  
 FT DISULFID 41 115 By similarity.  
 FT NON\_TER 117  
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 75.6%; Score 517; DB 1; Length 117;  
 Best Local Similarity 85.5%; Pred. No. 7.9e-43;

Matches 100; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MNFGSLIFLVVLKGVCEVKEVSGGLVPGASLKISCAASGFTFSNYGMSWVRQTS 60  
 Db 1 MNFGSLIFLVVLKGVCEVKEVSGGLVPGASLKISCAASGFTFSNYGMSWVRQTP 60  
 61 DKRLFWASISGSDSTFYADVNGKRFITSRNAXNTLYLQMSLSKSEDTALYYCAR 117  
 61 EKRLFWATISGSGSYTYPPDVKGRFTISRDNAXNTLYLQMSLSKSEDTALYYCAR 117

## RESULT 6

HV55\_MOUSE STANDARD; PRT; 117 AA.  
 ID HV55\_MOUSE  
 AC P18526;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region 345 precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;  
 RT "Early onset of somatic mutation in immunoglobulin VH genes during the  
 primary immune response.";  
 RL J. Exp. Med. 169:2007-2019(1989).  
 CC -1- MISCELLANEOUS; This sequence belongs to the VH7183 subfamily.  
 DR PIR; J0502; HVMS34.  
 DR HSSP; P01783; IIGC.  
 DR InterPro; IPR007110; I9-like.  
 DR InterPro; IPR003596; I9\_v.  
 DR Pfam; PF00047; I9; 1.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PSS0835; I9\_LIKE; 1.  
 KW Immunoglobulin V region; Signal.

FT CHAIN 1 19 Ig heavy chain V region 345.  
 FT SIGNAL 20 117  
 FT DOMAIN 20 49 Framework-1.  
 FT DOMAIN 50 54 Complementarity-determining-1.  
 FT DOMAIN 55 68 Framework-2.  
 FT DOMAIN 69 85 Complementarity-determining-2.  
 FT DOMAIN 86 117 Framework-3.  
 FT DISULFID 41 115 By similarity.  
 FT NON\_TER 117  
 SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 75.3%; Score 515; DB 1; Length 117;  
 Best Local Similarity 84.6%; Pred. No. 1.2e-42;

Matches 99; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MNFGLSLIFLVLTGKVGQCEVKVSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQTS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MNFGLRLIFVLTKGKCEVQVSGGGLVKGASIKLSCAASGFAFSSYDMSWVRQTP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DKLEWVASISGGSDSTFYADNVKGRFTISRBNKNTLYLQMSLSKSEDTALYYCAR 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EKLEWVASISGGSTYPPDYKGRFTISRBNKNTLYLQMSLSKSEDTAMYYCAR 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 7
HVS9_MOUSE STANDARD; PRT; 117 AA.
ID HVS9_MOUSE
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=9279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the
RT primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCBLANE05: This sequence belongs to the VH7.83 subfamily.
DR HSSP; P18529; 118K.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV_1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1
FT SIGNAL 19
FT DOMAIN 20 117 Ig heavy chain V region 7-39.
FT DOMAIN 20 49 Framework-1.
FT DOMAIN 50 54 Complementarity-determining-1.
FT DOMAIN 55 68 Framework-2.
FT DOMAIN 69 85 Complementarity-determining-2.
FT DOMAIN 86 117 Framework-3.
FT DISULPID 41 115 By similarity.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;
Query Match 74.6%; Score 510; DB 1; Length 117;
Best Local Similarity 84.6%; Pred. No. 3.9e-42;
Matches 99; Conservative 6; Mismatches 12; Indels 0; Gaps 0;
QY 1 MNFGLSLIFLVLTGKVGQCEVKVSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQTS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MNFGLSLIFVLTKGKCEVQVSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQTP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DKLEWVASISGGSDSTFYADNVKGRFTISRBNKNTLYLQMSLSKSEDTALYYCAR 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EKLEWVASISGGSTYPPDYKGRFTISRBNKNTLYLQMSLSKSEDTALYYCAR 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 8
Q91Z05 PRELIMINARY; PRT; 473 AA.
ID Q91Z05
AC Q91Z05;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE Expressed sequence AU044919.
GN Name=AU044919;
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner J., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueffing T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallegange D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary tumor;
RA Strausberg R.;
RX Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
DR PIR; S68213; S68213.
DR HSSP; P01783; 118K.
DR MGD; MGI:2144967; AU044919.
DR Pfam; PF07654; C1-sec; 3.
DR SMART; SM00406; CYTOCHROME_C; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PSS0290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932A12 CRC64;
Query Match 74.6%; Score 510; DB 2; Length 473;
Best Local Similarity 71.5%; Pred. No. 1.8e-41;
Matches 98; Conservative 19; Mismatches 16; Indels 4; Gaps 1;
QY 1 MNFGLSLIFLVLTGKVGQCEVKVSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQTS 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MDSRLNIVFLVLTKGQCEVQVSGGGLVKGASIKLSCAASGFTFSNYGMSWVRQAP 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DKLEWVASISGGSDSTFYADNVKGRFTISRBNKNTLYLQMSLSKSEDTALYYCAR-- 118
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EKLEWVASISGGSTYPPDYKGRFTISRBNKNTLYLQMSLSKSEDTALYYCAR 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 --DLFWNGQGTTLTVSS 133
   :|||||:|||||:
DB 121 LRRIDYWGQGTTLTVSS 137
   :|||||:|||||:
RESULT 9
Q91XE1 PRELIMINARY; PRT; 480 AA.
ID Q91XE1
AC Q91XE1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
DE Igh-V558 protein (Fragment).
GN Name=Igh-V558;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

```

[1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=FVB/N; TISSUE=Colon;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.D., Collins F.S., Wagner L.H., Derge J.G., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=FVB/N; TISSUE=Colon;  
 RC Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RA EMBL; BC010798; AAH10798.1; -.  
 DR HSSP; P01789; IMCP.  
 DR Pfam; PF07654; CI-sect; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 DR NON\_TER  
 FT 1  
 SQ SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Query Match 73.5%; Score 502.5; DB 2; Length 480;  
 Best Local Similarity 72.6%; Pred. No. 9.8e-41;  
 Matches 98; Conservative 17; Mismatches 17; Indels 3; Gaps 1;  
 Oy 2 NFGSLIFLVLYLVKGVCEVYVSSGGGLVPGASLKLSCAASGFTFSNYGSMVWRQSD 61  
 Db 1 NFGSLIFLVLYLVKGVCEVYVSSGGGLVPGASLKLSCAASGFTFSNYGSMVWRQSD 60  
 Oy 62 KRLKLVASISGGSDTFYADVNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCARDLL 121  
 Db 61 KRLKLVASISGGSDTFYADVNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCARDLL 120  
 Oy 122 N---WGQGTTLTVSS 133  
 Db 121 YFDVWAGAGTTTVSS 135

## RESULT 10

O6PDB8 PRELIMINARY; PRT; 485 AA.  
 AC O6PDB8;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 OS Hypothetical protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.D., Collins F.S., Wagner L.H., Derge J.G., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=FVB/N; TISSUE=Colon;  
 RC Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 RA EMBL; BC058814; AAH58814.1; -.  
 DR HSSP; P01661; IADQ.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_LIKE.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003606; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; CI-sect; 2.  
 DR SMART; SM00409; IG; 3.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 DR Hypothetical protein.  
 FT 1  
 SQ SEQUENCE 485 AA; 52472 MW; 81236FF3AD821056 CRC64;

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=FVB/N; TISSUE=Colon;  
 RC Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
 RA EMBL; BC058814; AAH58814.1; -.  
 DR HSSP; P01661; IADQ.  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG\_LIKE.  
 DR InterPro; IPR003597; IG\_C1.  
 DR InterPro; IPR003606; IG\_MHC.  
 DR InterPro; IPR003596; IG\_V.  
 DR Pfam; PF07654; CI-sect; 2.  
 DR SMART; SM00409; IG; 3.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 4.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_2.  
 DR Hypothetical protein.  
 FT 1  
 SQ SEQUENCE 485 AA; 52472 MW; 81236FF3AD821056 CRC64;

Query Match 72.3%; Score 494.5; DB 2; Length 485;  
 Best Local Similarity 69.3%; Pred. No. 6e-40;  
 Matches 97; Conservative 16; Mismatches 20; Indels 7; Gaps 1;  
 Oy 1 MNFGLSLIFLVLYLVKGVCEVYVSSGGGLVPGASLKLSCAASGFTFSNYGSMVWRQSD 60  
 Db 1 MDSRFLVFLVLYLVKGVCEVYVSSGGGLVPGASLKLSCAASGFTFSNYGSMVWRQSD 60  
 Oy 61 DRLKLVASISGGSDTFYADVNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCARDLL 120  
 Db 61 EKGLKLVASISGGSDTFYADVNVKGRFTISRANAKNTLYLQMSLSKSEDTALYYCARDLL 120  
 Oy 121 FN-----WGQGTTLTVSS 133  
 Db 121 SNYGAMDYWGQGTSTVTVSS 140

## RESULT 11

HV53 MOUSE STANDARD; PRT; 117 AA.  
 AC P18524;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V region RF precursor.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALE/cj;  
 RC MEDLINE=89279149; PubMed=2499654;  
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;

[illegible]





DR SMART; SM00406; IG; 1.  
DR PROSITE; PSS0835; IG LIKE; 5.  
DR PROSITE; PSS0290; IG MHC; UNKNOWN 3.  
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 71.3%; Score 487.5; DB 2; Length 597;  
Best Local Similarity 63.7%; Pred. No. 3,7e-39;  
Matches 93; Conservative 24; Mismatches 14; Indels 15; Gaps 2;

QY	1	MNFGSLIFLVLYKGVQCEVKYVESGGGLVYPGASLKLSCAAGFTFSNYGMSWVRQTS	60
Db	1	MEFGSLWFLVAILKGVQCEVLQESGGGLVYPGSLDLSCAAGFTFSNYAMWVRQAP	60
QY	61	DKRLWVASISGGDSTFYADNVKGRFTISRANKNTLYLQMSLKSDEPTALYYCARD--	118
Db	61	GKGLWVSAISGGSGSTFYADSVKGRFTISRDNSTRDTLYLQMSLRAEDTAVYYCAKDPR	120
QY	119	-----DLFNMGGGTTLYSS	133
Db	121	GYSASGNYTREDD--WCGGTLYTVSS	144

Search completed: May 25, 2005, 15:56:04  
Job time : 65.8298 secs